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OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 20:53:37 ; Search time 518 Seconds  
(without alignments)  
10434.389 Million cell updates/sec

Title: US-09-674-195C-1

Perfect score: 3862

Sequence: 1 ggaactgctggtccgata.....aacacctcaaaaggatcc 3862

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications\_NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	164	4.2	2037	10	US-09-974-300-2022
2	157.8	4.1	2262	10	US-09-815-242-6084
3	154.4	4.0	2253	10	US-09-815-242-9887
4	151.2	3.9	2130	10	US-09-815-242-4046
5	142.6	3.7	2537	9	US-10-099-352-1
6	141.2	3.7	4529	9	US-10-099-352-3
7	90.2	2.3	1596	9	US-09-938-842A-604
8	88.8	2.3	1506	9	US-09-738-626-285
9	88.8	2.3	3309400	9	US-09-738-626-1
10	87	2.3	1738	9	US-10-101-736-2
11	87	2.3	1738	9	US-09-834-659-2
12	87	2.3	1738	10	US-09-834-656-2
13	83.4	2.2	1780	9	US-09-895-913A-75
14	80.4	2.1	1458	10	US-09-974-300-2082
15	75	1.9	462	10	US-09-974-300-6436
16	71.6	1.9	696	10	US-09-974-300-6399
17	71.6	1.9	1623	9	US-09-974-300-6367
18	66	1.7	8062	9	US-10-108-605-294
19	64.4	1.7	714	9	US-09-727-855B-8

c	20	64	1.7	5277	10	US-09-070-927A-262	Sequence 262, App
	21	63.8	1.7	942	10	US-09-974-300-2033	Sequence 2033, App
	22	62.6	1.6	1830121	9	US-10-329-960-1	Sequence 1, Appli
	23	57.8	1.5	734	10	US-09-770-149-85	Sequence 85, Appli
	24	55.8	1.4	2014	9	US-10-099-352-4	Sequence 4, Appli
	25	54.6	1.4	590	9	US-10-255-536-249	Sequence 249, App
	26	52.4	1.4	417	10	US-09-960-352-8446	Sequence 8446, Ap
	27	52.4	1.4	488	9	US-09-918-995-34786	Sequence 34786, A
	28	52	1.3	951	9	US-09-727-855B-3	Sequence 3, Appli
	29	51.8	1.3	424	10	US-09-960-352-10087	Sequence 10087, A
c	30	51.8	1.3	604	9	US-09-796-692-8142	Sequence 8142, Ap
	31	51.8	1.3	604	9	US-10-040-862-8142	Sequence 8142, Ap
c	32	51	1.3	1049	10	US-09-770-445-164	Sequence 164, App
	33	50.2	1.3	413	10	US-09-960-352-9570	Sequence 9570, Ap
	34	50.2	1.3	416	10	US-09-960-352-13154	Sequence 13154, A
	35	49	1.3	3883	9	US-10-099-352-6	Sequence 6, Appli
	36	48.6	1.3	395	10	US-09-960-352-3954	Sequence 3954, Ap
	37	48.6	1.3	411	10	US-09-960-352-9819	Sequence 9819, Ap
	38	48.6	1.3	424	10	US-09-960-352-6122	Sequence 6122, Ap
	39	48.6	1.3	432	10	US-09-960-352-13881	Sequence 13881, A
	40	48.6	1.3	442	10	US-09-960-352-5449	Sequence 5449, Ap
	41	48.6	1.3	732	10	US-09-974-300-6435	Sequence 6435, Ap
	42	48.2	1.2	370	10	US-09-878-574-2807	Sequence 2807, Ap
c	43	47	1.2	520	9	US-10-184-644-332	Sequence 332, App
	44	47	1.2	520	9	US-10-184-644-332	Sequence 332, App
c	45	46.6	1.2	1200	10	US-09-815-242-4132	Sequence 4132, Ap

#### ALIGNMENTS

##### RESULT 1

US-09-974-300-2022  
; Sequence 2022, Application US/09974300  
; Patent No. US20020146721A1  
; GENERAL INFORMATION:  
; APPLICANT: Berka, Randy M.  
; APPLICANT: Clausen, Ib Groth  
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene  
; FILE OF INVENTION: Expression  
; FILE REFERENCE: 10085.500-US  
; CURRENT APPLICATION NUMBER: US/09/974, 300  
; CURRENT FILING DATE: 2001-10-05  
; PRIOR APPLICATION NUMBER: 09/680, 598  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/279, 526  
; PRIOR FILING DATE: 2001-03-27  
; NUMBER OF SEQ ID NOS: 8481  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2022  
; LENGTH: 2037  
; TYPE: DNA  
; ORGANISM: Bacillus licheniformis  
US-09-974-300-2022

Query Match 4.2%; Score 164; DB 10; Length 2037;  
Best Local Similarity 61.4%; Pred. No. 8.5e-36;  
Matches 263; Conservative 0; Mismatches 165; Indels 0; Gaps 0;

QY	1158	GGCAATGATATATATCGTCGGAAACAAACGTTCCAGTCTTCTTCATTTCAGGACGCTATTCAA	1217
Db	396	GGGAACATATGATCTTGTGCGCAACACATCCCGTTTCTTCATTTCAGGATGCCATCAAG	455
QY	1218	TTCCCTGATTTGATTCAGCTGTCAAGCGCGCAACAGACAGTGAATTCCTCCAGGCTGCA	1277
Db	456	TTCCCTGATTCGTCGACGCTTTAAACCGGAACGAATCCGCGATCTCT	515
QY	1278	ACTGCACATGATACGGCATGGGATTTCTTCAGCCAGCAGCCAGCTCATTTGCATGCCCTC	1337
Db	516	ACGGCGCAGCATACGCTTTTGGGACTTTGTCCCAACATGAAGAACGCCCCACATGATC	575
QY	1338	TTCTGGGCAATGTCAGGACATGGAATCCCTGCTCAATGCGTCATGTTGATGGGTGGGC	1397

Db 576 ATGTGACCAATCTGTACACAGGGCGATTCCCGAAGCTACAGGATGATGGAGGCTTCGGC 635  
QY 1398 GTCCATACCTTCGACTTGTACCGAGAGGGCAACTCGACCTTGTGTCAAAGTTTCGCTGG 1457  
Db 636 GTTCATACGTTTCAGGTTTGTAAAGAAAGGCAAGCGCACCTTTGTAAATTTCACTGG 695  
QY 1458 AAGACCTCTCAAGAGAGAGCGGCGCTGGTATGGAGAGGACACAGGCTCTTTGGCGGAAAG 1517  
Db 696 AAGCCGCTCTCGCGCTCCATTGCTGCTGGGAGGAAAGCGAGACAAATCGCGGAAAA 755  
QY 1518 AATCCCGGATTCATCGACAAAGACCTCTGGGATGCCATTGAATCTGGGAAGGTACCCCTGAG 1577  
Db 756 GATCCCGGATTCATCGACCGCGCGATCTGTGGGAGCGATCTGGAAGCGATGAAGTGAG 815  
QY 1578 TGGGAGGT 1585  
Db 816 TATGAGCT 823

## RESULT 2

US-09-815-242-6084  
; Sequence 6084, Application US/09815242  
; Patent No. US20020061569A1

## GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Karl L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard

## TITLE OF INVENTION: Identification of Essential Genes in

; FILE REFERENCE: ELITRA.011A

; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 14110

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6084

; LENGTH: 2262

; TYPE: DNA

; ORGANISM: Escherichia coli

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(2262)

US-09-815-242-6084

Query Match 4.1%; Score 157.8; DB 10; Length 2262;

Best Local Similarity 60.7%; Pred. No. 5.5e-34;

Matches 258; Conservative 0; Mismatches 167; Indels 0; Gaps 0;

QY 1158 GGCAATCTAGATATCGTGGAAACAGGTTCCAGTCTTCTTCATTCAGGACGCTATCAA 1217

Db 580 GGATTTTTCAGTCTGGTGGCAATACACCCCAATCTCTTTATCCAGGATCGCATAAA 639

QY 1218 TTCCTGATTGATTCACGCTGTCAAGCCGCAACACAGACAGTGAATTCGCCAGGTGCA 1277

Db 640 TTCCCGATTTTGTTCATGCGGTAAACACAGACCGGCAATTCACCAAGGCCAA 699

QY 1278 ACTGCACATGATAGCGCATGGGATTTCTTCAGCCAGCAGCCAGCTCAATTCGATGCCCTC 1337  
Db 700 AGTGCCACCATGACTTTCTGGGATTTATGTTCTGCAACCTGAAACTCTGCACAAAGTG 759  
QY 1338 TTCTGGGCATGTCAGGACATGGAATCCCTCGCTCAATGGCTCATGTTGATGGTGGGC 1397  
Db 760 ATGTGGCGGATGTCGATCGCGCATCCCCCGAGTTACCGCACCATGGAAGCTTTGGT 819  
QY 1398 GTCCATACCTTCGACTTGTACCGAGAGGGCAACTCGACCTTGGTCAAGTTTCGCTGG 1457  
Db 820 ATTACACCTTCGCTCTGATTATGCGGAAGGAGCAACGTTGTACGTTTCCACTGG 879  
QY 1458 AAGACCTCTCAAGAGAGAGCGGCTGGTATGGAAAGAGCAGCAGGCTCTTGGCGGAAAG 1517  
Db 880 AAACCACTGGCAGGTAAAGCCTCACTCGTTGGGATGAAGCACAAAACCTCACCGGACGT 939  
QY 1518 AATCCCGGATTCATCGACAAAGACCTCTGGGATGCCATTGAATCTGGAAGGTACCCCTGAG 1577  
Db 940 GACCCGAGTTCACCGCGCGAGTTGTGGGAAGCCATTGAAGCAGCGGATTTTCGGAA 999  
QY 1578 TGGGA 1582  
Db 1000 TAGCA 1004

## RESULT 3

US-09-815-242-9887

; Sequence 9887, Application US/09815242

; Patent No. US20020061569A1

## GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Karl L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard

## TITLE OF INVENTION: Identification of Essential Genes in

; FILE REFERENCE: ELITRA.011A

; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 14110

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 9887

; LENGTH: 2253

; TYPE: DNA

; ORGANISM: Salmonella typhi

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(2253)

US-09-815-242-9887

Query Match 4.0%; Score 154.4; DB 10; Length 2253;

Best Local Similarity 60.0%; Pred. No. 5.2e-33;

Matches 257; Conservative 0; Mismatches 171; Indels 0; Gaps 0;



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Db      599  TTTCCAGATTTTGTTCATGCTGTGAAGCCGGAACCTCATAACGAAAGTCCCCAGGACAA 658
QY      1278  ACTGCAGATGATACGGCATGGGATTTCCTCAGCCAGCAGCCAGCTCATTTGATGCCCTC 1337
Db      659  ACAGCACATAACAACACTTCCTGGGACTTGTATATATATATATATATATATATATATATAT 718
QY      1338  TTTCTGGGCAATGTCAGAGCATGGAATCCCTCGCTCAATCGCTCATTTGATGGGTGGGC 1397
Db      719  ATGTGGGCTATGTCCGACAGGGCTATTCGGGATCATATATCGGATGATGATGATGATGATG 778
QY      1398  GTCATATACCTTCGGACTTCACCGAGAGGCAACTCGACCTTGGTCAAGTTTCGCTGG 1457
Db      779  GTTAATACATTTGTTTGTGTGTAATAACAAGGAAAGACATTTTCGTTAAGTTTCACTGG 838
QY      1458  AAGACCTTCCAAGGAGAGCGGCTGTGTATGGGAAGAGGACAGGCTCTTGGCGGAAG 1517
Db      839  ATGCGGAACTTGGGGTTTCATTCGCTGGTCCCGGATGATCAATCAAACTTGGTGGCCAG 898
QY      1518  AATCCCGACTTCCATCGACAGCAACCTCTGGGATGCCATTGGAATCTGGAAGTACCTGAG 1577
Db      899  GACCCAGACTTCCACCGTAAGATCTAATGGAGGCAATCGACAATAAGGTGTACCCGAA 958
QY      1578  TCGGAGGTAAAGATGA 1594
Db      959  TGGAAAGTTTGGAAATCA 975

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## RESULT 6

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US-10-099-352-3
; Sequence 3, Application US/10099352
; Publication No. US20030082569A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Clayton H.
; APPLICANT: York, J. Lyndal
; APPLICANT: McEwen, Joan E.
; TITLE OF INVENTION: Histoplasma Capsulation Catalase Sequences and Their Use in the D
; FILE OF INVENTION: of Histoplasma Capsulation and Histoplasmosis
; CURRENT APPLICATION NUMBER: US/10/099,352
; PRIOR FILING DATE: 2002-03-13
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 4529
; TYPE: DNA
; ORGANISM: Histoplasma capsulatum CATA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (80)..(80)
; OTHER INFORMATION: "n" - any nucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (127)..(127)
; OTHER INFORMATION: "n" - any nucleotide
US-10-099-352-3

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Query Match      3.78; Score 141.2; DB 9; Length 4529;
Best Local Similarity 50.8%; Pred. No. 5.5e-29;
Matches 377; Conservative 0; Mismatches 348; Indels 17; Gaps 1;

QY      853  TTCTGAGCGCGGCTCATGCTCGAGGAGCTGGTGCCCATGCGGTATTCACATCTCATATA 912
Db      1433  TCCAGAACGTGTGTCCATGCGACGAGGACAGCTGTTTGGGCACTTCAAGCTCTCG 1492
QY      913  ATAACGTGCTGATATACAGCGCATCTTCTTTGAACCGCGGAGGAAAGCAGACACAG 972
Db      1493  AGAGCGCGGACAGCTGACGCTCGCTGGTCTTAACGTGACAGCTCCCGAAGTCTCCG 1552
QY      973  TATTCTGCGGTTTCTACAGTGGTGGAGCAGGCGAGTGTGACTGTGCTCGCGATA 1032

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Db      1553  TGTTCGTTGGTTCACCGTCCAGGGCAGCAAAAGGAGTTCGATACAGTCCGTGATG 1612
QY      1033  TCCACGGATTTGCGACCCGCTGTATACCGATGAAGCAATTTTGGTAAGCATATATCG 1092
Db      1613  TCAGAGGTTTCGCTACCAAAATTCATACGGRAAGGCAACTGGATCTTTGTTGCAATA 1672
QY      1093  TGGTAGTCTACTATACAGCACAACAAATATGAATACAAACCCAGGACCTAGGCTGAC 1152
Db      1673  ACATTTCCTGTATTTCTTCAATTCAGATGCTGTGAATTCACAGATTTTGGTAAGTATGAT 1732
QY      1153  TACTCGCAATGTAGATATCGTGGAAACAACGTTCCAGTCTTCTTCAATTCAGGACGCTA 1212
Db      1733  TGATATCCCATTTCTTCAATTCAGATTTTTCGTTGATCGTTTTCACAACTCGAC---- 1788
QY      1213  TTCATTCCTCGATTTGATTCACGCTGTCAAGCGCAACCAAGAGAGTGAATTTCCCCAGG 1272
Db      1789  -----ATTAGTTTCATGCTGTGAAGCCGGAACCTCATAACGNAAGTTCCTCCAGG 1835
QY      1273  CTGCAACTGCACATGATACGCGATGGGATTTCTCAGCCAGCAGCCAGCTCATTTGGATG 1332
Db      1836  GACAAACAGCACATAACAACTTCTGGGACTTTGTATATATGCTATATATGCTATGCTGATG 1895
QY      1333  CCCTCTTCTGGGCAATGTGACAGACATGGAATCCCTCGCTCAATCGCTCATGTTGATGSGT 1392
Db      1896  TGTTCATGTGGCTATGTCGGACAGGCTATTCGCGCATCATATCGGATGATGCAAGAT 1955
QY      1393  GGGCGGTCCATACCTTCGGACTTGTCAAGGAGGAGGCAACTGACCTTGGTCAAGTTTC 1452
Db      1956  TTGTTGTTAATACCTTTGTTTGGTGAATAAACAAGGGAAGACATTTCTGTTAAGTTTC 2015
QY      1453  GCTGGAAGACCTCCAAAGGAAGACGGGCTGTGTTGGGAGAGGACACAGCTTGGCG 1512
Db      2016  ACTGATGCGGAACTTTGGGTTTCATTCGCTGTGTCCTCCCGATGATCATTTCAAACTTGGTG 2075
QY      1513  GAAGAATCCGAGCTTCCATCGACAGACCTCTGGGATGCTGATGCTGGAAGGTACC 1572
Db      2076  GCCAGACCCAGAGTTCCACCGTAAGATCTAATGGAGGCAATCGACAATAAGGTGTACC 2135
QY      1573  CTGAGTGGGAGTAAAGATGA 1594
Db      2136  CGAATGGAAGTTGGAAATCA 2157

```

## RESULT 7

```

US-09-938-842A-604
; Sequence 604, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Wang, Joel
; APPLICANT: Krepes, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR FILING DATE: 2000-08-24
; PRIOR FILING DATE: 2000-08-24
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 604
; LENGTH: 1596
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-604

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Query Match      2.3%; Score 90.2; DB 9; Length 1596;
Best Local Similarity 52.9%; Pred. No. 1.1e-14;
Matches 225; Conservative 0; Mismatches 186; Indels 12; Gaps 1;

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D <sub>B</sub>	364	G G C A A C T A G C A C A T C T G G G T A A C A A C A C C C C A A C C T T C T T C C T T C G T G A C G C A T G A A G	423
Q <sub>Y</sub>	1218	T T C C C T G A T T T G A T T C A C G C T G T C A A G C C G C A A C A G A C A G T G A A A T T C C C C A G G T G C A	1277
D <sub>B</sub>	424	T T C C C G G A C T T C A T C C A C T C A C A G A A G G T C T C A A C A A G A A C G G T T G C G C G A T G C A - - -	480
Q <sub>Y</sub>	1278	A C T G C A C A T G A T A C G G C A T G G G A T T T C C T C A G C C A G C A G C C C A G C A C T A T T G C A T G C C C T C	1337
D <sub>B</sub>	481	- - - - - G A C A T G A C T G G G A T T T C T G G A C C C G G C A C C T G A A C T G C A C C A C C A G G T G	531
Q <sub>Y</sub>	1338	T T C T G G C A A T G T C A G G A C A T G G A A T C C C T F C G T C A A T G C G T C A T G T T G A T T G G T G G G G C	1397
D <sub>B</sub>	532	A C C T A C C T G A T G G G T G A C C C G G T A C C C C T A A G A C C T C C C C C A C C A G G A C G G G T T C C G C	591
Q <sub>Y</sub>	1398	G T C C A T A C C T T C C G A C T T G T A C C G A G A G G G C A A C T C G A C C T T G G T C A G T T T C G T G G	1457
D <sub>B</sub>	592	T C C A C A C C T T C C A G T G E A T T A A C G C T G A A G C C A A G C C A G T T T G G G T T A A G T A C C A C T T C	651
Q <sub>Y</sub>	1458	A A G A C C C T C C A A G A A C G A A C G G G C T G T A T G G G A A G A G G C A C A G G C T T T G G C G G A A A G	1517
D <sub>B</sub>	652	A A G A C C G C C A C G G G C T G G G A T T G T C A C C G A T C A G A C G C A A A A G G T T G C A G C G A G	711
Q <sub>Y</sub>	1518	A A T C C C G A C T T C C A T C A C A C A C C T C T G G S A T G C C A T T G A A T C T G S A A G G T A C C C T G A G	1577
D <sub>B</sub>	712	A A C C C T G A C T A C C A G C G G A A G A C C T C T A C A A C G T A T T G A A A C G G C G A C T T C C C A A T C	771
Q <sub>Y</sub>	1578	T G G A G G T A A	1587
D <sub>B</sub>	772	T G G G A C G T A	781

RESULT 9  
US-09-738-626-1  
: Sequence 1, Application US/09738626  
: Publication No. US20020197605A1  
: GENERAL INFORMATION:  
: APPLICANT: NAKAGAWA, SATOSHI  
: APPLICANT: MIZOGUCHI, HIROSHI  
: APPLICANT: ANDO, SEIKO  
: APPLICANT: HAYASHI, MIKIRO  
: APPLICANT: OCHIAI, KEIKO  
: APPLICANT: YOKOI, HARUHIKO  
: APPLICANT: TATEISHI, NAKOHO  
: APPLICANT: SENOH, AKIHIRO  
: APPLICANT: IKEDA, MASATO  
: APPLICANT: OZAKI, AKIO  
: TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
: FILE REFERENCE: 249-125  
: CURRENT APPLICATION NUMBER: US/09/738,626  
: CURRENT FILING DATE: 2000-12-18  
: PRIOR APPLICATION NUMBER: JP 99/377484  
: PRIOR FILING DATE: 1999-12-16  
: PRIOR APPLICATION NUMBER: JP 00/159162  
: PRIOR FILING DATE: 2000-04-07  
: PRIOR APPLICATION NUMBER: JP 00/280988  
: PRIOR FILING DATE: 2000-08-03  
: NUMBER OF SEQ ID NOS: 7059  
: SOFTWARE: PatentIn ver. 3.0  
: SEQ ID NO 1  
: LENGTH: 3309400  
: TYPE: DNA  
: ORGANISM: Corynebacterium glutamicum  
US-09-738-626-1

	Query Match	2.3%	Score 88.8;	DB 9;	Length 3309400;
	Best Local Similarity 52.6%;		Pred. No. 1e-11;		
	Matches 226;	Conservative	Mismatches 192;	Indels 12;	Gaps 1
QY	1158	GGCAATGTAGATATCGTCGGAAACAAGTTTCCAGTCTCTTCTTATTTAGAGCGCTATTCAA	121		
DB	274729	GGCAATCTACGACATCTCTGGGTATCAACACCGCCAACTTCTTCCTTCGTGCGGCGCATGAG	274		
QY	1218	TTCCCTGATTGTGATTTCAGCTGTCAAGCCGCAACCGACAGTGAATTTCCCGAGGCTGCA	121		

[illegible]

RESULT 10  
 US-10-101-736-2  
 ; Sequence 2, Application US/10101736  
 ; Publication No. US20030041351A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yoshihisa KASUKABE, Izumi IHARA, Yoshihiko MAEKAWA (Toyobo  
 ; APPLICANT: Co., Ltd.); Randy Dale Allen (Texas tech University)  
 ; TITLE OF INVENTION: Cotton plants with improved cotton fiber characteristics and meth  
 ; FILE OF INVENTION: for producing cotton fibers from these cotton plants  
 ; FILE REFERENCE:  
 ; CURRENT APPLICATION NUMBER: US/10/101.736  
 ; CURRENT FILING DATE: 2002-05-21  
 ; NUMBER OF SEQ ID NOS: 3  
 ; SEQ ID NO 2  
 ; LENGTH: 1738  
 ; TYPE: DNA  
 ; ORGANISM: Pisum sativum  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (57)...(1541)  
 ; PUBLICATION INFORMATION:  
 ; AUTHORS: Sibel H. Isin and Randy D. Allen  
 ; TITLE: Isolation and characterization of a pea catalase cDNA  
 ; JOURNAL: Plant Molecular Biology  
 ; VOLUME: 17  
 ; PAGES: 1263-1265  
 ; DATE: 1991  
 US-10-101-736-2

[illegible]

QY	1338	TTCTGGGCAATGTCTAGGACATGGGAATCCCTCGCTCAATCGCTCATGTTGATGGGTGGGC	1397
Db	615	TCCTTCTCTATTGTATGATGTGGGTGTCCCAACAAGATTATAGGCATATGATGTTTGGGA	674
QY	1398	GTCCATACCTTCGGACTTGTACCGAGGAGGCGAAGCTCGACCTTGGTCAAGTTTCGCTGG	1457
Db	675	GTTTACACATACACCCCTGATCAACAAGGCTGGAAATCGGTGTATGTCAAAATTTCACTGG	734
QY	1458	AAGACCTTCCAAGGAGAGCGGGCCCTGGTATGGGAAGAGGACACAGGCTCTTGGCGGAAG	1517
Db	735	AAGCCCACTGTGGTGTGAAGTGTCTATTGGAGGAGGAGGCCATTCAGTGGGAGGATCC	794
QY	1518	AATCCCGACTTCCATCGACAGACCTCTGGGATGCCATTAATCTGGAAGTACCCCTGAG	1577
Db	795	ACCACAGCCATGCTACTAAAGACCTTTATGACTCAATTGCTGTGTAACATATCCTGAG	854
QY	1578	TGGGA	1582
Db	855	TGGAA	859

RESULT 11  
 US-09-834-659-2  
 ; Sequence 2, Application US/09834659  
 ; Publication NO. US20030074697A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yoshihisa KASUKABE, Izumi IHARA, Yoshihiko MAEKAWA (Toyobo  
 ; APPLICANT: Co., Ltd.); Randy Dale Allen (Texas tech University)  
 ; TITLE OF INVENTION: Cotton plants with improved cotton fiber characteristics and  
 ; TITLE OF INVENTION: For producing cotton fibers from these cotton plants  
 ; FILE REFERENCE: 204552015600  
 ; CURRENT APPLICATION NUMBER: US/09/834,659  
 ; CURRENT FILING DATE: 2001-04-16  
 ; PRIOR APPLICATION NUMBER: US/09/347,669  
 ; PRIOR FILING DATE: 1999-07-05  
 ; NUMBER OF SEQ ID NOS: 3  
 ; SEQ ID NO. 2  
 ; LENGTH: 1738  
 ; TYPE: DNA  
 ; ORGANISM: Pisum sativum  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (57)...(1541)  
 ; PUBLICATION INFORMATION:  
 ; AUTHORS: Sibel H. Isin and Randy D. Allen  
 ; TITLE: Isolation and characterization of a pea catalase cDNA  
 ; JOURNAL: Plant Molecular Biology  
 ; VOLUME: 17  
 ; PAGES: 1263-1265  
 ; DATE: 1991  
 ; US-09-834-659-2

Query Match	2.3%	Score 87	DB 9	Length 1738
Best Local Similarity	52.5%	Prod. No. 9.4e-14		
Matches 223	Conservative 0	Mismatches 190	Indels 12	Gaps 17
Qy	1158	GGCAATGTAGATATCGTCGGAAACAAGTTCACGCTCTTCTTCATTTCAGGACGCTATTCAA	1217	
Db	447	GGTAACATATGACCTGTGTGGNAACACTTCCCGCTCTTCTCGTTCATGACGGTATGAAT	506	
Qy	1218	TTCCCTCATTTGATTTCACGCTGTCAACGCCGCAACCAGACAGATGAAATTTCCCAAGCGTGCA	1277	
Db	507	TTTCCAGATATGTCCATGTCTTTAAACCCAATCCCAAGACCCACATCCAGGAGAAATTTGG	566	
Qy	1278	ACTGCACATGATACGGCATGGGATTTCTTCAGCCAGCAGCCAGCTCATTTGCATGCCCTC	1337	
Db	567	AGAATTCCTT-----GATTTCCTCAACTTCCAGNAACCTTCACATGCTC	614	
Qy	1338	TTCTGGSCAATGTCAGGACATGNAATCCCTCGCTCAATGCGTGAATGGTGGGGC	1397	
Db	615	TCCTTCCTATTTCATGATGTGGGTGTCCCAAGATTTAAGGCATATGGAATGTTTGGGA	674	
Qy	1398	GTCCATACCTTCGCACTGTTCACCGACGAGGGCAACTCGACCTTGTGTCAAGTTTCGCTGG	1457	

1518 AATCCCGACTTCATCGACAGACCTCTGGGATGCGCAATTCGAATCTGTGAAGGATACCTGAG 1577  
1578 TGGGA 1582  
855 TGGAA 859

RESULT 13  
US-09-895-913A-75  
; Sequence 75, Application US/09895913A  
; Patent No. US20020160456A1  
; GENERAL INFORMATION:  
; APPLICANT: Kleanthous, Harold  
; APPLICANT: Al-Garawi, Amal  
; APPLICANT: Miller, Charles  
; APPLICANT: Tomb, Jean Francois  
; TITLE OF INVENTION: Identification of Polynucleotides  
; TITLE OF INVENTION: Encoding No. US20020160456A1 Helicobacter Polypeptides in t  
; FILE REFERENCE: 06132/043002  
; CURRENT APPLICATION NUMBER: US/09/895,913A  
; CURRENT FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 08/881,227  
; PRIOR FILING DATE: 1997-06-24  
; NUMBER OF SEQ ID NOS: 368  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 75  
; LENGTH: 1780  
; TYPE: DNA  
; ORGANISM: Helicobacter pylori  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (195)...(1709)  
US-09-895-913A-75

Query Match 2.2%; Score 83.4; DB 9; Length 1780;  
Best Local Similarity 51.7%; Pred. No. 1e-12;  
Matches 223; Conservative 0; Mismatches 196; Indels 12; Gaps 1;

1158 GCGAATGTAGATATCGTCGGAACAAACGTTCCAGTCTTCTTCATTCAGGAGCGTATTCAA 1217  
558 GGTAACTGGGATTTAGTGGGGAACACACGCGCTGTTCTTATCCGTGATCGATCAA 617  
1218 TTCCCTGATTTGATTCACGCTGTCAAGCGGCAACACAGAGTGAATTCCTCCAGGCTCA 1277  
618 TTCCCTGATTTGATTCACACTCAAAACGAGATCCTCAAAACCAATTTGCTTAAC----- 671  
1278 ACTGCACATGATACGCGATGGGATTTCTCCAGCGAGCCAGCTCATTTGATGCCCTC 1337  
672 -----CATGACATGGTATGGGATTTTGGAGTATGTTCTTGAAGCTTATACCAAGTA 725  
1338 TTCTGGGCAATGTACGAGCATGGAATTCCTCGCTCAATCGCTCATGTTGATGGGTGGGC 1397  
726 ACATGGGTTATGAGCATAGGGGATTTCTAAATCTTTCCGACACATGATGTTGTTGCG 785  
1398 GTCCATACCTTCGAGCTTGTACCGGAGGAGGCACTCGACCTTGTCAAGTTGCTGCTGG 1457  
786 AGCCACACTTTCAGTCTTATCAACGCGAAAGCGGTAATTTGGGTGAATTTCCACTTT 845  
1458 AAGACCTCCCAAGGAAGAGCGGCTTGGTATGGGAAGAGGACAGGCTCTTGGCGGAAAG 1517  
846 CACACCATGCAAGCGGTTAAGCATTTGACTAAGCAAGAGCCGCAAGATTTAGGAAGTAT 905  
1518 AATCCCGACTTCATCGACAGACCTCTGGGATGCGCAATTCGAATCTGTGAAGGATACCTGAG 1577  
906 GATCCGGATTCGAATCAAGAGGATTTATTCATGCGATCGTAGAGGGATTTCCCAAAA 965  
1578 TGGAGGTAAG 1588  
966 TGGAAATTAAG 976

675 GTTAACACATACACCTGATCAACAGGCTGGAATAACGGGTGATGCAAAATTCACCTGG 734  
1458 AAGACCTCCCAAGGAAGAGCGGCTGTGATGGGAAGGACACAGGCTCTTGGCGGAAAG 1517  
735 AAGCCACCTGTGGGTGCTGAAGTCTATTGGGAAGAGGCCATTCAGGTGGGAGGATCC 794  
1518 AATCCCGACTTCATCGACAGACCTCTGGGATGCGCAATTCGAATCTGTGAAGGATACCTGAG 1577  
795 AACCACAGCATGCTACTAAAGACCTTTATGACTCAATTTGCTGCTGGTAACTATCCTGAG 854  
1578 TGGGA 1582  
855 TGGAA 859

RESULT 12  
US-09-834-656-2  
; Sequence 2, Application US/09834656  
; Patent No. US2002004999A1  
; GENERAL INFORMATION:  
; APPLICANT: Yoshihisa KASURABE, Izumi IHARA, Yoshihiko MAEKAWA (Toyobo Co., Ltd.);  
; APPLICANT: Randy Dale Allen (Texas Tech University)  
; TITLE OF INVENTION: Cotton plants with improved cotton fiber characteristics and meth  
; TITLE OF INVENTION: producing cotton fibers from these cotton plants  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/834,656  
; CURRENT FILING DATE: 2001-08-07  
; NUMBER OF SEQ ID NOS: 3  
; SEQ ID NO 2  
; LENGTH: 1738  
; TYPE: DNA  
; ORGANISM: Pisum sativum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (57)...(1541)  
; PUBLICATION INFORMATION:  
; AUTHORS: Sibel H. Isin and Randy D. Allen  
; TITLE: Isolation and characterization of a pea catalase cDNA  
; JOURNAL: Plant Molecular Biology  
; VOLUME: 17  
; PAGES: 1263-1265  
; DATE: 1991  
US-09-834-656-2

Query Match 2.3%; Score 87; DB 10; Length 1738;  
Best Local Similarity 52.5%; Pred. No. 9.4e-14;  
Matches 223; Conservative 0; Mismatches 190; Indels 12; Gaps 1;

1158 GCGAATGTAGATATCGTCGGAACAAACGTTCCAGTCTTCTTCATTCAGGAGCGTATTCAA 1217  
447 GGTAACTATGACCTTTGTTGGAACAACTTTCCGCTCTTCTTCGTTTCATGACGATGAAT 506  
1218 TTCCCTGATTTGATTCACGCTGTCAAGCGGCAACACAGAGTGAATTCCTCCAGGCTCA 1277  
507 TTTCAGATATGGTCCATGCTCTTAAACCCCAATCCCGAGACCCACATCCAGGAGAAATGG 566  
1278 ACTGCACATGATACGCGATGGGATTTCTCCAGCGAGCGCCAGCTCATTTGATGCCCTC 1337  
567 AGAATTCCTT-----GATTTCTTCAACATTTCCAGAAAGCCTTCACATGCTC 614  
1338 TTCTGGGCAATGTACGAGCATGGAATTCCTCGCTCAATCGCTCATGTTGATGGGTGGGC 1397  
615 TCCTTCTTATTTGATGATGTTGGTGTCCCAAGATTTATAGGCATATGGATGGTTTGGGA 674  
1398 GTCCATACCTTCGAGCTTGTACCGGAGGAGGCACTCGACCTTGTGTCAGTTCGCTGG 1457  
675 GTTAACACATACACCTGATCAACAGGCTGGAATTCGTTGTCATGTCATTCATTCAGTGG 734  
1458 AAGACCTCCCAAGGAAGAGCGGCTTGGTATGGGAAGAGGACAGGCTCTTGGCGGAAAG 1517  
735 AAGCCACCTGTGGTGTGAAGTGTCTATTGGGAAGAGGCAATTCAGGTGGGAGGATCC 794

## RESULT 14

US-09-974-300-2082  
; Sequence 2082, Application US/09974300  
; Patent No. US20020146721A1  
; GENERAL INFORMATION:  
; APPLICANT: Berka, Randy M.  
; APPLICANT: Clausen, Ib Groth  
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene  
; FILE REFERENCE: 10085.500-US  
; CURRENT APPLICATION NUMBER: US/09/974,300  
; CURRENT FILING DATE: 2001-10-05  
; PRIOR APPLICATION NUMBER: 09/680,598  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/279,526  
; PRIOR FILING DATE: 2001-03-27  
; NUMBER OF SEQ ID NOS: 8481  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2082  
; LENGTH: 1458  
; TYPE: DNA  
; ORGANISM: Bacillus licheniformis  
US-09-974-300-2082

Query Match 2.1%; Score 80.4; DB 10; Length 1458;  
Best Local Similarity 51.4%; Pred. No. 6.4e-12;  
Matches 220; Conservative 0; Mismatches 196; Indels 12; Gaps 1;

QY	1158	GGCAATGATAGATATCGTCGGGAAACAACTGTCAGTCTTCTTCATTCAGGACGCTATTC	1217
DB	364	GGGAACATATGATCTCGTTGGAAACATACACCTGTTTCTTATCCGGGATGCGATTAA	423
QY	1218	TTCCCTGATTGATTCACGCTGTCAAGCCGCAACAGACAGTGAATTCGCCAGGCTGCA	1277
DB	424	TTCCCTGACTTCATTCATACACAAAGCGCATCCGCTCACACATTTGAAAAACCCG	480
QY	1278	ACTGCACATGATAGGCGATGGGATTTCTCTCAGCCAGAGCCGCTCATTCGATGCCCTC	1337
DB	481	-----GATCGGTATGGATTTTGGTTCATTTGCTGATCCCTGCACACAGGTA	531
QY	1338	TTCTGGGCAATGTCAGACATGGAATCCCTCGCTCAATGGCTCATGTTGATGGTGGGC	1397
DB	532	ACCATCTGATGTGTGACAGGGGATCCCTGCGACTTACCGGCACATGCGCGCTTCGGC	591
QY	1398	GTCATACCTTCCGACTTGTACCGAGGAGGCACTCGACCTTGGTCAAGTTTCGCTGG	1457
DB	592	TCCACACATTCAAATGGTGAATGCCAAGGAGAGGCGCTGGATCAAAATACCACTTC	651
QY	1458	AAGACCTCCAGGAAGAGCGGCTGTTATGGGAAGGACACAGGCTCTTGGCGGAAG	1517
DB	652	AAACAGAACAGGCATTAATAAACCTGACCGAAGAGTGGGGACAAGATTGCAAGTGAA	711
QY	1518	AATCCCGACTTCCATCCACAAGACCTCTGGATGCCATGAATCTGGAAGGTACCTGAG	1577
DB	712	AACCCGATTCACACACAGGACTTGTATGAGCGGATTGAAAAAGGCGACTTCCCGGCA	771
QY	1578	TGGAGGT 1585	
DB	772	TGGAAGCT 779	

## RESULT 15

US-09-974-300-6436  
; Sequence 6436, Application US/09974300  
; Patent No. US20020146721A1  
; GENERAL INFORMATION:  
; APPLICANT: Berka, Randy M.  
; APPLICANT: Clausen, Ib Groth  
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene  
; FILE REFERENCE: 10085.500-US

; CURRENT APPLICATION NUMBER: US/09/974,300  
; CURRENT FILING DATE: 2001-10-05  
; PRIOR APPLICATION NUMBER: 09/680,598  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/279,526  
; PRIOR FILING DATE: 2001-03-27  
; NUMBER OF SEQ ID NOS: 8481  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6436  
; LENGTH: 462  
; TYPE: DNA  
; ORGANISM: Bacillus clausii  
US-09-974-300-6436

Query Match 1.9%; Score 75; DB 10; Length 462;  
Best Local Similarity 56.2%; Pred. No. 9.3e-11;  
Matches 141; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

QY	829	TCCGCTAATTCATTTTACGCGAGTTTCTGTAGCGCGCGTCCATGCTCGAGGAGCTGGT	888
DB	109	TCGCCCCATTTTGACCGTGAACGGATTCCAGAACGGTTGTCCATGCGCGGGGCTGGT	168
QY	889	CCCATGGCGTATTCACATCTATATAACTGGTCAATATACAGCCGCTATCTTCTTGA	948
DB	169	CCCATGGCGTATTTAAAGTGAATAAACAATATGAAGCCCTATACAAAAGCAAACTTTCT	228
QY	949	ACGGCGCAGGAAGCAGACACAGTATTCGTGCGGTTTCTACAGTCGCTGGTAGCAGAG	1008
DB	229	CTGAAGATGGGAAGAAACACCTGTTTGTCCGCTTCTCAACGGTCATACACGGCGGTA	288
QY	1009	GCAGTGTGTACTCTGTCTGCGGATATCCACGGATTCGCGACCCCTCTGTATACCATGA	1068
DB	289	CTTCTCCAGAGACGCTTCGCGATCCACGGGGATTTTCCGTTAAGTTTATACAGAAGA	348
QY	1069	GCAATTTGGT 1079	
DB	349	GAAATTATGAT 359	

Search completed: June 12, 2003, 01:27:00  
Job time : 534 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 17:43:15 ; Search time 5081 Seconds  
(without alignments)  
12309.972 Million cell updates/sec

Title: US-09-674-195C-1  
Perfect score: 3862  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues  
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 1: em\_estba.\*
- 2: em\_esthum.\*
- 3: em\_estin.\*
- 4: em\_estnu.\*
- 5: em\_estov.\*
- 6: em\_estpl.\*
- 7: em\_estro.\*
- 8: em\_hic.\*
- 9: gb\_est1.\*
- 10: gb\_est2.\*
- 11: gb\_hic.\*
- 12: gb\_est3.\*
- 13: gb\_est4.\*
- 14: gb\_est5.\*
- 15: em\_estfun.\*
- 16: em\_estom.\*
- 17: gb\_gss.\*
- 18: em\_gss\_hum.\*
- 19: em\_gss\_inv.\*
- 20: em\_gss\_pln.\*
- 21: em\_gss\_vrt.\*
- 22: em\_gss\_fun.\*
- 23: em\_gss\_mam.\*
- 24: em\_gss\_mus.\*
- 25: em\_gss\_other.\*
- 26: em\_gss\_pro.\*
- 27: em\_gss\_rod.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	142.6	3.7	547	14	BQ142781 fmhlc.pk0
3	138.2	3.6	489	17	BH389231 AG-ND-146
4	111.4	2.9	413	14	BQ143257 fmhlc.pk0
5	99.6	2.6	606	10	BE518097 WHE0810.H
6	99.6	2.6	746	12	BG605498 WHE2332_E

7	98	2.5	588	12	BG593639
8	98	2.5	591	12	BG262801
9	98	2.5	713	12	BF630622
10	96.4	2.5	502	12	AW758424
11	96.4	2.5	632	12	BF052861
12	95.8	2.5	822	14	BQ903589
13	95.4	2.5	456	9	AL826874
14	94.8	2.5	569	10	BE430693
15	94.8	2.5	702	13	BM404604
16	94	2.4	555	13	BJ388480
17	94	2.4	620	17	AQ448020
18	94	2.4	676	10	AV926103
19	93.2	2.4	570	10	AW217463
20	93.2	2.4	603	9	AI352816
21	93.2	2.4	731	13	BI935128
22	93	2.4	486	13	BJ478364
23	93	2.4	516	10	AV942041
24	93	2.4	559	13	BJ481863
25	93	2.4	580	10	AV940363
26	93	2.4	620	10	AV941687
27	93	2.4	670	10	AV942040
28	91.8	2.4	672	14	BQ472158
29	91.8	2.4	691	13	BM134440
30	91	2.4	532	13	BI433414
31	91	2.4	575	9	AI772135
32	90.8	2.4	657	13	BI943487
33	90.6	2.3	613	13	BJ480537
34	90.4	2.3	478	10	AV939611
35	90.4	2.3	526	9	AL817679
36	90.2	2.3	478	10	AV526803
37	90	2.3	437	13	BM134400
38	89.2	2.3	330	17	AZ577487
39	89.2	2.3	695	10	BE038083
40	.89	2.3	420	13	BM135203
41	88.8	2.3	592	10	AW042684
42	87.6	2.3	240	14	BM69031
43	87.6	2.3	398	12	BF473965
44	87	2.3	561	13	BM113806
45	86	2.2	471	9	AU197265

ALIGNMENTS

RESULT 1  
A1209912

LOCUS  
DEFINITION

311 bp mRNA linear EST 19-OCT-1998  
f012a1.r1 Aspergillus nidulans 24hr asexual developmental and  
vegetative cDNA lambda zap library Emericella nidulans cDNA clone  
f012a1 5', mRNA sequence.

ACCESSION  
VERSION

A1209912  
A1209912.1 GI:3771854

KEYWORDS  
SOURCE

EST.  
Emericella nidulans.

ORGANISM

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Eurotiales; Trichocomaceae; Emericella.

REFERENCE  
AUTHORS

1 (bases 1 to 311)  
Kupfer, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R.,  
Prude, R. and Roe, B.

TITLE  
JOURNAL

An Aspergillus nidulans EST Database  
Unpublished (1998)

COMMENT

Other ESTs: f012a1.fl  
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu  
Department of Chemistry and Biochemistry  
Advanced Center for Genome Technology, University of Oklahoma  
620 Parrington Oval, Norman, OK 73019, USA  
Tel: 405 325 4912  
Fax: 405 325 7762  
Email: broe@ou.edu  
We anticipate the future release of the cDNA clones to the Fungal  
Genetics Stock Center  
Seq primer: T3



Seq primer: M13 For

Class: BAC ends.

Location/Qualifiers

1. .489

/organism="Anopheles gambiae"

/strain="PEST"

/db\_xref="taxon:7165"

/clone="AG-ND-146J5"

/clone\_lib="ND-TM"

/note="Vector: pECBAC1; Site\_1: HindIII"

BASE COUNT 92 a 166 c 141 g 90 t

ORIGIN

Query Match 3.6%; Score 138.2; DB 17; Length 489;

Best Local Similarity 63.3%; Pred. No. 1.3e-18;

Matches 212; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

QY 1158 GGCAATGTAGATATCGTCGGAACACACGTTCCAGTCTTCTTTCATTCAGGACGCTATTCAA 1217

DB 155 GGCAATGTGGATCTCGTCGGCAACAATCCCGTCTTCTTTCATTCAGGATCGATCAAG 214

QY 1218 TTCCCTGATTTGATTCACGCTGTCAAGCGGCAACAGACAGTGAATTTCCCGAGGTGCA 1277

DB 215 TTCCCGGACGTATTCACCGCCGGAAGATGGAGGCGGATCGCGGCTATCCCGAGGCGG 274

QY 1278 ACTGCACATGATAGCGCATGGGATTTCTTCAGCAGCAGCCAGCTCATTTGCATGCCCTC 1337

DB 275 ACCCGGACGACACCTCTTGGGACATCATCAGCTGATCGCCGATCCACCCATATGATC 334

QY 1338 TTCTGGGCAATGTTCAGGACATGAATCCCTCGCTCAATCGGTCATGTTGATGGTGGGCG 1397

DB 335 ATGTGGGCGATGTGGACCGCACGCTTGGCGGCGCACCTTGGCCACTATGAGGGGTTGCGC 394

QY 1398 GTCCATACCTTCGAGCTTGTACCGGAGGAGGCACTCGACCTTGTCAAGTTTCGCTGG 1457

DB 395 GTCCACACCTTTCGCTTCATCAACAAGGAGGCAAGACCTTTCGTCAGTTCCACTGG 454

QY 1458 AAGACCCCTCAAGAGAGCGGCGCTGGTATGGGA 1492

DB 455 AAGCCGAAGCAGGCGTTCCTCGACGATCTGGGA 489

RESULT 4

BQ143257

LOCUS

DEFINITION BQ143257 413 bp mRNA linear EST 24-APR-2002

fbhlc.pk002.p12 Metarhizium anisopliae sf. acridum ARSEF 324

Metarhizium anisopliae var. acridum cDNA, mRNA sequence.

ACCESSION BQ143257.1 GI:20280316

VERSION EST.

KEYWORDS Metarhizium anisopliae var. acridum.

SOURCE Metarhizium anisopliae var. acridum

ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreales; Clavicipitaceae; mitosporic Clavicipitaceae;

Metarhizium.

REFERENCE 1 (bases 1 to 413)

Freimoser F.M., Screen S., Baga S., Hu G. and St. Leger R.J.

EST analysis of genes expressed by two different insect pathogenic

fungi during optimized secretion of proteins

Unpublished (2002)

JOURNAL

COMMENT Contact: Freimoser F. M.

Department of Entomology

University of Maryland

4112 Plant Sciences Building, College Park, MD 20742, USA

Tel: 301 405 16 13

Fax: 301 314 92 90

Email: ff34@umd.edu

Location/Qualifiers

1. .413

/organism="Metarhizium anisopliae var. acridum"

/strain="ARSEF 324"

/db\_xref="taxon:92637"

/clone\_lib="Metarhizium anisopliae sf. acridum ARSEF 324"

FEATURES

source

/note="Vector: Unizap; Metarhizium anisopliae sf. acridum was grown on insect cuticle and chitin for 24 hours. A cDNA library was constructed in the unidirectional Lambda vector Unizap."

BASE COUNT 109 a 133 c 85 g 82 t 4 others

ORIGIN

Query Match 2.9%; Score 111.4; DB 14; Length 413;

Best Local Similarity 60.9%; Pred. No. 5.6e-13;

Matches 213; Conservative 0; Mismatches 134; Indels 3; Gaps 2;

QY 2186 ATTAAATATCCCGTCTGCACAGGACAAATGTTATCCCTTAACACCGCGCATATACA 2245

DB 55 AATAACAACAGAGATGTTGGCGCACAGAACTTGTATCACAAGAACTGTCCTTATACT 114

QY 2246 CCCAACTAATGAGCAGGATTCCTCAACAAGCCACCGACCCATAACAGAGGATTC 2305

DB 115 CCCAACTCTCTGAACAGAGGATTCCTCAAGCAGCCAAACCGACTCAAGCAAGGCTTC 174

QY 2306 TTACCCGACCTGGCGGCTATGTTAAATGGACCACTAGTGGCGGAGCTCAGCCCGAGTTC 2365

DB 175 TTACCCGCTCCCGCGCGCAGGCTTCTGGTCTCTCGAGAGACGACGAAGCAGCACTTTC 234

QY 2366 AACGACGCTGTGTCCTCAACCGGCTCTCTTCTACAACTCACTCAGGTC-TTTCGAGAAGCA 2424

DB 235 CAGGACCACTGGAGCGGCTGCTGTCTTCAATTCATCCACCCCATTTGAACAGCA 294

QY 2425 ATTCTCTGTCACAGCGATCGCTTCGAAACATCCACACGCGGAGTGAACCGTGCCTAA 2484

DB 295 ATTCTCTGTCACAGCGATCGCTTCGAAACATCCACACGCGGAGTGAACCGTGCCTAA 352

QY 2485 GAACGTATCATATCCAGCTGAACCGGCTCGACAACGACCTCGCCCGCGCG 2534

DB 353 AAACGCTCTGGTACAGCTCAACAATAATCAGCANGACATCCCGTCCCG 402

RESULT 5

BES18097

LOCUS

DEFINITION WHE0810\_H01\_0022s Wheat vernalized crown cDNA library Triticum

aestivum cDNA clone WHE0810\_H01\_002, mRNA sequence.

ACCESSION BES18097

VERSION BES18097.1 GI:9742043

KEYWORDS bread wheat.

SOURCE Triticum aestivum

ORGANISM Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae

; Triticeae; Triticum.

REFERENCE 1 (bases 1 to 606)

Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han

, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J.,

Seaton, C.L. and Tong, J.C.

The structure and function of the expressed portion of the wheat

genomes - Vernalized crown cDNA library

Unpublished (2000)

CONTACT: Olin Anderson

US Department of Agriculture, Agriculture Research Service, Pacific

West Area, Western Regional Research Center

800 Buchanan Street, Albany, CA 94710, USA

Tel: 5105595773

Fax: 5105595818

Email: oanderson@pw.usda.gov

Sequence have been trimmed to remove vector sequence and low

quality sequence with phred score less than 20

Seq primer: Stratagene SK primer.

Location/Qualifiers

1. .606

/organism="Triticum aestivum"

/cultivar="Chinese Spring"

/db\_xref="taxon:4565"

/clone="WHE0810\_H01\_002"

/clone\_lib="Wheat vernalized crown cDNA library"

FEATURES

source

/tissue\_type="Crown tissue of seedling"  
 /dev\_stage="Five-week old seedling"  
 /lab\_host="E. coli SOLR"  
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid:  
 Site.1: EcoRI; Site.2: XhoI; Seeds were germinated and  
 grown at 4 C for 5 weeks. The tissue, total RNA, and  
 poly(A) RNA were prepared, a cDNA library was made, and  
 the cDNA clones were in vivo excised to give pBluescript  
 phagemids in the TJ Close lab (Choi, Close, Fenton) at  
 the University of California, Riverside. Plasmid DNA  
 preparations and DNA sequencing were performed in the OD  
 Anderson lab (all other authors)."  
 108 a 239 c. 155 g 104 t



Db 204 TTCCTCTCTTCGACGAGCTCGGCATCCCAACCGACTACCGCCACATGACGGCTTCGCG 263

QY 1398 GTCCATACCTTCGACCTGTCACCGACGAGGCGCACTCGACCTTGCTCAAGTTTCGCTGG 1457

Db 264 GTCAACACCTACACCTTCGTCCTCCGCGCTGCGCAAGTCCCACTAGCTCAAGTTCACCTGG 323

QY 1458 AGACCCCTCAAGGAGGCGGCTGTGTATGGGAGAGGACAGGCTCTTGGCGGAAG 1517

Db 324 AGGCCACCTCGCGGCTCAGCTGCCTCATGGACGAGGAGCCACCTCGTGGCGGCAAG 383

QY 1518 AATCCCGACTTCATCGACAGACCTCTGGATGCGCATTTGAATCTGGAAAGTACCTGAG 1577

Db 384 ATATACAGCAGCCACCGACCTCTACGACTCCATCGACGCGGCAACTTCCCGAG 443

QY 1578 TGGGAGGT 1585

Db 444 TGGAGCT 451

RESULT 9  
BF30622  
LOCUS  
DEFINITION  
713 bp mRNA linear EST 22-OCT-2001  
HVSMB0012E16f Hordeum vulgare seedling shoot EST library  
HVCDA0002 (Dehydration stress) Hordeum vulgare cDNA clone  
HVSMB0012E16f, mRNA sequence.  
ACCESSION  
BF30622.2 GI:13091362  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Hordeum vulgare.  
Hordeum vulgare  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae  
1 (bases 1 to 713)  
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu  
Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton  
R.D., Oates, R. and Main, D.  
Development of a genetically and physically anchored EST resource  
for barley genomics: Morex drought-stressed seedling shoot cDNA  
library  
Unpublished (2001)  
On Dec 19, 2000 this sequence version replaced gi:11894780.

COMMENT  
Contact: Wing RA  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: rwing@clemson.edu  
Total hq bases = 530  
Seq primer: AATTAACCCCTCACTAAAGGG  
High quality sequence stop: 664.  
Location/Qualifiers  
1. .713  
/organism="Hordeum vulgare"  
/cultivar="Morex"  
/db\_xref="taxon:4513"  
/clone\_lib="Hordeum vulgare seedling shoot EST library  
HVCDA0002 (Dehydration stress)"  
/tissue\_type="Seedling shoot"  
/lab\_host="TJC121"  
/note="Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;  
Seeds were surface sterilized then germinated under axenic  
conditions in the dark at room temperature on filter paper  
with water, nystatin and cefotaxime in covered  
crystallization dishes. Five-day old seedlings were  
incubated at 90% RH for 24 hr. Shoots were then harvested,  
total RNA was prepared, poly(A) RNA was purified, one  
primary unamplified cDNA library was made, 600000 pfu were  
in vivo excised to give paluescript SK(-) cDNA phagemids.  
These steps were performed in the RJ Close laboratory at  
the University of California, Riverside (Choi, Close,

Penton). Phagemids were plated and picked at the Clemson  
University Genomics Institute (CUGI) (Begum, Palmer,  
Frisch, Atkins and Wing). Plasmid DNA preparations, DNA  
sequencing and sequence analysis were performed at CUGI  
(Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).  
The sequence has been trimmed to remove vector sequence  
and contains a minimum of 100 bases of phred value 20 or  
above. For more details on library preparation and  
sequence analysis see  
<http://www.genome.clemson.edu/projects/barley>. To order  
this clone see <http://www.genome.clemson.edu/orders>. Also  
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)  
Genetically and physically anchored EST resources for  
barley genomics. Barley Genetics Newsletter 31:29-30.  
(<http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html>).

BASE COUNT 126 a 294 c 175 g 118 t

ORIGIN

Query Match 2.58; Score 98; DB 12; Length 713;  
Best Local Similarity 54.08; Pred. No. 3.6e-10;  
Matches 231; Conservative 0; Mismatches 185; Indels 12; Gaps 1;

QY 1158 GGCAATGATAGATATCGTGGAAACAACGTTCCAGTCTCTTCATTCAGGACGCTATCA 1217

Db 203 GGCAACTGGGACCTGCTCGGCAACACTTCCCGCTCTCTTCATTCGCGAGGCATCAAG 262

QY 1218 TTCCCTGATTGATTACGCTGTCAAGCCCAACAGACAGTGAATTTCCCAAGGCTGCA 1277

Db 263 TTCCCGACGCTCATCCACGCTTCAAGCCCAACCAAGTCCCAAGTTCGAGGAGT----- 317

QY 1278 ACTGCACATGATACGGGATTCCTCAGCAGCAGCCAGCCAGCTCATTCGATGCCCTC 1337

Db 318 -----ACTGGCGCGTCTTCGACTTCCTCCACACCCCGAGAGCCCTCCACACCTTC 370

QY 1338 TTCTGGCAATGTCAGACATGGAATCCCTCGCTCAATGCGTCAATGTTGGTGGGGG 1397

Db 371 TTCTTCTCTTCGACGACGCTCGGCATCCCGACCGACTACCGCCACATGAGCGCTTCGGC 430

QY 1398 GTCCATACCTTCGACTTGTACCGGAGGAGGCACTCGACCTTGTGTCAGTTTCCTGG 1457

Db 431 GTCAACACCTACACCTTCGCTCTCCCGCGGCACTCCCACTACCTCAAGTTCCTACTGG 490

QY 1458 AAGACCTCCAGGAAGAGCGGCTGGTATGGGAAGAGGACAGGCTCTTGGCGGAAG 1517

Db 491 CGCCCACTTCGCGGCTCAGCTGCCTCATGGAGGAGGAGCAACCTCTGTTGGCGCAAG 550

QY 1518 AATCCCGACTTCATCGACAAAGCCTCTGGGATGCCATTTGAATCTGGAAGGTACCTGAG 1577

Db 551 AACCAAGCAGCCAGCAGGAGGCTCTACGACTCCATCGACGCGGCAACTTCCCGGAG 610

QY 1578 TGGGAGGT 1585

Db 611 TGGAGCT 618

RESULT 10  
AW758424  
LOCUS  
DEFINITION  
502 bp mRNA linear EST 03-MAY-2000  
reinhardtii cDNA, mRNA sequence.  
ACCESSION  
AW758424  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Chlamydomonas reinhardtii.  
Chlamydomonas reinhardtii  
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
1 (bases 1 to 502)  
Grosman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P.,  
McDermott, J.P., Silflow, C., Stern, D. and Surzycki, R.  
Analysis of the Chlamydomonas reinhardtii genome: A Model,  
Unicellular System for Analyzing Gene Function and Regulation in  
Vascular Plants; project phase 2



Db	391	G-AGGCCCAACKGSGGCGTCAKSGCCTCATGAGCAGCAGGAGCCACGCTCTCKGCGCGCA	449
Qy	1517	GAATCCCGACTTCATCGACGAAGACCTCTGGGATGACCATTTGAATCTGGAGGTACCTGA	1576
Db	450	RAACACAGCCAGCCACCCAGRCCTCKAGRCCTSATCGGCGCGCAACTTCGCCGA	509
Qy	1577	GTGGGAGGT	1585
Db	510	GTGGAAGCT	518
RESULT 13			
AL826874			
LOCUS	AL826874	p:638	Triticum aestivum cDNA clone G01_p638_plate_10, mRNA sequence.
ACCESSION	AL826874		
VERSION	AL826874.1	GI:21838395	
KEYWORDS	EST.		
SOURCE	bread wheat.		
ORGANISM	Triticum aestivum		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.		
AUTHORS	1 (bases 1 to 456)		
	Wilson, L., Bewick, R., Shepherd, S., Barker, G., Parker, J., Owen, P., Edwards, D., Coghill, J., Holdsworth, M., Lenton, J., Shewry, P. and Edwards, K.		
TITLE	A BSRSC-funded wheat EST resource for the academic community		
JOURNAL	Unpublished (2002)		
COMMENT	Contact: Barker G		
	Institute of Arable Crop Research		
	Long Ashton, Bristol BS41 9AF United Kingdom.		
FEATURES	Location/Qualifiers		
source	1..456		
	/organism="Triticum aestivum"		
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Best Local Similarity	53.5%;	Pred. No. 1.3e-09;	
Matches	229;	Conservative 0;	Mismatches 187; Indels 12; Gaps 1;
Qy	1158	GGCAATGTAGATATCGTCGGAACAACGTTCCAGTCTTCTTCATTTCAGGACGCTATTCAA	1217
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Qy	1218	TTCCCTGATTGATTCACGCTGTCAAGCGCAACACAGACAGTGAATATCCCAAGCGTCA	1277
Db	71	TTCCCGAGCGTCATCCAGCGCTTCAAGCCCAACCCCAAGTCCCACGTCCAGAGT	125
Qy	1278	ACTGCACATATACGGCATGGGATTTCTCTAGCCAGCAGCCAGCTCATTCATGCGCCTC	1337
Db	126	-----ACTGGCGGCTTTCGACTTCTCTCCCAACCAACCCCGAGAGCGCTCCACACCTTC	178
Qy	1338	TTCTGGGCAATGTTCAGGACATGGAATCCCTCGCTCAATGCGTCAATGTTGATGGGTGGGC	1397
Db	179	TTCTCTCTTCAGGACGTCGGCATCCCAACCACTACCCCAATATGGACGGCTTCGGC	238
Qy	1398	GTCNATACCTTCGAGTTGTCCAGCAGAGGGCAACTCGACCTTGGTCAAGTTTCGCTGG	1457
Db	239	GTCAACACTACACTTGTCTCCGCGCGCGCAAGGCCCACTACGTCAAGTTCCACTGG	298
Qy	1458	AAGACCCCTCCAAGNAGAGCGGCGCTGGTATGGGAAGGACACAGGCTCTTTGGCGGAAG	1517
Db	299	CGCCCCACTCGCGGCTGAGCTCATGGAACGACGAGCGCACCCCTCGTCGCGCGCAAG	358



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QY 1338 TTCTGGGCAATGTCAGGACATGGAATCCCTCGCTCAATGCGTCATGTTGATGGTGGGC 1397
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QY 1398 GTCCATACCTTCGACTTGTCAACCGAGGCGCAACTCGACCTTGGTCAAGTTTCGCTGG 1457
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251 GTCCACACATTCACATTTGATCAACAGGGCTGGGAAATCAACTTATGTGAAGTTCCACTGG 310
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Db      |      |      |      |      |      |      |      |      |      |
311 AGCCCAACATGTGGTGTCAAGTCTTGTGGGAAGAGGCAATCCGAGTCGGAGAGCA 370
QY 1518 AATCCGACTTCATCGACAGACCTCTGGGATGGCATTGAATCTGGAAGGTACCTGAG 1577
Db      |      |      |      |      |      |      |      |      |      |
371 AATCAGGCCATGCTACTCAGGACCTCTATGACTCTATTGCAGCTGGAATTTATCCTGAA 430
QY 1578 TGGGAGGT 1585
Db      |      |      |
431 TGGAGCT 438

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Job time : 5091 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 17:56:36 ; Search time 8067 Seconds  
(without alignments)  
12036.728 Million cell updates/sec

Title: US-09-674-195C-1

Perfect score: 3862

Sequence: 1 ggcactctgctgcgcgata.....aacaccttcaaaagatccc 3862

Scoring table: IDENTITY\_NUC

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Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Listing first 45 summaries

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83: /cgn2\_6/ptodata/1/pna/US6039\_COMB.seq.\*

84: /cgn2\_6/ptodata/1/pna/US6040\_COMB.seq.\*

85: /cgn2\_6/ptodata/1/pna/US6041\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	439	11.4	3107	3	US-07-845-990-1	Sequence 1, Appli
2	396	10.3	1739	80	US-60-360-039-36590	Sequence 36590, A
3	396	10.3	3594	57	US-60-138-103-6172	Sequence 6172, Ap
4	396	10.3	8336	18	US-09-404-520-4942	Sequence 4942, Ap
5	345.6	8.9	2258	80	US-60-360-039-27243	Sequence 27243, A
6	343.8	8.9	2152	18	US-09-404-520-28164	Sequence 28164, A
7	318.6	8.2	789	18	US-09-417-507-19771	Sequence 19771, A
8	286	7.2	828	52	US-60-082-300-9502	Sequence 9502, Ap
9	279.4	7.2	1186	20	US-09-533-559-5719	Sequence 5719, Ap
10	259.8	6.7	1146	26	US-09-675-784A-1693	Sequence 1693, Ap
11	252.6	6.5	850	52	US-60-082-300-2192	Sequence 2192, Ap
12	240.2	6.2	1185	20	US-09-533-559-5840	Sequence 5840, Ap
13	236.8	6.1	447	18	US-09-417-507-19777	Sequence 19777, A
14	214.8	5.6	534	18	US-09-417-507-19769	Sequence 19769, A
15	199.2	5.2	522	18	US-09-417-507-19772	Sequence 19772, A
16	195.8	5.1	687	56	US-60-126-265-1924	Sequence 1924, A
17	178.4	4.6	2071	80	US-60-360-039-42972	Sequence 42972, A
18	178.4	4.6	2151	34	US-09-902-540-9468	Sequence 9468, Ap
19	178.4	4.6	13466	34	US-09-902-540-1007	Sequence 1007, Ap
20	173.8	4.5	2319	80	US-60-360-039-47146	Sequence 47146, A
21	172.2	4.5	2283	16	US-09-252-691-3735	Sequence 3735, Ap

22 172.2 4.5 2283 16 US-09-252-691C-3735 Sequence 3735, Ap  
 23 172 4.5 2052 80 US-60-360-039-44226 Sequence 44226, A  
 24 168.8 4.4 2061 80 US-60-360-039-47050 Sequence 47050, A  
 25 167.4 4.3 2232 18 US-09-404-520-28071 Sequence 28071, A  
 26 167.2 4.3 2233 18 US-09-489-039A-701 Sequence 701, App  
 27 164 4.2 1923 80 US-60-360-039-31575 Sequence 31575, A  
 28 164 4.2 2037 36 US-09-974-300-2022 Sequence 2022, Ap  
 29 162.6 4.2 2109 80 US-60-360-039-33598 Sequence 33598, A  
 30 162.4 4.2 933 80 US-60-360-039-33235 Sequence 33235, A  
 31 161 4.2 2128 80 US-60-360-039-34178 Sequence 34178, A  
 32 161 4.2 2148 17 US-09-328-352-2704 Sequence 2704, Ap  
 33 159.4 4.1 2055 38 US-10-015-127-9433 Sequence 9433, Ap  
 34 159.4 4.1 2097 80 US-60-360-039-41486 Sequence 41486, A  
 35 159.4 4.1 2118 80 US-60-360-039-33952 Sequence 33952, A  
 36 159.4 4.1 13814 38 US-10-015-127-483 Sequence 483, App  
 37 158.4 4.1 2136 80 US-60-360-039-40960 Sequence 40960, A  
 38 157.8 4.1 2262 1 PCT-US02-03987-6084 Sequence 6084, Ap  
 39 157.8 4.1 2262 31 US-09-815-242-6084 Sequence 6084, Ap  
 40 157.8 4.1 2262 39 US-10-072-851-6084 Sequence 6084, Ap  
 41 157.8 4.1 2262 80 US-60-360-039-24541 Sequence 24541, A  
 42 156.2 4.0 721 80 US-60-360-039-40088 Sequence 40088, A  
 43 156.2 4.0 717 26 US-09-663-779-409 Sequence 409, App  
 44 156 4.0 2349 42 US-10-219-999-25224 Sequence 25224, A  
 45 154.6 4.0 2103 80 US-60-360-039-39039 Sequence 39039, A

# ALIGNMENTS

RESULT 1  
 US-07-845-990-1  
 : Sequence 1, Application US/07845990  
 : GENERAL INFORMATION:  
 : APPLICANT: BERKA, RANDY M  
 : APPLICANT: FOWLER, TIMOTHY  
 : APPLICANT: VAHA-VAHE, PEKA  
 : TITLE OF INVENTION: USE OF ASPERGILLUS NIGER CATALASE-R FOR  
 : TITLE OF INVENTION: HYDROGEN PEROXIDE NEUTRALIZATION  
 : NUMBER OF SEQUENCES: 5  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: GENECOR INTERNATIONAL, INC.  
 : STREET: 180 KIMBALL WAY  
 : CITY: SOUTH SAN FRANCISCO  
 : STATE: CALIFORNIA  
 : COUNTRY: U.S.A.  
 : ZIP: 94080  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patent In Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/07/845,990  
 : FILING DATE: 19920304  
 : CLASSIFICATION: 435  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: HORN MS, MARGARET A  
 : REGISTRATION NUMBER: 33,401  
 : REFERENCE/DOCKET NUMBER: GC209-US1  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 415-742-7536  
 : TELEFAX: 415-742-7217  
 : INFORMATION FOR SEQ ID NO: 1:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 3107 base pairs  
 : TYPE: NUCLEIC ACID  
 : STRANDEDNESS: double  
 : TOPOLOGY: linear  
 : FEATURE:  
 : NAME/KEY: CDS  
 : LOCATION: Join(327..620, 683..907, 969..1385, 1440..1604,  
 : LOCATION: 1654..2745)  
 : US-07-845-990-1

Query Match 11.4%; Score 439; DB 3; Length 3107;  
 Best Local Similarity 54.9%; Pred. No. 1.le-86;  
 Matches 1195; Conservative 0; Mismatches 760; Indels 220; Gaps 8;  
 QY 494 ATGCGGTGCTCAAGCTTATCTCGCTCGGCGGGTGTGTTCTTGCAGCCCTGTCCTTAC 553  
 DB 327 ATGCGCTCAATTTTGGCTTTTGGCAGCTGTGTGTATGCTGGGGCTCAATGCCCTTAC 386  
 QY 554 ATGTAGGGGAGATGCTAGCGGTGAGAAAGGCCCTCGATCGCGCCCATCACACTCTC 613  
 DB 387 CTGTGCGGTGAATGAGTTTACCAGGAGGAGCAATGCTGGC-----GATACCAT 440  
 QY 614 TCCGACCCCTACGAGCAGTTTCTTAGCAAGTTTATATGAGATGAGATGAACAGTCGGTGA 673  
 DB 441 GAGGTCAAGGAGCAGCCCATTCACAACACCCCTGTATGTAATGACACCCGCTAGCTACATG 500  
 QY 674 ACNAGGAGCTGGGTGCTCCCATCGAGGACCAACACAGCTCAAGGCTGGAATAGAGC 733  
 DB 501 ACTACCGACTTTGGGCACTCCGATCTCCGACACAGAGCTCTCAAGGCCGGGCCGCTGT 560  
 QY 734 CCAACTCTACTTGAAGATTTTATCTCCGCCCAAGAGATTCAACACTTTGATCATGAGAGG 793  
 DB 561 CCTACCTGTGGAGGACTTATCTCCGTCAGAGCTTCAGGGGTTCCACCATGAGCCT 620  
 QY 794 GTATGTAGATACA----AAATATGTGACCGGTGTGCAATCCGCTAATTTCAATTTTACGC 849  
 DB 621 GTAAGTACAGTAAGTCTGCGGTGTGTAGTAACAATAAATGACCCAGTGGTTTCAAT 680  
 QY 850 AGGTTCTGAGCGCGCTCCATGCTCGAGGAGCTGGTCCCATGGCTGATTCACATCTCT 909  
 DB 681 AGGTCCCGAGCGCTGCGGCGGCTGCGGCTGCGGCTGCTATGTTACTTTCAATCTCT 740  
 QY 910 ATAATAACTGTGCGAATATCACAGCGCATCTCTTGAACCGCGGAGGAGGAGACACAC 969  
 DB 741 ACCTCGGCTGCTGCAAGCTCACGGCTGCGGCTTCTTGAAGTGCACAGATAAGGAGACCC 800  
 QY 970 CAGTATTCGTGGCGGTTTCTACAGTCTGCTGTTAGCAGAGGAGCTGTGTTACTTGTCTCGG 1029  
 DB 801 CTATGTTCTGCTCTCTCTACTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTGCTG 860  
 QY 1030 ATATCCACGAGTTTGGGACCGCTCTGTATACCGCATGAAGGCAATTTTGTAGCATATA 1089  
 DB 861 ATGTTACGCTGACGCTTGTGCGGTTCTACACTGACGAGGTTACTATGTTA----- 911  
 QY 1090 TCGTGTAGTACTACTATACAGACACAAATATGATACAAACCCAGGACCTAGGCT 1149  
 DB 912 -----TCTTGATATGTTGTCACCCCAACAATAATTCATATGCTAATACAGATATGCT 962  
 QY 1150 GACTACTCGGCAATGTAGATATCGTGGAAACACGTTCCAGTCTTCTTCTTCTTCTTCTT 1209  
 DB 963 -----CTACTAGACATGCTGCGGTATCAATTTGCGCCCTTCTTCTTCTTCTTCTT 1011  
 QY 1210 CTATTTCAATTTCCCTGATTTGATTCAGCTGTCAAGCGGCAACCCAGAGTGAATTTCCCC 1269  
 DB 1012 CCATCCAGTTTCCCGGATCTTGTCCACGCCATCAAGGCCATGCCCCAACAATGAGATCCCC 1071  
 QY 1270 AGGCTGCAACTGCACATGATACGCGATGGATTTCTCAGCCAGCAGCCAGCTCATTCG 1329  
 DB 1072 AGGCGGTACTGCACACACTTCCGCTTTGGGACTTCTTACGACGAGAGCAGCTGCCCTCC 1131  
 QY 1330 ATGCGCTCTTCTGGGCAATGTAGGACATGGAATCCCTCGCTCAATGCGGTCTGTTGATG 1389  
 DB 1132 ACAGTGCCTTGTGGCTGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1191  
 QY 1390 GGTGGGCGCTCCATACCTTCCGACTTGTACCGAGGAGGCAACTCGACCTTGGTCAAGT 1449  
 DB 1192 GCTACGAGTCCACAGCTTCCGCTTTCGCTGCTGCAATGTCCTTCCAAAGTGTGCGAA 1251  
 QY 1450 TTCCTGGAAGACCTTCCAGGAAGAGCGGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1509  
 DB 1252 CACCTTGGNAAGTCCCAACAGGGTGTTCGCAGTCTGGGTGTGGGATGAAGCTCAGGCCGCTG 1311







1155 CTGGCAATGTAGATATCGTCGGAACAACAGTTCCAGTCTCTTCATTCAGGAGCGTATT 1214  
1178 -----GATATCGTCGCTTAACAACATCCCTCTTTTCATCCAGGATGCCATC 1131  
1215 CAATTCCTGATTTGATTCACGCTGTCAGCCGCAACACAGACAGTGAATTCCTCCAGGCT 1274  
1130 CAGTTCCTCCGACCTTGATCCACGCGCTCAAGCCCAAGGCGGATCGTGAATTCCTCCAGGCT 1071  
1275 GCAATTCGACATGATAGCGGATGATTTCTCTCAGCCAGAGCCAGCTCATTTGCATGCC 1334  
1070 GCCACGCCCATGACGCCGCTGGGATTTCTTCAGCCAGCAGCCCTCGATCTTCACACC 1011  
1335 CTCTTCGCGCAATGTCAGGACATGGAATCCCTCGCTCAATGCGTCAATGCTGATGATGGTGG 1394  
1010 CTGCTCTGGGCGCATGGCGGCTACAGGTATCCCGGCTTCGTTCCGCGACGTCGATGGGTTTC 951  
1395 GGGCTCCATACCTTCCTCCAGTGTACACCGAGGAGGCAACTCGACCTTGGTCAAGTTTCGC 1454  
950 GGTGTGCACACTTTCCTCCGCTCGTCAAGGAGTGGCTCCACCAAGCTCGTCAAGTTTCAC 891  
1455 TGAAGACCTCTCAAGGAAGAGGCGCTGCTGATGGAAGAGGACAGGCTCTTTGGCGGA 1514  
890 TGAAGACCTCTCAAGGTTGGCAAGTATGCTGCGGAGGAGCTCAGCAATTTCTGGC 831  
1515 AAGATCCGACCTTCATCGACAGACCTCTGGGATGCCATGGAATCTGGAAGTACCT 1574  
830 AAGAACCCGACACTACATCGCCAGGATCTGTTGAGTCGATGAGGCTGCGCGGTACCT 771  
1575 GAGTGGGAGGTAAAGATGATTTCCCAATCATTTAGTCTGACAGTGTTCCTGCTCT 1634  
770 GAGTGGGAGGTATGGTACCTCT----- 749  
1635 GTCGGTGTCTTTCTCTCTTTCTATATCTTCACTAAGACTGACTTATATACGTTT 1694  
748 -----TATTTCTACTACATCGGAAGATTTAC 720  
1695 TACTCATATAGCTGGGCTTCAATGTGTGAATGAAGCAGATCAATCAAGTTTGATTTG 1754  
719 TGACCGGACGCTTAAGCTGCAATCATGACGAGGAGGACAGTTCGCTGCTTGGCTTCG 660  
1755 ATCTATTAGATCCCAACCAATATCCAGAGAACTTGTCTTTCACCCCAATCGAA 1814  
659 ACCTTTTCGACCTTACCAAGATGTCCTGAGGAATACGTCCTTACCCCATGACCCCGCTGGCA 600  
1815 AATGCTCTGAACCGCAACCAAAAGTTATTTGCGCAACTGAGCAGATGATGTTG 1874  
599 AGATGACCTCAACCGCAACCCCGCAACTTTTCCGAGACTGACGAGCTCATGTAG 540  
1875 GTCACCCCTATATATTTGGAATATGAATACATGATAGTAGATGAAGGATATATCTA 1934  
539 GCTTCTCTCTCCCTTC-----TGATCTCTCTCTTTGCGGTTCTTAAC 495  
1935 AATATATTTCCACAGTTTCAACAGGTCATGTAGTTCGCGGAATCGATTTTCAGGATGAC 1994  
494 AGTA-----ACAGTTTCCACCCGCGCACGTCGTGCGGTGTGTGACTTTCACCGAGAT 442  
1995 CTTTGTCTTCCAGGCGCTTGTACTCTCTACCTTGCACACTCAATTTGAATGCGCATGGAGT 2054  
441 CCCCTTCTCAGTATGAGCGGCGAGCAAACTTTTTTGTCTTTTACCTAA----- 389  
2055 CCCAACTTCGAGCAACTGCGGATCAACAGACCCCGCATCCGATTCATTAACAACATCGC 2114  
388 GCTGACTCGAAGCAGGAGGACGCTTTTTCAGCTACCTTGCACACCCAGCTCAACCGCAATGGT 329  
2115 GACGGTGTGTAAGTACTTCTCACCTACCATGTCAACTTCCATCTTGTACCCCAATCGAT 2174  
328 GCGCGCAACTTTGAGAGTTGCGCATCAACAGCGCGCGGTGCTATTTAC----- 278  
2175 TTGTATAGATTAATCAATCCCGCTCTGACAGGACAAATGTTTCAATCCCTCTTAACACGG 2234  
277 -----NACAACACCGTGACGGTGTGCGCAGATGTTTATCTCCGCTGAACCCG 229  
2235 CCGCATATACCCCACTCAATGAGCAACGGATTTCCCAACAGCAACCGGACCCATTA 2294

228 ATCGGTACACCCCAACACAGCTGAAGGATCAACCCCTCAACAGGCGCAACAGCAGCTCGG 169  
2295 ACAGAGATTTCTCACCGCACCTGGGCTATGTAATGACACACCTAGTGCAGGAGCTCA 2354  
168 GTCGGGATTTCTTACTGCTCTGACCGTACTGCCAACGGCAATCTTTGCGGTGCGCAAGA 109  
2355 GCCCGAGCTTCAACGAGCTGCTGGTCCCAACCGGCTCTTCTTCAAACTCACTCACGCTCT 2414  
108 GCTCCACCTTCGATGATGCTTGTGCGAGCCCGGCTTTTCTGGAACCTCTTCTTCCCG 49  
2415 TCAGAGAAGCAATTTCTGCTCAACGCCATGCGCTTCGAAACTCC 2458  
48 CCAGAGAAGCAATTTCTGCTGCTCAACGCCATTCGCTTCGCCACCGGC 5

RESULT 5  
US-60-360-039-27243  
; Sequence 27243, Application US/60360039  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Chen, Xianfeng  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
; FILE REFERENCE: 38-10(52052)A  
; CURRENT APPLICATION NUMBER: US/60/360,039  
; CURRENT FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 27243  
; LENGTH: 2258  
; TYPE: DNA  
; ORGANISM: Neurospora crassa  
US-60-360-039-27243

Query Match 8.9%; Score 345.6; DB 80; Length 2258;  
Best Local Similarity 52.7%; Pred. No. 6.4e-66;  
Matches 1230; Conservative 0; Mismatches 779; Indels 327; Gaps 9;

629 CAGTTTCTTACGAGTTTACATTTGACGATGACAGCTCGGTGCTTAACACGAGCTGGGT 688  
106 CAGAGGTTGAAGAGGTTGAGTTGACGACACGCGCAATTCATGACACAGATTTCCGGC 165  
689 GGTCCCATCAGGACCAACACAGCTGAAGCTGGAATAGAGCCCACTCTACTTTGAG 748  
166 GGCACATTCAGGACAGTTGCTGTAAGGCTGGTGGCGGCTCGACATTTGCTTTGAG 225  
749 GATTTTATCTCCGCCAGAGATTCACACTTTTATCATGAGAGGCTATGATACACAA 808  
226 GACTTCATCTCCGTCAGAGCTCCAGCACTTCGACCATGAGCGGTATGCTTCCCTGC 285  
809 ATATG-----TGACCGTTTGAAATCCGCTAATTAATTTT--ACCGAGTTCTCTGAGC 861  
286 CATGGCCCAATTAGCATCAAGAACTCTTAGTAAAGAAAGTTTATACAGATTCGCCAGA 345  
862 GCGCGCTCATGCTCGAGGAGCTGGTCCCATGCGCTATTACATCTATAAATCACTGGT 921  
346 GAGTGTTCATGCGCGGTGGTGGCGGTGCCACCGTATCTTCACAGTTATGCGGAGCTGGT 405  
922 CGAATATACAGCGGCTCTTCTTTGAACCGCGGAGGAGACACAGCAGTATTCGTGC 981  
406 CCAACATCACCGCGCTCTCTCTGCGGCGCAAGGACAAACACCGCTCTTCTGCTC 465  
982 GGTTTTCTACAGCTGCTGAGGAGGCTGTTGACTCTGCTCGCGATATCCAGGAT 1041  
466 GCTTCTTACCGGTGCGGTTCCAGGGGTTCCCGCGACACTGCGCGGTATGTTCAAGGCT 525  
1042 TTGCGACCGCTCTGATACCGGATGAAGCAATTTTGGTAAGCAATATATCGTGTGATCA 1101  
526 TCGCCAGAGATGATGTTGACCA-----CGTAACACCCCTTCCCTTC 569

QY	1102	TACTCATACAGCACAAACAATATGATATCAAAACCCAGGACCTAGGCTGACTACTCGGCA	1161
Db	570	ACCTCTTCACAGGGGGTTAACTTGACTTCAGCTATACGACGAG-----GGCA	618
QY	1162	ATGTAGATATCGTCGGAACAACGGTCCAGTCTTTCATTATCAGGACGCTATTCAATTCC	1221
Db	619	ACTTTGATATCGTCGGCAACAACATTCCTCGTCTTTTTCATCCAGGATGCCATCCGCTTCC	678
QY	1222	CTGATTTGATTCACGCTGTCAAGCGCAACACGACAGTAGTGAATTTCCCAAGGTGCAACTG	1281
Db	679	CCGACCTTATTCACCTCGTCAAGCCTAGCCCCGACCAATGAGGTTCCCAAGCGCGCACCG	738
QY	1282	CACATGATACGGCATGGGATTTCTCAGCCAGCAGCCAGCTCATTTGCATGCCCTCTTCT	1341
Db	739	CCACAGACTCCGCTTGGGACTTCTTCAGCTCCAGCCCTCCGGCTCTCCACACCTCTTCT	798
QY	1342	GGGCAATGTCAGGACATGGAATCCCTCGTCTCAATGGCTCATGTGTGATGGTGGGGGGTCC	1401
Db	799	GGGCCATGTCTGCAACGGTATTTCGCCGAGCTACCGTCAATGGATGGTTTCGGTATCC	858
QY	1402	ATACCTTCGCACTTGCACCGAGGAGGCAATCGACCTTGGTCAAGTTTCGGTGGGAAGA	1461
Db	859	ATACCTTCCTCTGGTGACCGAGGAGCGGAAGTCCAAAGCTGCTCAAGTGGCAATTTGGAAGA	918
QY	1462	CCCTCCAAGGAGAGGGGCGCTGGTATGGGAAGGACAGAGCTCTTGGCGGAAAAAATC	1521
Db	919	CGAAACAGGGAAAGGCGCTCTCGTCTGGAGGAGGCTCAAGTCTCTCGCGCAAGACG	978
QY	1522	CCGACTTCATCCACAAGACCTCTCGGATGCCATTTGAATCTGGAAGGTACCTTGAATGGG	1581
Db	979	CCGACTTCCACCTCAGGATCTCTGGGAGCGCTATCGAGTCCGGAACGGCCCTTCATGGG	1038
QY	1582	AGGTAAGATATGATTCCCCCAATCATTAGTTCTGACAGTGTTTCTCTGCTGTCTCGGTT	1641
Db	1039	-----	1038
QY	1642	GCTCTTTTTCGTCCTTTTCTATATCTTCAACTAAGACTGACTTATATACGTTTACTCAT	1701
Db	1039	-----	1038
QY	1702	ATAGCTGGGCTTTCAAATTTGGTGAATCAAGCAGATCAATCCAAGTTTGATTTCGATCTATT	1761
Db	1039	--AGCTCGCGTTCAGCTTATTTCACGAGGACAAGGCCAGGCTTACGGCTTTCGACCTTCT	1096
QY	1762	AGATCCCAACAAATCATCCAGAGAAGCTTGTTCTCTTCACCCCAATCGGAAAAATGTT	1821
Db	1097	TGATCCCAACCAAGTCTCTTCCCGAGGAGTTGCGCCCTCTCCAGGTTCTCGGTGAGATGAC	1156
QY	1822	CTTGAACGGAACCCAAAAGTTATTTCGGAACCTGACAGATCATGGTTGGTCCACC	1881
Db	1157	CCTCAACCGAACCCCTATGACTACTTCGCGAGACCGGACGATC-----	1202
QY	1882	CCCTATATATTTGGAAATATGAATACATGTATAGCTAGATGAAGCGTATATCTAAATATAT	1941
Db	1203	-----	1202
QY	1942	TTCCACAGTTCCAAACAGGTCATGTAGTTTCGGGAATCGATTTACGGATGACCCTTGC	2001
Db	1203	-----TCCTTCCAGCCCGGCGACATTTGTCGGGGGCTGCATTTACCCGAGGATCCCGCTGC	1257
QY	2002	TTCAGGCGCGCTTGTACTCCTACTTTCAGACTCAATTTGAATCGCCATGGAGGTCCCAACT	2061
Db	1258	TGCAGGTCGTCTCTACAGCTACCTCGACACCCAGCTCAACCGCCACAGGGGCCCACT	1317
QY	2062	TCGAGCAACTGCGGATCAACAGACCCCGCATCCCATTTCCATACAAACAATCGCGAGGTG	2121
Db	1318	TTGAGCAGCTCCCCATCAACCGCGCTGTCTCTGGCGTCCACAACAACCCAGCGCAGGT-	1376
QY	2122	CTGGTAAGCTACTTCTCACTACCATCACTTCACTTCCATCTTGACCCAATCGATTTGTATA	2181
Db	1377	-----	1376
QY	2182	GAGTATTAACTCCCGTCTGCACAGGACAAAATGTTTCACTCCCTCTAAACACGCGCCATA	2241

Db	1377	-----CAAGCCAGGCTTGGATCCACAAGAATCATCCACCACTA	1414
Qy	2242	TACACCCAACTCAATGAGCAACGATTCCCACACAAGCCAAACGGACCATCAACAGAGG	2301
Db	1415	CAGCCCGTCTTACCTCAACAAGGGCTACCTGCCAGGCCAACAGACCGTCTGGCCGGG	1474
Qy	2302	ATTTCTTACCGCACCTGGGCGTATGTTAAATGAGCACCACTAGTCGGGAGCTACGCCGAG	2361
Db	1475	CTTCTTCACTACCCCGCGCCGACCGCGTCTGGCGTCTCAACCGGAGCTCAGCGCCAC	1534
Qy	2362	CTTCAACGAGGCTCTGGTCCCAACCGGCTCTCTTCTACAACTCACTACGGTCTTTCGAGAA	2421
Db	1535	CTTTGAGCAGCACTACACCCAGGCCCCGGCTCTTTCTTAACCTCGCTCACCOCCTCGAGCA	1594
Qy	2422	GCAATTCCTCGTCAACGCCATGGGCTTCGAAAACTCCACGTGCGGAGTGAACACCGTGGC	2481
Db	1595	GCAGTTGCTATCAACGCGATCGCTTCGAGGCCAGCCAGCTCACCACGAGCAGGTCAA	1654
Qy	2482	TAGAAGCTCATCATCCAGCTGAACCGCGTCGACAAGACCTCTGCCCGCGCTCGCGCT	2541
Db	1655	GAGAAGGTTCTCGAGCAGCTTAACAAGATCTCCAAGGAGCTGSCCAAGCGCTGGCCGT	1714
Qy	2542	AGCTATCGGCGTCGAACCCCCCATCCCGGACCCAAACCTTCTACCAACAAGGCAACCGT	2601
Db	1715	TGGGCTCGGCTCTGAGGCGGCCGAGCCGACCGGACCGGACCTACTAGCACAAATGTCACCG	1774
Qy	2602	CCCCATCGGCACTTGGCACGAACTCTCTCGGCTCGAGGGGCTGAAATCGCCCTCCT	2661
Db	1775	CGGGTTTCCATCTTCAACGAGAGCTTCCCCACCATCGCCACCCCTCGGCTCGGCGTCT	1834
Qy	2662	---GACAAGAGACGAGTCTAGCTTCAGATCGGGGAGCAGCTCTCGGCGCCGCTTTAACAG	2718
Db	1835	CTCCACCACCAAGGCGGCTCCCTCGACAAGGCCAAGGCCCTCAAGGAGCAGCTCAGAA	1894
Qy	2719	CGCCACAACAAGTAGATATGCTCTCTAGTGGGCTCATCGCTTGATCCCCAACGCGGCGT	2778
Db	1895	GGACGGGCTCAAGGTACACCTCATCGCCGAGTACCTTGCCAGCGGGTCTCACCAGACCTA	1954
Qy	2779	GAACATGACCTATTTCGGGCGCCGAGGCTCGATCTTCGATGCGGTGATCGTCTCGGCGG	2838
Db	1955	CTCGGTGCGGACGCCACCGCTTTCGATGCCGTTCGTGGCGCGAGGGGCTGAGCGCGT	2014
Qy	2839	CGTGCTCACAGCGCCTCAA-----CGCAATACCCAAGAGGTCGCCCGCTCAGGATTAT	2892
Db	2015	CTTCAGCGGCAAGGGGCCCATGAGCCCTCTTTTCCCTGTGTGCCGTCTTAGCCAGATTCT	2074
Qy	2893	TACGGATGCATACGCTATCGGAAGCCGTTGGCGCGCTCGGTGACGGTAGCAATG	2948
Db	2075	TACTGATGTTACCGTTGGGGTTAAGCCGTTGCTGCCGTGCGCAGCGCCCAAGAAGG	2130

## RESULT 6

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US-09-404-520-28164
; Sequence 28164, Application US/09404520
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Ghodssi, Azita
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: McIninch, James
; APPLICANT: Timberlake, William E.
; APPLICANT: Yu, Jaehyuk
; TITLE OF INVENTION: Emericella nidulana
; FILE REFERENCE: 38-10(15498)A
; CURRENT APPLICATION NUMBER: US/09/404,
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 44345
; SEQ ID NO 28164
; LENGTH: 2152
; TYPE: DNA
; ORGANISM: Aspergillus nidulans
US-09-404-520-28164

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Query Match 8.9%; Score 343.8; DB 18; Length 2152;  
Best Local Similarity 52.0%; Pred. No. 1.6e-65;  
Matches 1296; Conservative 0; Mismatches 757; Indels 438; Gaps 6;

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QY 615 CCGACCTACCGACAGTTCTTAGCAAGTTTTCATCTGACGATGACAGTCCGCTGTAA 674
DB 100 CCGAGGCACCTGAGGAATTTCTGCGAGTACTACCTTGACGACGAGGACTCGTACCTGA 159
QY 675 CAACGGAGTGGGTGCCATCCATCAGAGGACCAACACAGCTGAAGGCTGGAATAGAGGCC 734
DB 160 CGACTGAGTGGCGGCCCAATTGAGGACACGAGAGTCTCAAGCGGTCGCGCGGT 219
QY 735 CAACCTACTGAGGATTTTATCTTCGCCCAAGAGATTCACACTTTGATCATGAGAGG 794
DB 220 CTACCCCTGCTGGAAGACTTTATCTTCGTCGAGAGATCCAGGATTCGACCAGGCG-- 277
QY 795 TATGTAGATACAAATATGTGACCGTGTGCAATCCGCTAATTCAAATTTACGACGTT 854
DB 278 -----GGTC 281
QY 855 CCTGAGCGCGGTCCTATGCTCGAGGAGCTGGTGCCATGGCGATTCACATCCTATAAT 914
DB 282 CCGAGCGTGGTCCATGCTCGGGTGCGAGTGCCACGCTGCTTCACCTCGTACGCG 341
QY 915 AACTGGTCAATATCACAGCGGCATCCTTCTTGAACGGCGGAGGAAAGCACACAGCAGTA 974
DB 342 GACTTCTCCACATACACCGCGCTCTCTCTCTGCTGAGGTAAGGAGACCCCGCTC 401
QY 975 TTCGTGCGGTTTCTACAGTGCCTGAGTACAGAGGAGTGTGACTCTGCTCGGATATC 1034
DB 402 TTCGTGCGGTTCTGACCGCTCGCGGAGTCTGGGAGTCTGACCTCGCGCGGATGTC 461
QY 1035 CACGATTTGGACCGGCTCTGTATACCGATGAAGGCAATTTGGTAAGCATATATCTGT 1094
DB 462 CACGGTTTCGCCACCGCTTTTACACTGACGAGGCACTTT----- 503
QY 1095 GTAGTCACTATCAACAGCACACAATATGAATACAAACCCAGGACCTAGGTGACTA 1154
DB 504 ----- 503
QY 1155 CTCGCAATGATGATATCGTCGGAACAAACGTTCCAGTCTTCTTCAATCAGAGGCTATT 1214
DB 504 -----GATATCGTCGGTAACAACATTCCTCGTCTTTTCATCCAGGATGCCATC 551
QY 1215 CAATTCCTGATTTGATTCAGCTGTCAAGCGGCAACAGACAGTGAATTTCCCGAGCT 1274
DB 552 CAGTTCCCGGACCTGATCCAGCGCTCAAGCCCAAGGCGGATCGTGAATCCCGAGGCT 611
QY 1275 GCAACTGCACATGATACGGCATGGGATTTCTCAGCCAGAGCCAGCTCATTTGCATGCC 1334
DB 612 GCCAGGCCCATAGCGCGCTGGGATTTCTTACCGAGAGCCCTCGACTCTTCACACC 671
QY 1335 CTCCTTCTGGCAATGTCAGGACATGGAAATCCCTCGCTCAATGCGTCAATGTTGATGGGTGG 1394
DB 672 CTGCTCTGGCCATGGCGGTCACGGTATCCCGGTTCTGTTCCGCCAGCTCGATGGGTTTC 731
QY 1395 GCGCTCATACCTCCGACTTGTACCGAGGAGGCAACTCGACCTTGGTCAAGTTTTCGC 1454
DB 732 GGTGTGCACACTTTCGGCTGTCACGGAGGATGGCTCCACCAAGCTCGTCAAGTTCCAC 791
QY 1455 TGAAGACCCCTCAAGGAAGAGCGGCTGTGATGGGAAGGACAGGCTCTTGGCGGA 1514
DB 792 TGAAGACCCCTGCAAGGTTTGGCAAGTATGTTGAGGAGGAGCTCAGCAATTTCTGGC 851
QY 1515 AAGATCCCGACTTCCATCGACAAGACCTCTGGGATGCCATTTGAATCTGGAAGGTACCT 1574
DB 852 AAGAACCCCGACTACATCGCCAGGATCTGTTTCGAGTCGATGAGGCTGGCGGTACCT 911
QY 1575 GAGTGGGAGGTAAGATATGATTCGCCCAATCATATAGTTCGACAGTGTCTCTGCTCT 1634
DB 912 GAGTGGG----- 918
QY 1635 GTCGGTTCTCTTTCGTCCTTTTCTATATATCTTCAACTAAGACTGACTTTATATACGTTT 1694
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DB 919 ----- 918
QY 1695 TACTCATATAGCTGGCTTTCAATTTGGTGAATGAAGCAGATCAATCCAAGTTTGTATTCG 1754
DB 919 -----ACCTTAAGCTGCAATCATGAGCAGAGGAGGACCATGTCGGCTTTGGCTTCG 969
QY 1755 ATCTATTAGATCCCAACCAAAATCATCCAGAGAAGTGTTCCTTTTACCCCAATTCGGA 1814
DB 970 ACCTTTTCGACCCCTACCAAGATTGTCCTGAGGAATACGTCCCATTGACCCCGCTGGCA 1029
QY 1815 AATGTGCTTGAACCGAAACCCAAAGTTATTTTGGCGGAACCTGAGCAGATCATGTTG 1874
DB 1030 AGATGACCCCTCAACCGCAACCCCGCAACTATTTTGGCGAGACTGAGCAGGTCTAT----- 1084
QY 1875 GTCACACCCCTATATATTGGAATATGAATACATGTATAGCTAGATGAAGGTATATCTA 1934
DB 1085 ----- 1084
QY 1935 AATATATTTCCACAGTTCCAAACAGGTCATGTAGTTTCGCGGAATTCGATTTTCCACGATGAC 1994
DB 1085 -----GTTCCAAACCCCGGCACGCTCGTGGTGGTGTGACTTTCACCGAGGAT 1130
QY 1995 CCTTTGCTTCAGGCGCGCTTGTACTCTACCTTGACACTCAATTTGAATCGCCATGAGGT 2054
DB 1131 CCCCTTCTTCAGGAGACGCTTTTTCAGCTACCTTGACACCCAGCTCAACCCGCAATGGTGGC 1190
QY 2055 CCCAACTTCGAGCAACTGCCGATCAACAGACCCCGCATCCCATTTCCATTAACAACAAATCGC 2114
DB 1191 CCGAACTTTGAGCAGTTGCCCATCAACAGCGCGCGGTGCTATTCACAACAACACCGT 1250
QY 2115 GACGGTGTGTGTAAGCTACTTCTCACCTACCATGCTCAACTTCCATCTTGACCCAAATGAT 2174
DB 1251 GACGGTGTGCGCCAG----- 1265
QY 2175 TTGTATAGAGTATTAAACATCCCGCTCTGCACAGGACAAATGTTTCATCCCTTAACACGG 2234
DB 1266 -----ATGTTTCATTCGCTGAACCCCG 1287
QY 2235 CCGCATATACACCAACTCAATGACAAACGATTCCCAACAACAGCCAGCCGACCCATA 2294
DB 1288 ATGCTACAGCCCCCAACACGCTGAAGGATCAACCCCTCAACAGGCCAACACAGACTGGG 1347
QY 2295 ACAGAGGATTTTCACCGCACCTGGCGGTATGGTAAATGGACCACTAGTGGCGGAGTCA 2354
DB 1348 GTCGCGGATTTCTTACTGCTCTGACCGTACTGCAACGGCAATCTTGTGGCTGCCAAGA 1407
QY 2355 GCCGAGGTTCAACAGACGCTGCTGCCAAACCGCTCTCTTACAACCTCACTCAACGGTCT 2414
DB 1408 GCTCCACCTTCGATGATGCTTGGTGGCAGCCCGGCTTTCTGGAACCTCTCTTCTCCCG 1467
QY 2415 TCGAAGAGCAATTCCTCGTCAACGCGATGCGCTTCGAAACCTCCACGTCGCGGAGTANA 2474
DB 1468 CCGAGAAGCACTTCGTGTCACGCAATTCGCTTCGAAACGCAATGTTGAAGAGCGATG 1527
QY 2475 CCGTGGTGAAGCTCATCATCAGCTGAACCGGTCGACAGACCTCCCGCGCGCGG 2534
DB 1528 TCGTGAAGAACAGCTCATCTGCTCAGCTTAATCGAATCTCGAAGACGACTTCCACCGCG 1587
QY 2535 TCGCGTACGCTATCGGCGTGAACCCCATCCCGGACCCCAACCTTCTACCAACAACAGG 2594
DB 1588 TTGCCAAGCCCATCGGTGTTGATGCTCCGAGACCCGACACACTTACTACCAACAACA 1647
QY 2595 CAACCGTCCCATCGGCACCTTCGCGACGAATCTCTCTCGGCTCGAGGGTGAANAATCG 2634
DB 1648 CGACTCCAACATCGTGGCTTTGGCCACCGACTCCAGAGCTTGGCTGGCTTGAAGATTG 1707
QY 2655 CCCTCTCTGACAGACAGCAGCTAGCTTCAGATTCGCGGACAGCTCGCGGCGCGGTTTA 2714
DB 1708 CCGTACTTGTCTCTGTTGACGACAGAGGAATCTTTCAGCGCGGCTACTGCTCTGAAGCGG 1767
QY 2715 ACAGCGCAACAACAAAGTAGATATCGTCTAGTGGGCTCATCGTTGATCCCAACCGG 2774
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Db 1768 AGCTCTCAACAGCAACCTGACAGTCATTGTGCTGCTGAAAGCTT-----CTCCAAG 1821  
QY 2775 GCGTGAACATGACCTATTTCGCGCGCGGAGCTGCTGATCTTCGATGCGGTGATCGTCTGCG 2834  
Db 1822 GCGTGAACAGCACTACTCTGCTCTGAGCGCATTCAGTTTGACGCGCTGCTGTTGCGCC 1881  
QY 2835 GGGGCTGCTACGAGCGCTCAACGAATACCCAAAGAGTGTGCGCGCTCAGGATATTA 2894  
Db 1882 CTGGAGCGAGAGCTTTCGGTGTCAAGTCCGCGGCAACTCCAGCTCAACCCCTCTACC 1941  
QY 2895 CGGATGCATACGCTATGAAAGCCGTTGGCGCGCTGCTGACGTCGATGAAGCC 2954  
Db 1942 CTGCGCGCGCTCCCTCGAATCCCTGCTGTGATGCTTTCGCTTCGCTGAGCAGTCTG 2001  
QY 2955 TTCTGAGCTCTTATGCGCGCTGCTGGGAGTGCCTGAAATGGCTGGACCAAGCCGCTG 3014  
Db 2002 CTCTTGGCAGCGCTCCACTGCTTTCGACAAGCTGTTATCAACCGCGTTCGAGGGCG 2061  
QY 3015 TGTATATTCCACGATGAGTGAAGCTAGTTAGAGTGTCTTGGACGATTCAGCG 3074  
Db 2062 TGTAGCTTCCGATCCCTGGAGAGAGCTTTGCCAACAACCTCGAGGAGGTCTGACCG 2121  
QY 3075 CATATCGTCTTGAATCGTTCCCGTTGGA 3105  
Db 2122 TGTTCAGTTCTGATGCTTTCGCTGGA 2152

RESULT 7  
US-09-417-507-19771  
; Sequence 19771, Application US/09417507  
; GENERAL INFORMATION:  
; APPLICANT: KEITH G. WEINSTOCK ET AL.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ASPERGILLUS  
; FILE REFERENCE: PATH99-10  
; CURRENT APPLICATION NUMBER: US/09/417,507  
; CURRENT FILING DATE: 1999-10-14  
; NUMBER OF SEQ ID NOS: 44312  
; SEQ ID NO 19771  
; LENGTH: 789  
; TYPE: DNA  
; ORGANISM: A.fumigatus  
US-09-417-507-19771

Query Match 8.2%; Score 318.6; DB 18; Length 789;  
Best Local Similarity 66.6%; Pred. No. 4.6e-60;  
Matches 508; Conservative 0; Mismatches 214; Indels 41; Gaps 2;

QY 845 TACGAGGTTCTGAGCGCGCTCATGCTCGAGGAGCTGTGCGCATGGCGTATTCTAC 904  
Db 23 TTCTGAGTTCGCGAGCTGCGGTCCATGCCGCTGCTGCGCGCGCATGGAGTCTTAC 82  
QY 905 ATCCCTATAATACTGTGCTGAATATCACAGCGCATCTTCTTGAACGGCGGAGGAAGCA 964  
Db 83 TCCATATGCGACTTCTGAACATCACTCGGCTCTTCTTCCGCAAGGAAGGAAGCA 142  
QY 965 GACACGATTTCTGCGGTTTTCTACAGTCTGCTGAGCAGGAGTGTGACTCTGC 1024  
Db 143 AACCCCTGATTGTCGCTTCTCGAGGTCGCGAGGAGGAGTGTGCGATCTGC 202  
QY 1025 TCGGATATCCAGGATTTGCGACCGCTGTATACCGATGAAGCAATTTGGTAAGCA 1084  
Db 203 CGGTGATGTTACGGTTTTGCGACTCGTTTCTATACCGAGGAGCAATTCGTT 257  
QY 1085 TTATATCGTGTAGTACTATACACGACCAACAATAATGATATACAACCCAGCACT 1144  
Db 258 -----ACGTGGTCAATTCGACAACTACAT 284  
QY 1145 AGCTGACTACTCGGCAATGATGATATCGTGAACAACAGTCTTCCAGTCTTCTTCAATCA 1204  
Db 285 CGTCTGCTAAGTGCA---TAGATATCGTTGGAACAATATCCCTGTATTCTTCAATCA 341  
QY 1205 GGAGCTATTCATTCCTGATTGATTGATTCACGCTGTCAAGCGCGCAACACAGAGTGAAT 1264

Db 342 GGATGCTATCTCTTCCCGGATCTGATCCAGCGCTCAAGCCGAGAGGTGACACGAGAT 401  
QY 1265 TCCCAGAGCTCAACTGCACATGATACGCGATGGGATTTCTTCAGCCAGCCAGCTC 1324  
Db 402 CCTCAGGCTGCATGCTCATGACTCGGCTGGGACTTTTCAGCCAGCAGCCAGCA 461  
QY 1325 ATTGCATCCCTCTTCTTGGCAATTCAGGACATGGAATCCCTCGCTCAATCGCTCATGT 1384  
Db 462 GATGCACACACTGCTCTGGCTATCTTGGCATGGCATTCCTGTTCTTTCGACATGT 521  
QY 1385 TGATGGTGGGCGCTCATACCTTCGAGCTTGTACCGAGAGGGAACCTGACCTTGT 1444  
Db 522 TGATGGTTCGCTGTGATACCTTCGATTCGATTCGATTCGATTCGATTCGATTCGAT 581  
QY 1445 CAAATTTCTGCTGAGAGCCCTCAAGAGAGAGCGGCTTGGTATGGAGAGGCGACAGC 1504  
Db 582 CAAATTTCTGCTGAGAGCTTTCGAGGCGAGGCGAGGCTGCTGGAGAGGCGCGCA 641  
QY 1505 TCTTGGCGAAGAAATCCGACTTCCATCGAAGAGCCTCTGGGATGCGCATTTGAATCTGG 1564  
Db 642 GACCTCTGCGAAGAAATCTGACTTCTGCTGAGGATTTGACGATTCGATTCGATTCGAT 701  
QY 1565 AAGGTACCTGAGTGGGAGGTAAGATATGATTCCTCCCAATCA 1607  
Db 702 ACGCTATCGGAGTGGGAAGTAAGTCTGCTTCCATCGTCAATCA 744

## RESULT 8

US-60-082-300-9502/c  
; Sequence 9502, Application US/60082300  
; GENERAL INFORMATION:  
; APPLICANT: LAGACHE, ROBERT E.  
; APPLICANT: CORLEY, NEIL C.  
; APPLICANT: RUSSO, FRANK D.  
; APPLICANT: HANN, AMY L.  
; APPLICANT: HEATH, JOE D.  
; APPLICANT: BROOKS, GREGORY L.  
; APPLICANT: FINNEY, JACQUELINE  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF ASPERGILLUS FUMIGATUS  
; TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF  
; NUMBER OF SEQUENCES: 21910  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/60/082,300  
; FILING DATE: HERewith  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CERRONE, MICHAEL C.  
; REGISTRATION NUMBER: 39,132  
; REFERENCE/DOCKET NUMBER: PM-00014 P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 9502:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 828 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: genomic DNA  
; IMMEDIATE SOURCE:



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Db 652 TCCTTGGGACTTCTTTCAGCCAGCAGCCAGTTCCTCGACACCTCTGCTGGGCCATGTC 711
QY 1352 AGGACATGAATCCCTCGCTCAATCGTCAATGCTGATGCTGGGGGCGGCTCCATACCTTCGG 1411
Db 712 CGGCCATGATTCGCCGCGCTCTCTTGGCCACGCTGATGCTGGTATGCCACACTTCGG 771
QY 1412 ACTTGTACCGGAGGAGGCAACTCGACCTTGTCAAGTTTCGCTGGAAGACCTCCAAAG 1471
Db 772 CTTCGCTACTGACACGGTGACTCCCAAGCTGCTCAAGTTCCACTGGAAGTCTCGANGG 831
QY 1472 AAGAGCGGCTGCTGATGGGAAGAGGACAGGCTCTTGGCGAAGAAAGATCCGACTTCCA 1531
Db 832 TAAAGCCCAACATGGTCTGGGAAGAGCGCAACAGGCTCTTGGCAAGAACCCCGACTTCAT 891
QY 1532 TCGCAAGACCTCTGGGATGCCATTAATCTGGAAGGTACCTGAGTGGGAGGT 1585
Db 892 GCGCCAAAGTCTCTCGAAGGATCGAGCGGGGAGATACCTGTAATGGGAGCT 945

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RESULT 10

US-09-675-784A-1693  
 ; Sequence 1693, Application US/09675784A  
 ; GENERAL INFORMATION:

APPLICANT: HARE, ROBERTA S.  
 APPLICANT: SHAW, KAREN J.  
 APPLICANT: SHIMER JR., GEORGE H.  
 APPLICANT: KESSLER, MARCO  
 APPLICANT: NOLLING, JORK  
 APPLICANT: ZENG, QIANDONG  
 APPLICANT: GRENE, JONATHAN R.  
 TITLE OF INVENTION: ASPERGILLUS FUMIGATUS NUCLEIC ACIDS AND POLYPEPTIDES,  
 TITLE OF INVENTION: AND USES THEREOF  
 FILE REFERENCE: 2976-4020US1  
 CURRENT APPLICATION NUMBER: US/09/675,784A  
 PRIOR FILING DATE: 2000-09-29  
 PRIOR APPLICATION NUMBER: 60/156,338  
 PRIOR FILING DATE: 1999-09-29  
 NUMBER OF SEQ ID NOS: 13925  
 SEQ ID NO 1693  
 LENGTH: 1146  
 TYPE: DNA  
 ORGANISM: Aspergillus fumigatus  
 US-09-675-784A-1693

Query Match 6.7%; Score 259.8; DB 26; Length 1146;  
 Best Local Similarity 58.3%; Pred. No. 6.6e-47;  
 Matches 594; Conservative 0; Mismatches 277; Indels 148; Gaps 2;

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QY 564 AGATCCCTAGCGGTGAGAAAGGCGCCCTCGATCGCGCCGATGACACTCTCTCCGACCCTA 623
Db 131 ATATGACCGGGAGGCTCAACCGCTCGTGATGATATATCCGATGGGAGCGCTGCGCGAGCCA 190
QY 624 CGGACCACTTCTTACGAAAGTTTACATTTGACGATGAACAGTGGTGTCTAACAAGGAGC 683
Db 191 CAGAGGAATCTTGTCCAGTATTTATCTCAACAGCAATGATGCTTATGACGCTCCGAGC 250
QY 684 TGGTGTGCTCATCGAGGACCAACAGCCTGAAGCTGGAATAGAGGCCCAACTCTAC 743
Db 251 TGGGCGGCTTATCGAAGATCAGATAGTCTCAGTGGCGGAGCGTGTGCTCCACCTGCG 310
QY 744 TTGAGGATTTATCTTCCGCGCAGAGATTCACACTTTGATCATCAGAGGGTATGTAGAT 803
Db 311 TCGAAGATTTATTTCTCGTCAAAAGATACAGCGTTTTCGACCATGACGCGGTC----- 363
QY 804 ACAAATATATGACCGGTGTTTCAAAATCGCTTAATTCATTTTACCGAGTTTCGAGCGC 863
Db 364 -----CCGAGCGT 372
QY 864 GCGTCCATGCTCAGGAGCTGGTGGCCATGGCGCTATTCACATCTATATAAATGCTGTCG 923
Db 373 GCGGTCCATGCTGCTGGTGGCGGCGCCATGGAGTCTTCACTTATATGCGGACTTCTCG 432

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QY 924 AATATCACAGCGCGCATCTTCTTGAACGGCGAGGAAAGACACACACCACTATTCGTCCGG 983
Db 433 AACATCACTGCGGCTTCTTCTGCGCAAGGAAGCAAGCAACCCCTGATTTATTTCTCCGC 492
QY 984 TTTTCTACAGTGCCTGTGTAGCAGAGGAGGAGTGTGACTCTGCTCGGAGATATCCACGATTT 1043
Db 493 TTCTCGAGGCTGCGCAGGAGGAGAGTGTGCTCGGATCTGCGCCGCTGATGTTTCAACGTTT 552
QY 1044 GCGACCGCTCTGTATACCGATGAAGCAATTTTGTGTAAGCAATATATCGTGTGATGAT 1103
Db 553 GCGACTCTCTTCTATACCGAGGAGGCAAT----- 583
QY 1104 CTCATAACAGCAACAATAATATACAAACCCAGGACCTAGGCTGACTACTCGGCAT 1163
Db 584 ----- 583
QY 1164 GTAGATATCGTGGGAAACAAGTTCCAGTCTTCTTCTTTCAGGAGCGCTATTCATTTCCCT 1223
Db 584 -TCGATATCGTTGGAAACAATAATCCCTGTATTTCTTTCATCCAGGATGCTATCTCTCCCC 642
QY 1224 GATTTGATTCAGCTGTCAAGCCGCAACAGCAGTGAATTTCCCGAGCTGCAACTGCA 1283
Db 643 GATCTGATCCAGCGCGCTCAAGCCGAGAGGTGACAAAGAGATCCCTCAGCTGCCACTGCT 702
QY 1284 CATGATACGGCATGGGATTTCTCTCAGCCAGCAGCCAGCTCATTTGCATGCCCTCTCTCG 1343
Db 703 CATGACTCGGCTGGGACTTTCTCAGCCAGCAGCCAGCAGCATGATGCACACATGCTCTGG 762
QY 1344 GCAATGTCAAGACATGGAATCCCTCGCTCAATGCTCATGTTGATGGGTGGGCGCTCCAT 1403
Db 763 GCTATGTCTGGCATGGCATTCCTGCTTCTTCCGACATGTTGATGGGTGCGTGGCAT 822
QY 1404 ACCTTCCGACTGTCTCAGCAGGAGGCAACTCGACCTTGGTCAAGTTTTCGCTGGAGACC 1463
Db 823 ACCTTCCGATTCGTACAGATGACGCTGCATCAAGCTCGTCAAAATTTTCACTGGAAGTCT 882
QY 1464 CTCGAAGGAAGAGCGGCGCTGTGATGGAAGAGGACAGGCTCTTTGGGGAAGAAATCCC 1523
Db 883 TTGAGGCAAGGCGGAGCATGCTGCGGAGAGGCGGAGCAGACCTCTGGCAGAAATCCT 942
QY 1524 GACTTCCATCGCAAGACCTCTGGATGCCATTTGAATCTGGAAGTACCCCTGAGTGGGA 1582
Db 943 GACTTCATCGCTCAGGATTTGCACGATTTGCACGATCGAGGCTGGACGCTATCCGAGTGGGA 1001

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RESULT 11

US-60-082-300-2192/c

Sequence 2192, Application US/60082300  
 ; GENERAL INFORMATION:  
 APPLICANT: LAGACE, ROBERT E.  
 APPLICANT: CORLEY, NEIL C.  
 APPLICANT: RUSSO, FRANK D.  
 APPLICANT: HANW, AMY L.  
 APPLICANT: HEATH, JOE D.  
 APPLICANT: FINNEY, GREGORY L.  
 APPLICANT: BROOKS, JACQUELINE  
 TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF ASPERGILLUS FUMIGATUS  
 TITLE OF INVENTION: GENOME FRAGMENTS THEREOF, AND USES THEREOF  
 NUMBER OF SEQUENCES: 21910  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
 STREET: 3174 PORTER DRIVE  
 CITY: PALO ALTO  
 STATE: CALIFORNIA  
 COUNTRY: USA  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/60/082,300

FILING DATE: HEREWITH  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: CERRONE, MICHAEL C.  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PM-00014 P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 2192:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 850 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: genomic DNA  
IMMEDIATE SOURCE:  
CLONE: AFUlc2199  
US-60-082-300-2192

Query Match 6.5%; Score 252.6; DB 52; Length 850;  
Best Local Similarity 60.2%; Pred. No. 2.4e-45;  
Matches 500; Conservative 0; Mismatches 284; Indels 47; Gaps 3;

QY 1699 CATATAGCTGGCTTCAATTTGGTGAATGAGCAGATCAATCCAAAGTTTGAATTCGATCT 1758  
DB 785 CAATAGCTGGTGTGTAATCCATGATGAGGAGACCAATGCGGTTCGGTTTGACCT 726  
QY 1759 ATTAGATCCCAACAAATCATCCAGAGAACTGTTTCCTTACCCCAATCGGAAAAAT 1818  
DB 725 CTGGACCCCAAGAAGTCGTCCAGAGGAATCGTGCCTCATCACCAGTTGGCAGAT 666  
QY 1819 GGCTTTGAACCGAAACCCAAAAAGTTATTTGGCGAAACTGAGCAGATCATGTTGGTCC 1878  
DB 665 GCAACTGAACCGCAACCTCGCACTATTTGCTGAGACCGCAACAGTTATGTTGATG 609  
QY 1879 ACCCTTATATTTGGAAATGATACATGATATAGTATAGTGAAGCGTATATCTAATA 1938  
DB 608 GTGCCATCAGGAAGCTGATCAGAAATGAATCTGTAGTCTGAC 567  
QY 1939 TATTTCCACAGTTTCCACACAGGTGATAGTTGCGGAATCGAATTTCCAGGATGACCTT 1998  
DB 566 --TGCAACAGTTTCCACCTGGTGCACATTTGCGGTGTTGATCTTCACTGAAGACCTC 509  
QY 1999 TGCTTAGGGCGGCTTGTACTCTTACCTTGACACTCAATTAATCGCCATGGAGGTCCCA 2058  
DB 508 TCCTGCAAGCGCGTCTGTTTCTGTAACCTGGACACTAGCTGAACCGTCAACGGTGGCCCA 449  
QY 2059 ACTTCGAGCAACTCCGATCAACAGACCCGCGATCCCATCCATAACAACAATCGCGACG 2118  
DB 448 ACTTTGAACAACTCCCATCAACCACTCGCGTTCCCGTGCAACAACAACCGCGATG 389  
QY 2119 GTGCTGTAAGTACTTCTCACCCTACCATGTCAACTTCCACTTTGACCCCAATCGATTGT 2178  
DB 388 GAGCAGTGAGACTTTTCAACTTTTAAGCCAGTGTCTCCATTAATCTTTTCATATT 331  
QY 2179 ATAGAGTATTAAATCCCGTCTCCACAGCAAAATGTTCAATCCCTTAACACGGCCGC 2238  
DB 330 -----TCTGAGGCGCAAAATGTTCAATTCCTCCCTCAACCCCTCACGC 293  
QY 2239 ATATACACCAACTCAATGAGCAAGGATTCACCAACAGCCCAACCGGACCCATACAG 2298  
DB 292 GTATCGCCCAAGACCTTCGCTCAACGGTTCCCAAAAACAGCCCAACGACCGTCGCGCA 233  
QY 2299 AGGATTTCTACCCGACCTGGGCGTATGTTAAATGGACCACTAGTGGCGAGCTCAGCCC 2358  
DB 232 TGGCTTTTACAGCTCTTGACGCTACCAACAGTGGCAGCTTGTCCGTGGGTGAGCTC 173  
QY 2359 GAGCTTCAACGAGCTGTGGTCCCAACCGCGTCTTCTTACAACTCACTACAGGTCATCGA 2418  
DB 172 AAGCTTTGAGGATGCTGGTCTCAGCCACGGCTCTTCTACAATTTCTTTGTTCTCGCCA 113  
QY 2419 GAACCAATTCCTGCTCAACGCCATGCGCTTCGAAAACTCCCAACGTCGGGAGTGAACCGT 2478

DB 112 GAAGCAGTTGGTTATTGACCCATCCGCTTCGAAATGCAAACTTAAATCTCCCGTGT 53  
QY 2479 GCGTAAGAAGCTCATCATCCAGCTGAACCGCTGCAGACGACGCTCGCCG 2529  
DB 52 AAGAACACAGCTCATCATTCAGTTGAACCGCATCGATAGGACCTTGCAGG 2

RESULT 12  
US-09-533-559-5840  
Sequence 5840, Application US/09533559  
GENERAL INFORMATION:  
APPLICANT: Randy M. Berka  
APPLICANT: Michael W. Rey  
APPLICANT: Jeffrey R. Shuster  
APPLICANT: Sakari Kauppinen  
APPLICANT: Ib Groth Clausen  
APPLICANT: Peter Bjarke Olsen  
TITLE OF INVENTION: Methods for Monitoring Multiple Gene  
FILE REFERENCE: 5849.200-US  
CURRENT APPLICATION NUMBER: US/09/533,559  
EARLIER FILING DATE: 2000-03-22  
EARLIER APPLICATION NUMBER: 09/273,623  
NUMBER OF SEQ ID NOS: 7860  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5840  
LENGTH: 1185  
TYPE: DNA  
ORGANISM: Aspergillus oryzae  
US-09-533-559-5840

Query Match 6.2%; Score 240.2; DB 20; Length 1185;  
Best Local Similarity 61.8%; Pred. No. 1.6e-42;  
Matches 402; Conservative 0; Mismatches 243; Indels 6; Gaps 1;

QY 2189 AACATCCCTGTCGACAGGACAAATGTTTCATCCCTTAAACAGGCGCGCATATACACC 2248  
DB 180 AACAAACCGCATGGAGCGCCAGATGTTTCATCCCTGAAACCCCAACGCTACTCTCCG 239  
QY 2249 AACTCAATGAGCAACGGATTCCCAACAAGCAACGCGGACCCCAATACAGAGATTCTTC 2308  
DB 240 AACACCTCAACAGGCGCTCTCTTAAGCAGGCCAACCGACTGTGGCAAGGCGTCTTC 299  
QY 2309 ACCGCACTGGCGGTATGTAATGGACCACTAGTGGCGAGCTACGCCGAGCTTCAAC 2368  
DB 300 ACGCTCTGGAGCGGAGTCTACTGGCGGTTTCAACCGTCCGCTCAGCCGCTCTTCGAG 359  
QY 2369 GAGCTCTGGTCCCAACCGCGCTCTTCTACAACTCACTCAGGTCTTCGAGAGCAATTC 2428  
DB 360 GAGCTCTGGTCCGAGCGCGCTGTTCTACAACTCACTTACTCCCGCCGAACAGAGTTC 419  
QY 2429 CTGCTCAACGCCATCGCTTCGAAACTCCCACTGGGAGTGAAACCGTCCGTGAAGAC 2488  
DB 420 GTGCTCATGCTATTCGTTTGAAGACTCCACGTCAGAGCTCGGTCTGACGCAACAT 479  
QY 2489 GTCATCATCAGCTGAACCGCTGACACAGACTCGCCCGCGCTGCGCTAGCTATC 2548  
DB 480 GTCATCATCAGCTGAACCGCTGTCACACAGACTCGCCCGCGCTGCGCTATC 539  
QY 2549 GGGTCAACCCCATCCCGGACCCAACTTACCAACAACAGGCAACCGTCCCGCATC 2608  
DB 540 GGGTTCAGGAGCGCTGAGGCTGAGCCGACCTTACCAACAACAGGCAACCGTTCGAGCT 599  
QY 2609 GGCACCTTCGCGAGGAATCTCTCGCGCTGAGCGGCTGAAATTCGCCCTCTCTGACAAGA 2668  
DB 600 GGCACCTTCGCGAGGAGCTGAAGAGCTGATGAGACTGAAGGTGCTTCTTGGCTTCG 659  
QY 2669 GACGACGCTAGCTTTCACGATCGCGGAGCAGCTCCGGCGCGGTTTAAACAGCGCAACAAC 2728  
DB 660 GTTGAGACCCCTGCTCCATCCATCGAGGCGCCTCTGAGCTCAGCAAGCAGCTTCTCTGAGGAC 719

QY	2729	AAAGTAGATATCTCTAGTGGCTCATCGTTGATGCCAACGCGCGTGAACATGACC	2788
Db	720	GGCTTTGATGTTGTCGCTTG-----CGGACGCTCTGCCGATGCGCTTGATCAGACT	773
QY	2789	TATTCGCGCGCGACGGCTCGATCTTCGATGCCGTGATCGTCTCGCGCGC	2839
Db	774	TACTCCGGATCGGATGCCATCCATGTCGATGTCGTGATCGTCTCGCGCGCGC	824

RESULT 13  
US-09-417-507-19777/c  
; Sequence 19777. Application US/09417507  
; GENERAL INFORMATION:  
; APPLICANT: KEITH G. WEINSTOCK ET AL.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ASPERGILLUS  
; TITLE OF INVENTION: FUMIGATUS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: PATH499-10  
; CURRENT APPLICATION NUMBER: US/09/417,507  
; CURRENT FILING DATE: 1999-10-14  
; NUMBER OF SEQ ID NOS: 44312  
; SEQ ID NO 19777  
; LENGTH: 447  
; TYPE: DNA  
; ORGANISM: A.fumigatus  
US-09-417-507-19777

Query Match	6.1%	Score 236.8	DB 18	Length 447
Best Local Similarity	72.4%	Pred. No. 6.3e-42		
Matches 307	Conservative 0	Mismatches 117	Indels 0	Gaps 10
QY	1165	TAGATATCGGCGAAACAAGCTTCCAGTCTCTTCATTCAGGAGCGCTATTCAATTCCTG	1224	
DB	437	TAGATATCGTTGGAAACAATATCCCTGTATCTTCATCCAGGATGCTATCTCTTCCCG	378	
QY	1225	ATTGTATTCAGCGTGTCAAGCCGCAACGACAGTGAATTCGCCAGGCTGCAACTGCAC	1284	
DB	377	ATCTGATCCACGCGCTCAAGCCGACAGGTCACAACGAGATCCCTCAGGCTGCCACTGCTC	318	
QY	1285	ATGATACGGCATGGGATTTCTCAGCCAGCAGCCAGCTCATTTGCATGCCCTCTTCGGG	1344	
DB	317	ATGACTCGGCTGGGACTCTTCAGCCAGCAGCCAGCAGATTCGACACACTCTCTGGG	258	
QY	1345	CAATGTACGACATGGAATCCCTCGTCAATGCGTCAATGTGATGGGTGGGCGTCCATA	1404	
DB	257	CTATGTCGGGATGGCATTCCTTCGTTCTTCCGACATGTTGATGGTTCGGTGTGCATA	198	
QY	1405	CCTTCGCACTGTGTCACGAGGCGCACTCGACCTTGGTCAAGTTTCGTTGGAAGACCC	1464	
DB	197	CCTTCGCACTGTGACAGATGACGGTGCATCCAAAGTCTGTCAAATTTCACTGGAAGTCTT	138	
QY	1465	TCAAGGAAGAGCGGCCCTGGTATGGGAAGAGCAGACGCTCTTTGGCGAAGAAATCCCG	1524	
DB	137	TGCAGGCAAGGCCAGCATGGTCTGGGAAGAGCCGACGACCTCTGCGAAGATCTCTG	78	
QY	1525	ACTTCCATCGACAAGACCTCTGGGATGCCATTGAATCTGGAAGGTACCTGATGGGAGG	1584	
DB	77	ACTTTCATGGCTCAGGATTTGCACGATGCAATCGAGGCTGGAGGCTATCCGGAGTGGGAAG	18	
QY	1585	TAAG 1588		
DB	17	TAAG 14		

RESULT 14  
US-09-417-507-19769 . . .  
; Sequence 19769, Application US/09417507  
; GENERAL INFORMATION:  
; APPLICANT: KEITH G. WEINSTOCK ET AL.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ASPERGILLUS  
; TITLE OF INVENTION: FOMIGATUS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: PATH99-10  
; CURRENT APPLICATION NUMBER: US/09/417,507  
; CURRENT FILING DATE: 1999-10-14

```

; NUMBER OF SEQ ID NOS: 44312
; SEQ ID NO 19769
; LENGTH: 534
; TYPE: DNA
; ORGANISM: A.fumigatus
US-09-417-507-19769

```

```
Query Match      5.6%; Score 214.8; DB 18; Length 534;
Best Local Similarity 66.8%; Pred. No. 5.3e-37;
Matches 306; Conservative 0; Mismatches 152; Indels 0; Gaps 0;
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QY	2205	CAGGCAAAATGTTTCATCCCTCTAAACACAGCGCGCATATACACCAACTCAATGAGCAACG	2264
Db	17		76
QY	2265	GATTCGCCACAAACGCAACCGGACCCATTAACAGAGGATTCTTACCGCACCTTGGCGGTA	2324
Db	77		136
QY	2325	TGTTAAATGGACCACACTAGTTCGGCGAGTCTCAGCCGAGCTTTCACGAGCTCTGTTCCCAAC	2384
Db	137		196
QY	2385	CGGGTCTCTCTTCAACTCACTCACGGTCTTCGAGAGCAATTCCTCGTCAAGCGCCATGC	2444
Db	197	CACGGGTCTTCTACAATCTTTGGTTCTCGCGAGAGCAGTTCGTTATTTCAGCCCATCC	256
QY	2445	GCATTGAAAACTCCACGTGCGGAGTGAAACCGTGGTAGAGCGTCATCATCCAGTGTA	2504
Db	257		316
QY	2505	ACGCGTTCGACACGAGCTCGCGCGCGGTTCGCTAGCTATTCGGCGTGGAAACCCCAT	2564
Db	317	ACCGCATCGATAACGACCTTGCACGACGGCTTCGGCGCGCTATTGTTGTGCGCGAGCCCTG	376
QY	2565	CCCGCGACCCAACTCTTACCAACAAGCGACCGTCCCCATCGGCACCTTCGGCACGA	2624
Db	377	AGCCCGACCCGACCTTCTATCACACACAAAGACTGCCGATGTCGGCACTTTTGGAAACCA	436
QY	2625	ATCTCTCGCGCTCGAGGGCTGAAAATCGCCCTCCTG	2662
Db	437	AGCTGAAGAAGCTTGATGGCTCAAGGTCGGCGCTCTG	474

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RESULT 15
US-09-417-507-19772
; Sequence 19772, Application US/09417507
; GENERAL INFORMATION:
; APPLICANT: KEITH G. WEINSTOCK ET AL.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ASPERGILLUS
; TITLE OF INVENTION: FUMIGATUS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH99-10
; CURRENT APPLICATION NUMBER: US/09/417,507
; CURRENT FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 44312
; SEQ ID NO 19772
; LENGTH: 522
; TYPE: DNA
; ORGANISM: A. fumigatus
US-09-417-507-19772

```

	Query Match	5.2%;	Score 199.2;	DB 18;	Length 522;
	Best Local Similarity	63.9%;	Pred. No. 1.6e-33;		
	Matches 331;	Conservative 0;	Mismatches 163;	Indels 24;	Gaps 1;
QY	1946	ACAGTTCCAACACAGTCATGTAGTTCGCGGAATCGATTTCACGATGACCTTTGTCTCA			
Db	12	ACAGTTCCAACCTGGTCACATGTTCGCGTGGTGTGACTTCACCTGAAGACCTCTCCTGCA			
QY	2006	GGCGCGCTGTACTCTCTACCTTGACACTCAATGTAATGCCATGGAGGTCCCAACTTCGA			
Db	72	AGCGCGTCTGTGTTTCGTACTCTGGACACTCAGCTGGAACCGTCACGGTGGCCCCAACTTTGA			



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 17:52:40 ; Search time 168 Seconds  
(without alignments)  
7049.915 Million cell updates/sec

Title: US-09-674-195C-1

Perfect score: 3862

Sequence: 1 ggatcctgctgctccgata.....aacaccttcataaaggatcc 3862

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents\_NA.\*  
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2: /cgn2\_6/ptodata/1/lna/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/lna/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/lna/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/lna/PTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/lna/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	442.2	11.5	8533	1	US-07-846-181-6
2	442.2	11.5	8533	1	US-07-845-989-6
3	439	11.4	3107	1	US-07-846-181-4
4	439	11.4	3107	1	US-07-845-989-4
5	249.2	6.5	2794	1	US-08-435-925C-1
6	156.2	4.0	3466	3	US-09-027-166-10
7	88.2	2.3	1518	3	US-08-695-987-1
8	88.2	2.3	1518	4	US-09-421-238-1
9	86.6	2.2	1518	3	US-08-695-987-3
10	86.6	2.2	1518	4	US-09-421-238-3
11	85	2.2	1803	3	US-08-657-868B-2
12	85	2.2	1829	3	US-08-657-868B-1
13	84.6	2.2	1449	3	US-09-027-166-6
14	81.8	2.1	1810	3	US-08-657-868B-3
15	78.8	2.0	1243	4	US-09-615-192A-121
16	75	1.9	1452	3	US-09-027-166-8
17	73.8	1.9	1502	4	US-08-980-241-7
18	67	1.7	7218	1	US-08-232-463-14
19	64.2	1.7	6840	4	US-08-980-241-8
20	60.8	1.6	515	2	US-08-975-316-42
21	60.8	1.6	515	4	US-09-615-192A-42
22	60.8	1.6	515	4	US-09-615-192A-119
23	59.6	1.5	2423	2	US-08-385-486A-25
24	59.6	1.5	2423	4	US-08-880-342-25
25	57.4	1.4	2264	4	US-09-126-109-9
26	55	1.4	642	4	US-09-134-001C-2412
27	50.2	1.3	1926	4	US-09-249-585A-4

28 50.2 1.3 1931 2 US-09-130-114-2 Sequence 2, Appl 1  
29 48.8 1.3 487 2 US-08-975-316-44 Sequence 44, Appl 1  
30 48.8 1.3 487 4 US-09-615-192A-44 Sequence 44, Appl 1  
C 31 44.8 1.2 1881 4 US-09-434-288-5 Sequence 5, Appl 1  
C 32 44.6 1.2 4403765 4 US-09-103-840A-2 Sequence 2, Appl 1  
C 33 44.4 1.1 4411529 4 US-09-103-840A-1 Sequence 1, Appl 1  
34 43.6 1.1 925 3 US-08-858-003-1 Sequence 1, Appl 1  
35 43.6 1.1 925 3 US-09-078-166-1 Sequence 1, Appl 1  
36 43.6 1.1 925 4 US-08-997-467-1 Sequence 1, Appl 1  
37 43.2 1.1 15872 4 US-09-105-537-1 Sequence 1, Appl 1  
C 38 42.8 1.1 390 4 US-09-197-649-7 Sequence 7, Appl 1  
C 39 42.8 1.1 1158 4 US-09-372-422A-21 Sequence 21, Appl 1  
C 40 42.6 1.1 168575 4 US-09-426-290-1 Sequence 1, Appl 1  
41 40.6 1.1 1820 1 US-08-173-508-7 Sequence 7, Appl 1  
42 40.6 1.1 1821 2 US-08-265-310-7 Sequence 7, Appl 1  
43 40.6 1.1 1821 3 US-08-951-742-7 Sequence 7, Appl 1  
44 40.6 1.1 11220 4 US-09-105-537-32 Sequence 32, Appl 1  
45 40.6 1.1 36778 4 US-09-105-537-5 Sequence 5, Appl 1

## ALIGNMENTS

RESULT 1

US-07-846-181-6

; Sequence 6, Application US/07846181

; Patent No. 5360732

; GENERAL INFORMATION:

; APPLICANT: BERKA, RANDY M

; APPLICANT: FOWLER, TIMOTHY

; APPLICANT: REY, MICHAEL W

; TITLE OF INVENTION: PRODUCTION OF ASPERGILLUS NIGER

; TITLE OF INVENTION: CATALASE-R

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: GENECOR INTERNATIONAL, INC.

; STREET: 180 KIMBALL WAY

; CITY: SOUTH SAN FRANCISCO

; STATE: CA

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/846,181

; FILING DATE: 19920304

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: HORN Ms, MARGARET A

; REGISTRATION NUMBER: 33401

; REFERENCE/DOCKET NUMBER: GC204-US1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-742-7536

; TELEFAX: 415-742-7217

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8533 base pairs

; TYPE: NUCLEIC ACID

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-07-846-181-6

Query Match 11.5%; Score 442.2; DB 1; Length 8533;

Best Local Similarity 54.8%; Pred. No. 1.2e-106;

Matches 1209; Conservative 0; Mismatches 778; Indels 220; Gaps 8;

QY 462 AGCTTACTCCAGCTTCATTCAGGGGTAATAATCGGCTCGCTCAAGCTTATCTCGCCT 521

Db 1925 AGCTTATCCCGCCAGCATCATTTAGATCTCAGCAATCGCTTCTTCTGGCTTTTGGCAGCTG 1984

QY 522 CGCGGGTGTGTTCTGACGCTGTCCCTACATGTGAGGGAGATGCCCTAGGGTCAGA 581  
 Db 1985 TTGCTGTATCGTGGGCTCAATGCCCCCTACCTGTGGGTGAATGAGTTTACCCAGG 2044  
 QY 582 AAGCCCCCTCGATGCGCGGCATGACACTCTCTCCGACCCCTACGGACCAATTTCTTAGCA 641  
 Db 2045 AGCAGGACAATGCTGGC-----GATACCATTTAGGTTCAGGGACGACCCATGACACA 2098  
 QY 642 AGTTTACATGAGAGTGAACAGTCGGTGTACAAACGAGCGTGGGTGTCCTACGAGG 701  
 Db 2099 CCCTGTATGATGACACCGGTAGTACATGACTACCGACTTTGGCAGCTCCGATCTCCG 2158  
 QY 702 ACCAACACAGCTGAAGCTTGGAAATAGAGGCCCAACTCTACTTTGAGGATTTTATCTTC 761  
 Db 2159 ACCAGACAGTCTCAAGCGCGGCGCTGTCTACCCCTGTTGGAGGACTTTATCTTC 2218  
 QY 762 GCGAGAGATCAACACTTTGATCATGAGAGGGTATGTAGATACA-----AAATATGTAC 817  
 Db 2219 GTCAGAGCTTACGCGGTTCCGACCATGAGCGTGTAGTACAGTAACCTGCTGCGGTGTGA 2278  
 QY 818 CGTGTGCAATCGCTCAATTTACGAGGTTCCCTGAGCGCGCCGTCCTACATGCTCG 877  
 Db 2279 GTAACATAAATGACCCAGTGGTTTCAATTAGTCCCGAGGCGCTGCTCCAGCGCGG 2338  
 QY 878 AGGAGCTGGTCCCATGGCCTATTCACATCCTATATAAATGCTGTCGGAATATACACAGCCG 937  
 Db 2339 TGGTGGCGGTGCATATGTTACTTTCAAACTCTACCGCGACTGGTTCGAAACGTCACGGCTG 2398  
 QY 938 ATCCCTTCTGNACCGCGCAGGAAGACAGACACAGTATTCGTGGGTTTTCTACAGTCGC 997  
 Db 2399 CGATTTCTTAGTCCCAACCAATAGAGAGACCCCTATGTTGTGCGCTTCTACTGTGGT 2458  
 QY 998 TGGTAGCAGAGGAGTGTGACTCTGCTCGGATATCCAGGATTTCCGACCCGCTGTGA 1057  
 Db 2459 CGGTTCCGTGGTAGTGTGACACTGCGGTGATGTTTCACGGTCACGCTTGTGCGTTCTA 2518  
 QY 1058 TACCGATGAAGGCAATTTGGTGAAGCATATATCGTGGTAGTCAATCTATACACAGACA 1117  
 Db 2519 CACTGACGAGGTAACATGTA-----TCATTGATGTTGTCACCCAA 2560  
 QY 1118 ACAATATGAATACAAACCCAGGACCTAGGCTGACTACTCGGCAATGTAGATATCGTCGG 1177  
 Db 2561 CAATTAATCAATATGTTACAGATATGTCCT-----ACTAGACATCGTCGG 2609  
 QY 1178 AAACAAGCTTCAGTCTTCTTCAATTCAGGAGCTATTCATTCCTGATTTGATTCACGC 1237  
 Db 2610 TATCAATTTCCGCCCCCTTCTATCCAGGAGGCCATCCAGTTCCTCCGATCTTTGTCACGC 2669  
 QY 1238 TGTCAAGCGGCAACAGACAGTGAATTTCCCGAGGTCGAACCTGCATGATGATGAGGATG 1297  
 Db 2670 CATCAAGGCCATGCCCCAACAATGATGATCCCGCAGGCGGCTACTGCACACACTTCCGCTG 2729  
 QY 1298 GGATTTCTCAGCCAGGAGCCAGCTCATTTGCATGCTCTCTCTGCGCAATGTGAGGACA 1357  
 Db 2730 GGACTTTCTCAGCCAGCAGACATGCCCCCTCCACAGTGCCTTGTGGCTGATGTGTGTA 2789  
 QY 1358 TGGAACTCCCTCGCTCAATGCTGATGTTGATGGGTGGGCGCTCCATACCTTCCGACATGT 1417  
 Db 2790 CGGTATTCCTGTTCTTCCGACATGAAGGGCTACGGATCCACAGCTTCCGCTTCGT 2849  
 QY 1418 CACCGAGAGGCAACTCGACCTTTGGTCAAGTTTTCGTGGAGACCCCTCCCAAGGAAGAGC 1477  
 Db 2850 CGCTGCCAAATGGCACTTCCAAAGGTGGTCCGAACACCTTGGAAATCCCAACAGGGTGTTC 2909  
 QY 1478 GGGCTGGTATGGAAGGAGCAGAGCTTGTGGCGGAAGATCCCGACTTCCATCGACA 1537  
 Db 2910 CAGTCTGGTGGTGAAGCTCAGGCGCTGCTGGTGAAGAACAGTGAAGTACACCGGCA 2969  
 QY 1538 AGACCTCTGGGATGCCATTTGAATCTGGAAGGTAGCCCTGAGTGGGAGGTGAAGATATGATTC 1597  
 Db 2970 GGATCTGTACAAATGGATGCCCAATGGCCACTACCCGGAATACGAGGTACGCCAAT---- 3025

QY 1598 CCCAAATCANTAGTTCTGTGACAGTGTCTCTCTGCTGTGGTGTGCTCTTTTGTCTTTT 1657  
 Db 3026 -----CCCTGTGATGTCTATC 3040  
 QY 1658 TCTATATCTTCAACTAAGACTGACTTTATATACGTTTTTACTCATATAGCTGGGCTTTCAA 1717  
 Db 3041 GATAGAGC-----CTTTGCTGACAAATCCCTAGCTTCCAAAGGCCAG 3081  
 QY 1718 TTGGTGAATGAAGCAGATCAATCCAAATTTGATTTGATCTATAGATCCCAACCAAAATC 1777  
 Db 3082 ATCATGATGAGCTGACATGCTTCTGCTTGGCTTCGACCTTCTGGATCCCAACCAAGTTG 3141  
 QY 1778 ATCCAGAGAAGACTTGTCTCTTACCCCCAATCGGAAATATGCTTTGAAACGAAACCCA 1837  
 Db 3142 GTCCCCGAGGAGTGTGCTCTTACACTCTCTCGGAATGATGAGCTCAATGCAACCC 3201  
 QY 1838 AAAAGTATTTTCCGGAACCTGAGCAGATCATGTTGGTCCACCCCTATATATTGGAA 1897  
 Db 3202 ACCAACTACTTTGCTGAAGTTGAACAGGCTGGTGTATGTATCCCATTCAT----- 3253  
 QY 1898 TATGAATACATGATAGCTAGATCAAGCGTATATCTAAATATATTTCCACAGTTCCAACC 1957  
 Db 3254 -----CAATGCCAGACATAATCTAATCTCTGCTGAGTTCCAACC 3291  
 QY 1958 AGTCTAGTGTAGTTCGGGAATCGATTTTCAGGATGACCCCTTGTGTCAGGGCGCTGTGA 2017  
 Db 3292 CGGTACGCTGCTGCTGCTGCTTACCTTACCGCAGACCCCTGCTGCAAGGCGCTCTCT 3351  
 QY 2018 CTCTACTTTCGACACTCAATTTGAATGCCATGAGGTGCCAATTCGAGCAACTGCGGAT 2077  
 Db 3352 CTCTACTCTCGACACTCGTGTGACCCCTGACGGGTGCCACTTCGAGCAATTCGCCGT 3411  
 QY 2078 CAACAGACCCCGCATTCCTTCCATTAACAACATTCGCGACGGTGTGCTGTGAAGCTACTTCT 2137  
 Db 3412 CAACCGTCTCGCAAGCCGTTCAACAACAACACCGTGACG----- 3452  
 QY 2138 CACTACCATGTCACTTCCATCTTGACCAATCGATTTGTATAGAGTATTAACATCCCC 2197  
 Db 3453 ----- 3452  
 QY 2198 GTCTGCACAGGACAAATGTTTCATCCCTCTAAACAGCGCCGATATACACCACTCAATG 2257  
 Db 3453 -----GCTTCGCGCAGCAGATCCCAACCACTGCGCTTACACCCCAACAGCATG 3508  
 QY 2258 AGCAACGGATTTCCACAAACAGCAACCGGACCCATTAACAGAGATTTCTTCAACGACCT 2317  
 Db 3509 AGCAACGGTTTACCCATGCAAGCAACAGCAGACCCAGGCTCATGTTTCTTCAACGCGCC 3568  
 QY 2318 GGGGTATGTAATGACCACTAGTGGCGAGCTCAGCCGAGCTTCAACGAGCTCTGG 2377  
 Db 3569 TACCGTACGCTTCCGCGCATCTGCTCCGCGACAGCCGCGACTTCAATGACCACTGG 3628  
 QY 2378 TCCCAACCGGCTCTTCTTCAACTCACTCACTGCTTCGAGAGCAATTTCTGCTCAAC 2437  
 Db 3629 TCCAGCGCGCATGTTCTGGAATCTCTGATCCCCGCTGAGCAGAGATGTTGTGTCAC 3688  
 QY 2438 GCCATCGCTTCGAAAATCCCACTGCGGAGTGAACACCGTGGCTAAGAACGTCATCATC 2497  
 Db 3689 GCCATTGCTTTGAGAACTCCAAGTTAAACAGCCCAACGCTTCCGGAAGACGTTGTCAAC 3748  
 QY 2498 CAGCTGAACCGCTCGACAGGACCTCGCGCGCGCTGCGGTAGCTATCGGGGTGCA 2557  
 Db 3749 CAGCTGAACATGGTCAACAACACCTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 3808  
 QY 2558 CCCCATTCGCGGACCAACTTCTACCAACAAGCAACCGCTCCCACTCGGACCTTC 2617  
 Db 3809 GAGCCCTCCCAACCGCAGCTTACTACCTTCCAAAGACCTTCCACAGCTCGGTACCTTC 3868  
 QY 2618 GGCAGCAATCTCTCGGCTCGAGGCTGAAATTCGAAATTCGCTTCTGAC 2664  
 Db 3869 GGCAAGCCCTCTCAGCATCGAGGCTCTGCAAGTCTGCGCTTCTCTGCG 3915

## RESULT 2

```

US-07-845-989-6
; Sequence 6, Application US/07845989
; Patent No. 5360901
; GENERAL INFORMATION:
; APPLICANT: BERKA, RANDY M
; APPLICANT: FOWLER, TIMOTHY
; APPLICANT: REY, MICHAEL W
; TITLE OF INVENTION: PRODUCTION OF ASPERGILLUS NIGER
; TITLE OF INVENTION: CATALASE-R
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENENCOR INTERNATIONAL, INC.
; STREET: 180 KIMBALL WAY
; CITY: SOUTH SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/845,989
; FILING DATE: 19920304
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HORN MS, MARGARET A
; REGISTRATION NUMBER: 33401
; REFERENCE/DOCKET NUMBER: GC208-US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-742-7536
; TELEFAX: 415-742-7217
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8533 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; NS-07-845-989-6

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Query Match	11.5%;	Score	442.2;	DB 1;	Length	8533;
Best Local Similarity	54.8%;	Pred.	No. 1.2e-106;			
Matches 1209;	Conservative	0;	Mismatches	778;	Indels	220;
Gaps	8;					
QY	462	AGCTTACTCCAGCTTCAATTCAGGGGGTAAAAATCGGTCGCTCAGCTTATACTCGCCT	521			
Db	1925	AGCTTCATCCCCAGCATCATTAGATCTCAGCAATGCGTCATTTCTGGCTTTTGCCAGCTG	1984			
QY	522	CGSCGGGTGTGTTTCTGCAGCCTGTCCCTACATGTCAGGGGAGATGCCTAGCGGTACGA	581			
Db	1985	TTGCTGGTATCGGTGGGGTCAATGCCCTTACTCTGTGGGTGAAATGAGTTTCACCCAGG	2044			
QY	582	AAGGCCCTTCGATCGCCGCCATGACACTCTCTCCGACCCCTACGGACCAAGTTTCCTTAGCA	641			
Db	2045	AGCAGGACAAATGCTGSC-----GATACCATTGAGGTCACGGAGCAGCCCATTTGACAACA	2098			
QY	642	AGTTTACATTTGACGATGAACAGCTCGGTGCTACACAGGACAGCTGGGTGGTCCCATCGAGG	701			
Db	2099	CCCTGTATGTCAATGACACCGGTAGTACATGACTACCGACTTTGGCACTTCCGACTCTCCG	2158			
QY	702	ACCAACACACCCCTGAAGGCTTGAAATAGAGCCCAACTCTACTTGAGGATTTTATCTTCC	761			
Db	2159	ACCAGACCACTCAAGCCCGGGCCCGTGGTCTTACCCCTGTGGAGGACTTTTATCTTCC	2218			
QY	762	GCCAGAGAGTTCAACACTTTTGATCATGAGAGGGTATGTAGATACA-----AAATATGTGAC	817			
Db	2219	GTCAAGAGCTTACAGCGGTTTCGACCAAGAGCGGTGTAAGTACAGTAACGTGCTCCGGTGTA	2278			
QY	818	CGTGTTCGAATCCGCTTAATTCATTTTACGAGGTTTCTTGAGCGCGCCCTCCATGCTCG	877			

Db	2279	GTAACAATAAATTGACCCAGTGGTTTTCAATTAGGTCGCCGAGCGCGTCTGTCACGCGCCG	2338
QY	878	AGGAGCTGGTGCCCATGGCGTATTACATCTCCTATAATAACTTGGTCGAATATFCACAGCGCCG	937
Db	2339	TGTCGCGGTGCATATGGTACTTTTCAAAATCCTAGCCGCACTGGTGCAGACGTCCAGGGTTC	2398
QY	938	ATCCCTTCTTGAACGCGGAGGAAGACACACACACAGTATTCTGTCGGGTTTTCTACAGTCGC	997
Db	2399	CGATTTCTTTGATGGCAACGATAAGGAGACCCCTAATGTTCTGCTTCTCTACTGTGGT	2458
QY	998	TGTTAGCAGAGGCAGTGTGTACTCTGCTCGCGATATCCACGGATTTGCGACCCGTCGTATA	1057
Db	2459	CGGTTTTCCGTGTGTGTGTGACACTGCGGTGATCTTCACGCTACGCTTGTCTGGTTCTA	2518
QY	1058	TACCGATGAAGGCAATTTTGGTAAGCATTTATATCTGCTAGTCTCATCTCATACAGACACA	1117
Db	2519	CACTGACGAGGGTAACTATGGTA-----TCTTGTATGGTCAACCCAA	2560
QY	1118	ACAAATATGAATACAAACCCAGGACCTAGGCTGACTACTCGGCAATAGATATATGTCGG	1177
Db	2561	CAATAATTCAATACATGCTAAACAGATATGCTCT-----ACTAGACATCGTCGG	2609
QY	1178	AAACAACGTTCCAGTCTTCTTCAATTCAGACAGCCGTTTCAATTCCTTGATTTGATTCACGC	1237
Db	2610	TATCAATTTGCGCCCTTCTTATCCAGACGCCATCCAGTTCCCGGATCTTGTCCACGC	2669
QY	1238	TGTCAAAGCCCAACACAGACAGTGAATTTCCCAAGGCTGCAACTGCACATGATFACGGCATG	1297
Db	2670	CATCAAGCCCATGCCCAACAATGAGATCCCCAGGCGCTACTGCACACACTTCGCGTTG	2729
QY	1298	GGATTTCTCTCAGCCAGAGCCGACGCTCATTTGCATGCCCCCTTCTTGGGCAATGTCAGGACA	1357
Db	2730	GGACTTTCTTCAGCCAGCAGACACTCCCTCCACAGTGCCTTGTGGCTGATGCTCTGGTAA	2789
QY	1358	TGGAATCCCTCGCTCAATGGCTCATGTTGATGGTGGGGCTCCATACCTTCCGACTTGT	1417
Db	2790	CGGTATTTCTCTGTTCTTTCGCCACATGAACGCTACGAGTCCACAGCTTCCGCTTGT	2849
QY	1418	CACCGACGAGGGCAACTFCGACCTTGTCAAGTTTCGCTGGAGACCCCTCCAGGAAGACG	1477
Db	2850	CGCTGCCAATGGCACTTCCAAGGTGGTGCAGAACACCTTGGAGTCCCAACAGGGTGTGC	2909
QY	1478	GGGCCTGSTATGGGAAGAGGCACAGGCTCTTGGCGGAAGAATCCCGACTTCCATCGACA	1537
Db	2910	CAGTCTGGTGGGATGAAGCTCAGGCCGCTGCTGTGAACAGTGTACTACCCAGCCCA	2969
QY	1538	AGACCTCTGGGATGCCATTGAATCTGGAAGGTACCTCGAGTGGGAGGTGAAGATATGATTTC	1597
Db	2970	GGATCTGTACAAATCGATGCCAATGGCCACTACCCGAAATACAGAGTCCAGCCAAAT	3025
QY	1598	CCCCAAATCATAGTTCTGACAGTGTTCCTGCTCTGTCGGTGTCTTTTGGTCTTTT	1657
Db	3026	-----CCCTTGATGTCCTATC	3040
QY	1658	TCATATCTTCAACTAAGACTGACTTTATATACGTTTTTACTCATATAGTGGGCTTTCAA	1717
Db	3041	GATAGAGC-----CTTTTGTGACATCCCTAGCTCCCAAGCCCAAG	3081
QY	1718	TTGGTGAATGAAGCAGATCAATCCAAGTTTGATTTTCGATCTATAGATCCCACCAAAATC	1777
Db	3082	ATCATGGATGAGGTGACATGCTTCTGTTCCGGCTTCGACCTTCGTGATCCCAAGTTG	3141
QY	1778	ATCCAGAGAAGACTTGTTCCTTCCACCCCAATCGAAAAATGGTCTTGAACCCGAAACCCA	1837
Db	3142	GTCCCCGAGGAGTTGTCCTTACACTCTCTCGAATGATGGAGTCAATGCCAACCCC	3201
QY	1838	AAAAGTTATTTTGGCGAACTGAGCAGATCATGGTTGGTCCACCCCTATATATTTGGAA	1897
Db	3202	ACCAACTACTTGTGCTGAAGTTGAACAGGCTGGTGTATGTATCCCATTCAT-----	3253
QY	1898	TATGAATACATGTATAGCTAGATGAAGGGTATATCTAAATATATTTTCCACAGTCCCAACC	1957
Db	3254	-----CAAAATGCCAGACATAATCTAACTTCTGAGTTCCCAACC	3291

QY	1958	AGGTCATGTAGTTCGCGAAATCGATTTCACGGATGACCCCTTGCTTCAGGCGCGCTGTGA	2017
Db	3292	CGGTACAGTCTGTTCTGGCATGTACTTCACGAGACCCCTGCTGCAAGCGCGTCTCTT	3351
QY	2018	CTCCTACTCTGACACTCAATTTGAATCCGATGAGGTCCCACTTCGAGCAACTGCCGAT	2077
Db	3352	CTCCTACTCTGACACTCAGTTGACCGCTGACGGCGGTCCCACTTCGAGCAATCCCGT	3411
QY	2078	CAACGACCCCGCATCCCATTTCCATACAAACAATCGCGAGCGTCTGGTAAGCTACTTCT	2137
Db	3412	CAACCGTCTCGCAAGCCGTTCCACAACAACACCGTGAGC	3452
QY	2138	CACCTACCATGTCAACTTCCATCTTGACCCAAATCGATTTGTATAGAGTATTAAACATCCCC	2197
Db	3453	-----	3452
QY	2198	GTCTGCACAGGACAAATGTTTCATCCCTCTAAACACGGCGGCATATACACCCAACTCAATG	2257
Db	3453	----GCTTCGGCAGCAGCAGTCCCCACCACTGGGCTTACCCCCAACACGATG	3508
QY	2258	AGCAACGGATTCTCCACAAACGACCAACCGGACCCATAACAGAGGATTTCTACCGCACCT	2317
Db	3509	AGCAACGGTTACCCCATGTCAAGCCAAACAGACCCAGGGTCTATGGTTTCTTTCACCGCGCC	3568
QY	2318	GGCGGTATGTTAAATGGACCACTAGTGCAGAGCTCAGCCCGAGCTTCAACGACGTCGG	2377
Db	3569	TACCGGTACGTTCCGGCCATCTCGTCCGGCAGACCGCCGACCTTCANTGACCACTGG	3628
QY	2378	TCCCAACCGGGTCTCTTCTACAACTCACTACGGTTCGAGAAACAAATTCCTCGTCAAC	2437
Db	3629	TCCACGCGCGCATGTCTTGGAACTCTCTGATCCCGCTGAGCAGCAGATGTTGTCAAC	3688
QY	2438	GCCATCGGTTCCAAAACCTCCACAGTCGGAGTGAAACCGTCGGTAAGAACGTCAATC	2497
Db	3689	GCCATTGCTTTGAGAACTCCAAGTTTACACGCCCGAGTTTCGGAAGAAAGTTGTCAAC	3748
QY	2498	CAGCTAAACGGGTGCAACAGCACTTCGCCCGCGCGTGCAGCTAGCTATCGGCGTCGAA	2557
Db	3749	CAGCTGAACATGGTCAACAAACAACCTCGCGCGTCTGCTGCTGCTGGTCTCGAT	3808
QY	2558	CCCCATCCCGGACCCCAACCTTCTTACACAAACAAGGAACCGTCCCATCGGACCTTC	2617
Db	3809	GAGCCCTCCCCAAACCGACTTACTACACCTCCACACAGACCTCCACGTCGGTACCTTC	3868
QY	2618	GGCAAGATCTCCTGGGGTTCGACGGGTGAAATGCGCCCTGTGAC	2664
Db	3869	GGCAAGCCCTCTCTCAGCATCAGAGGTTGCAAGTCTCGGCTCTTCTGGC	3915

### RESULT 3

RESULT 3  
US-07-846-181-4

03 07 040-101-4  
; Sequence 4, Application US/07846181

; Patent No. 5360732

GENERAL INFORMATION:

APPLICANT: BERKA, RANDY M

APPLICANT: FOWLER, TIMOTHY

APPLICANT: REY, MICHAEL W

1. TITLE OF INVENTION: PRODUCTION OF ASPERGILLUS NIGER

; TITLE OF INVENTION: CATALASE-R

**NUMBER OF SEQUENCES:**

**; CORRESPONDENCE ADDRESS:**

ADDRESSEE: GENENCOR INTL

STREET: 180 KIMBALL WAY

CITY: SOUTH SAN FRANCISCO

; STATE: CA

COUNTRY: US

; ZIP: 94080  
; COMPUTER PROCESSOR:

COMPUTER READABLE FORM:

```

: MEDIUM TYPE: Floppy disk
:
: COMPUTER: IBM PC compatible
:

```

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/846.181  
 FILING DATE: 19920304  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: HORN MS, MARGARET A  
 REGISTRATION NUMBER: 33401  
 REFERENCE/DOCKET NUMBER: GC204-US1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-742-7536  
 TELEFAX: 415-742-7217  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3107 base pairs  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: join(327..620, 683...907, 969...1385, 1440..1604,  
 LOCATION: 1654..2745)  
 US-07-846-181-4

Query Match	11.4%;	Score 439;	DB 1;	Length 3107;
Best Local Similarity	54.9%;	Pred. No. 5.3e-106;		
Matches 1195;	Conservative 0;	Mismatches 760;	Indels 220;	Gaps 8;
QY	494	ATGGGTCGCTCAAGCTTATACTCGCCTCGCGGGGTGTGTTCTGCGAGCTGTGCCCTAC	553	
DB	327	ATGGCTCATTTCTGCTTTTCCAGCTGTTGCTGCTATCGCTGGGCTCAATGCCCTAC	386	
QY	554	ATGTCAGGGAGATGCCTAGCGGTGAGAAAGGCCCTCGCATGCCGCCATGACACTCTC	613	
DB	387	CTGTCGGGTGAATGAGTTTCACCCAGGAGCAGACAAATGCTGCG-----GATACCAAT	440	
QY	614	TCCGACCCCTACGGACCAAGTTCTTTAGCAAGTTTTACATGACGATGAACAGTCGGTGCTA	673	
DB	441	GAGTGCACGGAGCAGCCCATTTGACAAACCCCTGTATGTCATGACACCGGTAGCTACATG	500	
QY	674	ACAACGGACGTGGGTGTCCCATCGAGGACCAACACAGCCTGAAGGCTGGAAATAGAGGC	733	
DB	501	ACTACCGACTTTTGGCACTCCGATCTCCGACCAAGCCAGTCTCAAGGCCGGCCCCGTGGT	560	
QY	734	CCAACTCTACTTGAGGATTTTATCTCCGCCAGAAATTCAACACTTTTGATCATGAGAGG	793	
DB	561	CCTACCCCTGTGGAGGACTTTATCTCCGTGAGAAGCTTCAGCGGTTTCGACCATGACCGT	620	
QY	794	GTATGTAGATACA----AAATATGTGACCGTGTGTGCAAAATCCGCTAATTCANTTTACGC	849	
DB	621	GTAAGTACAGTAAGTCTGCGGTGTGTAGTAAACATTAATGACCCAGTGGTTTCAATT	680	
QY	850	AGGTTCTGAGCGGCGCTCCATGCTCGAGGAGCTGGTGCCCATGCGGTATTCACATCCCT	909	
DB	681	AGGTCCCGGAGCGCTGTCCAGCGCGTGTGCGCGTGCTATGTTACTTTTCAAAATCCT	740	
QY	910	ATAATACTGGTCGAATATCACAGCGCATCTTCTTGACGGCGGAGGAAACGACAC	969	
DB	741	ACGCGGACTGGTCGAAGCTCACGGCTGCCGATTTCTTGAGTGCCAACGATAAGAGACACC	800	
QY	970	CAGTATTCGGTCGGTTTTCTPACAGTCGCTGGTAGCAGAGGACAGTGTGACTCTGCTCGCG	1029	
DB	801	CTATGTTCTGTGCTTCTCTACTGTGTGCTGGTTTCGTTGCTAGTGTGTGACATGCGCGTG	860	
QY	1030	ATATCCACGGATTTGGGACCCGCTCTATACCGATGAAGGCAATTTTGGTAGCATATAA	1089	
DB	861	ATGTTCCAGGTCAGGTTGTGCGGTTCTACACTGACAGGGTAACTATAGTA-----	911	
QY	1090	TCGTGTAGTCATPACTATAACAGCACACAATAATGAATACAAACCCAGGACCTAGGCT	1149	
DB	912	-----TCTTGATATGGTCACCCCAACAATAATTCAATACATGCTACACATATGCT	962	
QY	1150	GACTACTCGGCATGTAGATATCGTCGGAAACAACGTTTCCAGTCTTCTTTCATTCAGGAC	1209	

Db 963 -----CTACTAGACATCTCGGTATCAATTTTCGCCCTTCTTTCATCCAGAGC 1011  
Qy 1210 CTATTCATATCCCTGATTTGATTCACGCTGTCAAGCCGCAACAGACAGTGAATTCGCC 1269  
Db 1012 CCATCCAGTTCCCGGATTTGTCACGCGCATCAAGCCCATGCGCAACATGAGATCCGCC 1071  
Qy 1270 AGGCTGCAATCGACATGATAGCGATGGGATTTCTTCAGCCAGCCAGCGCTCAATGC 1329  
Db 1072 AGGCGCTACTGACACACTTCCGCTTGGGACTTCTTCAGCCAGCAGAGCTCCGCCCTC 1131  
Qy 1330 ATGCCCTCTCTGGGCAATGTCAGGACATGGAATCCCTCGCTCAATGCGTCAATGTTGATG 1389  
Db 1132 ACAGTGCCTTGTGGCTGATGCTGTGACGCTATTCCTCGTCTTTCGCCACATGAAGC 1191  
Qy 1390 GGTGGGGCGTCATACCTTCCGACTGTTCACGAGGAGGGCACTCGACCTTGGTCAAGT 1449  
Db 1192 GCTACGGATGTCACAGCTTCCGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1251  
Qy 1450 TTCGCTGGAAGACCTCCAAAGGAGAGCGGCTGCTGATGGAGAGGACACAGGCTCTTG 1509  
Db 1252 CACCTTGGAGTCCCAACAGGCTGTGCGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1311  
Qy 1510 GCGGAAGAATCCCGACTTCCATCGACAGAGCTCTGGGATGCGCATTTGAATCTGGAAGT 1569  
Db 1312 CTGGTAAGAACAGTGAATACCAAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1371  
Qy 1570 ACCCTGAGTGGGAGTGAATATGATTTCCCAATCATTTAGTCTGACAGTGTTCCTCT 1629  
Db 1372 ACCCGAAATACGAGGTGACCCA----- 1393  
Qy 1630 GCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1689  
Db 1394 -----ATCCCTGATGCTATGATAGAGC-----TUTTT 1423  
Qy 1690 CGTFTTACTATATAGCTGGGCTTTCATTTGCTGATGATGAGCAGATCAATCAAGTTTCA 1749  
Db 1424 GCTGCAATCCCTAGCTCCAAAGCCAGATCATGATGAGGCTGATGCTTTCGTTTCGG 1483  
Qy 1750 TTTTCGATCTATTAGATCCCAACCAATATCATCCAGAGAACTTGTTCCTTTTTCACCCCAAT 1809  
Db 1484 CTTTCGACCTTCTGGATCCCAACCAAGTTGGTCCCGAGGAGTGTTCCTTACACTCTCT 1543  
Qy 1810 CGGAAATAGTCTTGAACCGAACCACCAAGTTATTTTGGCGAACTGAGCAGCATAT 1869  
Db 1544 CGGAATGATGAGCTCAATGCCAACCCCAACTACTTGTGTAAGTTGAACAGGCTGG 1603  
Qy 1870 GGTGCTGACCCCTTATATTTGGAATATGATATGATATGATATGATATGATATGATAT 1929  
Db 1604 TGATGATATTCCTCATTCAT-----CAATGCCAG 1633  
Qy 1930 ATCTAAATATATTTCCACAGTTCACACAGGCTCATGTAGTTCGCGGAATCGATTTCCAGG 1989  
Db 1634 ACATAATCACTTCTGAGTTCCACACCGGCTCACGCTGCTGCTGCTGCTGCTGCTGCTGCT 1693  
Qy 1990 ATGACCTTGTCTTTCAGGCGGCTTGTACTCTTACCTTACCTTACCTTACCTTACCTTAC 2049  
Db 1694 ACGACCCCTGCTGCAAGGCGCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1753  
Qy 2050 GAGTTCCTCACTTTCGAGCACTCGGATCAACAGACCCCGCTCCATTCATTAACAACA 2109  
Db 1754 GCGTTCCTCACTTTCGAGCAATCCCGTCAACCGTCTCGCAAGCCGCTTCACACACACA 1813  
Qy 2110 ATCCGAGCGGTGCTGTAAGCTACTTCTACCTACCATGTCATTCATCTTTGACCCAA 2169  
Db 1814 ACCGTGAG----- 1822  
Qy 2170 TCGATTTGTATAGATATTAACATCCCGCTGTCGACAGGACAAATGTTTCATCTTAA 2229  
Db 1823 -----GCTTCGCGCAGCAGCAGATCCCCACCA 1850  
Qy 2230 CACGCGCGCATATACCCCACTCAATGAGCAAGGATTCACCAACCAACCAACCGGAC 2289  
Db 1851 CNACTGGGCTTACACCCCAACACAGCATGAGCAAGGTTACCCCATGCAAGCCACACAG 1910

Qy 2290 CCATACAGAGGATTTCTTCCAGCAGCTTGGGCTATGTAAATGGACCACTAGTTCGCGA 2349  
Db 1911 CAGGCTATGTTTCTTCCAGCGGCTTACCGCTACGCTTCCGGCCATCTGTCGCGCA 1970  
Qy 2350 GCTCAGCCGAGCTTCAACAGAGCTGTGGTCCCAACCGCTCTTCTTCAACTCACTAC 2409  
Db 1971 GACCAGCCGAGCTTCAATGACCACTGTTGTTCCAGCCGCTGTTCTTGAAGTCTCTGAT 2030  
Qy 2410 GGTCTTCGAGAAACAATTTCTCTGTCAGCCATGCGCTTCCGAAACTTCCACGTGCGGAG 2469  
Db 2031 CCGCGTTCAGCAGAGATGTTGTCAGCGCATTTGTTGAGAACTTCAAGTTTAAACAG 2090  
Qy 2470 TGAACCGTTCGTAAGAACGTCATCTCAGCTTGAACCGCTGACAAAGACCTTCTTACCA 2529  
Db 2091 CCCCCAGTTTCGGAAGAAGCTTGTCAACCAAGCTTGAACATGTTCAACAACAACCTCGCGT 2150  
Qy 2530 CCGGCTCGCTAGCTATCAGCGCTGCAACCCCATCCCGGAGCCCACTTCTTACCA 2589  
Db 2151 CCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2210  
Qy 2590 CAAGGCAACGTCCTCCCATCGCACCTTTCGCGCAAGAACTCTCTGCGGCTCGACGGCTGAA 2649  
Db 2211 CAACAAGCTTCCAAAGCTTCGTAACCTTTCGCGCAAGCCCTCTCTCAGCATCGAGGCTGCA 2270  
Qy 2650 AATCGCTCTCTGAC 2664  
Db 2271 GGTGCTTCTCTGCG 2285

RESULT 4  
US-07-845-989-4  
; Sequence 4, Application US/07845989  
; Patent No. 5360901  
; GENERAL INFORMATION:  
; APPLICANT: BERKA, RANDY M  
; APPLICANT: FOWLER, TIMOTHY  
; APPLICANT: REY, MICHAEL W  
; TITLE OF INVENTION: PRODUCTION OF ASPERGILLUS NIGER  
; TITLE OF INVENTION: CATALASE-R  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENENCOR INTERNATIONAL, INC.  
; STREET: 180 KIMBALL WAY  
; CITY: SOUTH SAN FRANCISCO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/845,989  
; FILING DATE: 19920304  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HORN MS, MARGARET A  
; REGISTRATION NUMBER: 33401  
; REFERENCE/DOCKET NUMBER: GC208-US1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-742-7536  
; TELEFAX: 415-742-7217  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3107 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: join(327..620, 683..907, 969..1385, 1440..1604,





QY	1804	CCCAATCGGAAAAATGGTCTTGAACCGGAAACCCAAAAAGTTATTTTTGCAGAACTGACGA	1863
Db	1425	CCAGATTGTGCGATGAGTCCCAAGGCGCAAGCCCTTTGGCTTCGACTTGCCTGGACCCGCAAAA	1484
QY	1864	GATCATGGTTGGTCCACCCCTATATATTTCGGAATATGAATACATGATATAGCTAGATGAA	1923
Db	1485	GATCATCCCGAGGAGTAGCGCCCTCTTGACGAAGCTGGCGCTCTTTGAAGCTGGATCGCAA	1544
QY	1924	GGGTATATCTAAATATATTTCCAC-----AGTTCCAAACAGGTCATGTAGTTCG	1972
Db	1545	TCCGACCAACTACTTCGCCGAGAGCGGACAGGTGTCATGTTCCACCCCGGTTCATATCFCCG	1604
QY	1973	CGGAATCGATTTCAGGATGACCCCTTTGCTTCAGGGCCGCTTGTACTCTCTACCTTGACAC	2032
Db	1605	CGGCATCGACTTCACGGAGGATCCCTGCTACAGGGACGCTCTTTTCGTACCTTGACAC	1664
QY	2033	TCAATTGAATCGGCATCGAGGTCCCAACTTCGAGCAACTCCGATCCGATCAACAGACCCCGCAT	2092
Db	1665	GCAGCTGNAACGGGAATGGCGGCCCAACTTTGAGCAGCTGCCCATCAACATGCGCGGGT	1724
QY	2093	CCCAATTCGATAAACAATCGGACGGTGTGTGAAGTACTTCTCACCCTACCATGTCAA	2152
Db	1725	GCCGATTTCACAACAATAATCGCAGCGCGCGCCAGATGTTTCATCCACAGGAACAAGTA	1784
QY	2153	CTTCCATCTTGACCCCATCGATTGTATAGATTATTAACATCCCGCTGTCACAGACAA	2212
Db	1785	TCCTGTGAAGTCCCTC-----TTTGTGCTCGATCGTTGTGTGCGCGCTTGCTGA-----	1833
QY	2213	ATGTTTCATCCTCTAAACACGGCGGATATACACCAACTCAATAGCAACGGATTCACA	2272
Db	1834	-----CAGACGCGAGTACACTCCCACACCCCTGAAACAGTGGTTATCCG	1875
QY	2273	CAACAGCCCAACCGGACCCCAATAACAGAGGATTTTCACCGCACCTGGCGGTATGTTAAAT	2332
Db	1876	CGGCAAGCCCAACCAAAATGCGGACGCGGATTTCTCACAGCGCTGGCCGTACCGCCAGC	1935
QY	2333	GGACCACTAGTGTGCGGAGCTCAGCCGAGCTTCAACGAGCTGTGTTCCCAACCGGCTCTC	2392
Db	1936	GGTGGCTCTGCTGCTGAGGTGTGCCACAGATTTCAACGACCACTGTGTGCGAGCCGCTCTC	1995
QY	2393	TTCTACAACCTCACTACGCTTTTCGAGAAGCAATTCCTCGTCAACGCCCATGGCTTCGAA	2452
Db	1996	TTCTTCAACTCCCTCACTCCCGTCGAACAACAGTTCCTGCTCAAGCCCATGCGCTTCGAA	2055
QY	2453	AACTCCCACTGCGGAGTGAACCCGTGCGTAAAGAGTCATCATCCAGCTGAACCGCTC	2512
Db	2056	ATCAGCCTTGTGAAGTCGGAAGAAGTCAAGAAGAAGCTGCTCACCAGCTCAACCGCTC	2115
QY	2513	GACAAGCACTCGCCCGCCGCTGGCGGTAGCTATCGGGTTCGAACCCCATCCCGGAC	2572
Db	2116	AGCCATGAGTGGCGCTGCGGTGGCGCGCTATCGGCTTCGGCGCCCGCAGCGCGAC	2175
QY	2573	CGAACCTTCTACACAACAAGGCAACCGTCCCATCGGCACCTTCGGCACCAATCTCCTG	2632
Db	2176	GACACATATCTACCAACAACAAGACGGCTGCGCTCTCAATGTTGGAAGCGGGCCCTTG	2235
QY	2633	CGGCTCGAGGGTGAAATCGCCCTCTGTGACAAGAGCAGGTAGTGTCAACATCGCG	2692
Db	2236	CCTACCATC---AAGACTTCGCGTGGCGATCTCTGGCTACACGAGGAGTCTGAGGGCG	2292
QY	2693	GAGCAGCTCGGGCGCGGTTTAACAGCGCCCAACACAAGTAGATATCGTCTAGTGGGC	2752
Db	2293	CTGGATCAGCGCGCCAGCTCCGACCCCTCTGGAAAGAGCAGGGCTGTGGTCAACGGTT	2352
QY	2753	TCATCGCTTGATCCCAACCGGGGTGAACATGACCTATTCGGCGCGCAGCGGTCTGATC	2812
Db	2353	GTGGCTGAACCGCTCGCGAGGGGTAGACAGACGTACTCGACGGGGATGCCACGGGT	2412
QY	2813	TTTCGATGCGGTGATCGTGTGCGGGCGCTG-----CTCACGAGCGCCCTCA	2857
Db	2413	TTTCGAGCGGTGTGTGTGTGACAGGGCGCGGGCGGTGTGTGTCACGACCGGTCTGCTG	2472
QY	2858	ACGCAANTACCAAGAGGTGCCCCCTCAGGATATTATACGGATGTCATACGGGTATGGAAAG	2917

Db	2473	CGTTGTTCCCGACGGGCAGGCCGTGCAGATCTTTGTGGACGGGTATCGTGGGGAAG	2532
QY	2918	CCCGTTGGCGCGGTGAGCGTAGCAATGAACCCCTTCGTGACGTCCCTTATGGCGCCT	2977
Db	2533	CCGGTCCGTGTGTGTGGTGGGAAGTCGACGAGGTGTGGATGCCGGGATGTGCCGAA	2592
QY	2978	GGTGGGATCGCTCGAATGGCTGGACCGCCCGGTGTGTATAT	3021
Db	2593	GACGGGGACGGGGTGTATTCGGAGAGTCGGTGGACATGTTGT	2636

## RESULT 6

US-09-027-166-10  
Sequence 10, Application US/09027166  
Patent No. 602721  
GENERAL INFORMATION:  
APPLICANT: CHANG, Li-Yen Edward  
APPLICANT: HWONG, Ching-Long  
APPLICANT: LO, Cheng-Kai  
TITLE OF INVENTION: No. 602721el Catalase, The Gene Thereof and  
TITLE OF INVENTION: Composition Comprising The Same, And Process For Preparing  
TITLE OF INVENTION: Catalase Using Genetic Engineering Technology  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
STREET: 300 S. Wacker Drive Suite 3200  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/027,166  
FILING DATE: 20-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: TW 86100018  
FILING DATE: 03-JAN-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: CN 97120386.5  
FILING DATE: 11-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: CHAO, Mark  
REGISTRATION NUMBER: 37,293  
REFERENCE/DOCKET NUMBER: 98,180  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 913-0001  
TELEFAX: (312) 913-0002  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3466 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: not relevant  
MOLECULE TYPE: cdna  
US-09-027-166-10

[illegible]

QY 1278 ACTGCACATGATACGGCATGGGATTTCTCTCAGCAGAGCCAGCTCATTTGCATGCCCTC 1337  
Db 1520 AGTGGCCACGATACCTTTCTGGGATATGTTCTCTGCAACCTGAAACTCTGCACAAGCTG 1579  
QY 1338 TTCGGGCAATGTCAGGACATGGATCCCTCGCTCAATGGCTCATTTGATGGGTGGGC 1397  
Db 1580 ATGTGGGGATGTCGGATCGCGGCATCCCCCGCAGTTTACCCACCATGGAGGCTTCGGT 1639  
QY 1398 GTCCATACCTTCCGACTTGTTCACGACGAGGCGCAACTCTGACTTTGGTCAAGTTTCGGCTG 1457  
Db 1640 ATTCACACTTCCGCTGATTAATGTCGGAAGGCAACGTTGTACGTTTCCACTGG 1699  
QY 1458 AAGACCTCCAAAGGAAGAGCGGCTGTATGGGAGGACAGGCTCTTGGCGGAAG 1517  
Db 1700 AAACCACTGGCAGGTAAAGCCTCACTCGTTGGGATGAAGCACAAAACCTCACCGGAGCT 1759  
QY 1518 AATCCGACTTCCATCGACAAGACCTCTGGGATGCCATTGAATCTGGAAGGTACCTCTGAG 1577  
Db 1760 GACCGGACTTCCACCGCGCGAGTTGTGGGAGCCATTGAAGCAGGCGCATTTTCCGGAA 1819  
QY 1578 TGGGA 1582  
Db 1820 TAGCA 1824

RESULT 7  
US-09-695-987-1  
; Sequence 1, Application US/08695987  
; Patent No. 6005090  
; GENERAL INFORMATION:  
; APPLICANT: DODGE, Christopher V.  
; APPLICANT: LEE, Adrian  
; APPLICANT: RADCLIFF, Fiona J.  
; APPLICANT: HAZELL, Stuart L.  
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF HELIOBACTER  
; TITLE OF INVENTION: INFECTION  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY & LARDNER  
; STREET: 3000 K STREET, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/695,987  
; FILING DATE: 15-AUG-1996  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 17227/128  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1518 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; ORIGINAL SOURCE:  
; ORGANISM: Helicobacter pylori  
; STRAIN: HP 921023  
; FEATURE:  
; NAME/KEY: CDS

; LOCATION: 1..1515  
; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: 1..1515  
; US-08-695-987-1  
Query Match 2.3%; Score 88.2; DB 3; Length 1518;  
Best Local Similarity 52.4%; Pred. No. 1.8e-13;  
Matches 226; Conservative 0; Mismatches 193; Indels 12; Gaps 1;  
QY 1158 GGCATATGATATGTCGGAAACACAGTTCCTTCTTATTCAGGACGCTATTCAT 1217  
Db 364 GGTAACTGGGATTTAGTGGGAAACACAGCCTGTTTCTTTATCCGTATGGATCAAA 423  
QY 1218 TTCCTGATTTGATTCACGCTGTCAAGCCGCAACACAGAGTGAATTCCTCCAGGCTGCA 1277  
Db 424 TTCCTGATTTTCCACACTCAAAAACAGAGATCCTCAACCAATTTGCTAAC----- 477  
QY 1278 ACTGCACATGATAGGCGATGGATTTCTCTCAGCAGAGCCAGCTCATTTGCATGCCCTC 1337  
Db 478 -----CATGCACATGTTGGGATTTTGGAGCAATGTTCTCTGAAAGCTTATACCAAGTA 531  
QY 1338 TTCCTGGCAATGTCAGGACATGCCCTCGCTCAATGGCTCATTTGATGGGTGGGC 1397  
Db 532 ACATGGGTTATGAGCGATAGAGGTATCCCTTAATCTTTCCGCCACATGGATGTTTGGC 591  
QY 1398 GTCCATACCTTCCGACTTGTTCACGACGAGGCGCAACTCGACCTTGGTCAAGTTTCGCTG 1457  
Db 592 AGCCACACTTTCAGTCTTATCAACGCTAAAGGCGAAGCGTTTGGGTGAAATTCACCTTT 651  
QY 1458 AAGACCTCCAAAGGAAGAGCGGCTGTATGGGAGGACAGGCTCTTGGCGGAAG 1517  
Db 652 GAAACCATGCAAGCGGTTAAGCACTTGACTTAACGAAGAACCGCAGAAATCAGAAAGCAT 711  
QY 1518 AATCCGACTTCCATCGACAAGACCTCTGGGATGCCATTGAATCTGGAAGGTACCTCTGAG 1577  
Db 712 GATCCGATTCATCAAGGATTTATTCATCGGATCGTACGAGGGGATTTCCCAAAA 771  
QY 1578 TGGGAGTAA 1588  
Db 772 TGGAAATTAAG 782

RESULT 8  
US-09-421-238-1  
; Sequence 1, Application US/09421238  
; Patent No. 6468545  
; GENERAL INFORMATION:  
; APPLICANT: DODGE, Christopher V.  
; APPLICANT: LEE, Adrian  
; APPLICANT: RADCLIFF, Fiona J.  
; APPLICANT: HAZELL, Stuart L.  
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF HELIOBACTER  
; TITLE OF INVENTION: INFECTION  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY & LARDNER  
; STREET: 3000 K STREET, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/421,238  
; FILING DATE: 20-OCT-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/695,987

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; FILING DATE: 15-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17227/128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1518 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; STRAIN: HP 921023
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1515
; NAME/KEY: mat_peptide
; LOCATION: 1..1515
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-421-238-1

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Query Match      2.3%; Score 88.2; DB 4; Length 1518;
Best Local Similarity 52.4%; Pred. No. 1.8e-13;
Matches 226; Conservative 0; Mismatches 193; Indels 12; Gaps 1;

QY 1158 GCGAATGTAGATATCGTCGGAACAACGCTTCACGCTCTCTTCATTTCAGGACGCTATTCAA 1217
DB 364 GGTAACTGGGATTTAGTAGGGGAACAACAGCGCTGTTTTCTTTATCCGCTGATCGATCAA 423
QY 1218 TTCCTGTATTTGATTCACGCTGTCAAGCCGCAACAGACAGTGAATTCGCCAGGCTGCA 1277
DB 424 TTCCTGTATTTGATTCACGCTGTCAAGCCGCAACAGACAGTGAATTCGCCAGGCTGCA 1277
QY 1278 ACTGCACATGATAGCGGATGATTCCTCAGCCAGCAGCCAGCTCATTCGATGCGCTC 1337
DB 478 -----CATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 477
QY 1338 TTCCTGTATTTGATTCACGCTGTCAAGCCGCAACAGACAGTGAATTCGCCAGGCTGCA 1397
DB 532 ACATGGGTTATGAGCGATAGAGGTATCCCTAAATCTTCCGCCACATGATGATGATGATGAT 591
QY 1398 GTCCATACCTTCCGACTTTCACCGAGGCGGCAACTCGACCTTGTGTCATGATGATGATGAT 1457
DB 592 AGCCACACTTTCAGCTCTTATCAAGGCTTAAAGGCGCAACGCTTTTGGGTGAATTCACCTTT 651
QY 1458 AAGACCTTCCAAAGGAAGCGGCGCTGATGGAAGAGCAGCAGGCTCTTGGCGGAAG 1517
DB 652 GAAACCATGCAAGCGCTTAAGCACTTGACCTAAGCAAGAGAGCCGCAAGAAATTCAGAAAGCAT 711
QY 1518 AATCCGACTTCCATCAAGAACACCTTCTGGATGCCATTTGAATCTGGAAGGTACCTGAG 1577
DB 712 GATCCGATTCATCAAGAGGATTTATTCAATGCGATGCTAGAGGGGATTTCCCAAAA 771
QY 1578 TGGGAGGTAAG 1588
DB 772 TGGAAATTAAG 782

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RESULT 9
US-08-695-987-3
; Sequence 3, Application US/08695987
; Patent No. 6005090
; GENERAL INFORMATION:
; APPLICANT: DOIDGE, Christopher V.
; APPLICANT: LEE, Adrian
; APPLICANT: RADCLIFF, Fiona J.
; APPLICANT: HAZELL, Stuart L.

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; TITLE OF INVENTION: TREATMENT AND PREVENTION OF HELIOBACTER
; INFECTION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,987
; FILING DATE: 15-AUG-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17227/128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1518 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; STRAIN: RU1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1515
; NAME/KEY: mat_peptide
; LOCATION: 1..1515
; US-08-695-987-3

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Query Match      2.2%; Score 86.6; DB 3; Length 1518;
Best Local Similarity 52.2%; Pred. No. 4.7e-13;
Matches 225; Conservative 0; Mismatches 194; Indels 12; Gaps 1;

QY 1158 GCGAATGTAGATATCGTCGGAACAACGCTTCACGCTCTCTTCATTTCAGGACGCTATTCAA 1217
DB 364 GGTAACTGGGATTTAGTAGGGGAACAACAGCGCTGTTTTCTTTATCCGCTGATCGGATCAA 423
QY 1218 TTCCTGTATTTGATTCACGCTGTCAAGCCGCAACAGACAGTGAATTCGCCAGGCTGCA 1277
DB 424 TTCCTGTATTTGATTCACGCTGTCAAGCCGCAACAGACAGTGAATTCGCCAGGCTGCA 1277
QY 1278 ACTGCACATGATAGCGGATGATTCCTCAGCCAGCAGCCAGCTCATTCGATGCGCTC 1337
DB 478 -----CAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 477
QY 1338 TTCCTGTATTTGATTCACGCTGTCAAGCCGCAACAGACAGTGAATTCGCCAGGCTGCA 1397
DB 532 ACATGGGTTATGAGCGATAGAGGTATCCCTAAATCTTCCGCCACATGATGATGATGATGAT 591
QY 1398 GTCCATACCTTCCGACTTTCACCGAGGCGGCAACTCGACCTTGTGTCATGATGATGATGAT 1457
DB 592 AGCCACACTTTCAGCTCTTATCAAGGCTTAAAGGCGCAACGCTTTTGGGTGAATTCACCTTT 651
QY 1458 AAGACCTTCCAAAGGAAGCGGCGCTGATGGAAGAGCAGCAGGCTCTTGGCGGAAG 1517
DB 652 CACACCATGCAAGCGCTTAAGCACTTGACCTAAGCAAGAGAGCCGCAAGAAATTCAGAAATAT 711
QY 1518 AATCCGACTTCCATCAAGAACACCTTCTGGATGCCATTTGAATCTGGAAGGTACCTGAG 1577

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TITLE OF INVENTION: No. 602721el Catalase, The Gene Thereof and  
TITLE OF INVENTION: Composition Comprising The Same, And Process For Preparing  
TITLE OF INVENTION: Catalase Using Genetic Engineering Technology  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boenhen Hulbert & Berghoff  
STREET: 300 S. Wacker Drive Suite 3200  
CITY: Chicago, IL  
STATE: IL  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/027,166  
FILING DATE: 20-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: TW 86100018  
FILING DATE: 03-JAN-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: CN 97120386.5  
FILING DATE: 11-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: CHAO, Mark  
REGISTRATION NUMBER: 37,293  
REFERENCE/DOCKET NUMBER: 98,180  
TELEPHONE: (312) 913-0001  
TELEFAX: (312) 913-0002  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1449 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: not relevant  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1449  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 1..1449  
US-09-027-166-6

Query Match 2.2%; Score 84.6; DB 3; Length 1449;  
Best Local Similarity 59.3%; Pred. No. 1.5e-12;  
Matches 144; Conservative 0; Mismatches 99; Indels 0; Gaps 0;  
Qy 835 AATCAATTTACGAGGTTCTCGAGCGCGCTCCATGTCGAGGAGCTGGTGCCCATG 894  
Db 125 ACTTCAATAGAGACGTCCTCCAGACGCTGTGTCATGCGAAGGCGCTGGTGGCAG 184  
Qy 895 GCGTATTCACATCTTATAATCACTGGTGAATATCACAGCGCGATCTCTTGAACGCG 954  
Db 185 GCTATTTCGAGTAACAAACGATATGTCGAAATACACAAAGCGAAAGTGTAAACGCTG 244  
Qy 955 CAGGAAGCAGACACCATATTCGCGGTTTCTACAGTCTGCTGGTAGCAGAGCGAGT 1014  
Db 245 TTGGCAACGCGACGCTGATTCGTCGCTTCTCTACTGTGCGCGGTGAATGGGATCTG 304  
Qy 1015 TTGACTCTGCTCGGATATCCACGATTTGGACCGCTGTGTATACCGATGAAGCAATT 1074  
Db 305 CGGATACAGTCCGCGCGCGGCTTTTGGCGTCAATTTATACCGAAGAGAACT 364  
Qy 1075 TTG 1077  
Db 365 ATG 367

RESULT 14  
US-08-657-868B-3  
Sequence 3, Application US/08657868B  
Patent No. 6080556  
GENERAL INFORMATION:  
APPLICANT: SUGIYAMA, Tosihiro  
APPLICANT: KAWABATA, Tomohisa  
APPLICANT: HIRAYASU, Kazunari  
APPLICANT: TANAKA, Takumi  
TITLE OF INVENTION: POLYPEPTIDES, THEIR PRODUCTION  
TITLE OF INVENTION: AND USE  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/657,868B  
FILING DATE: 31-MAY-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 136465  
FILING DATE: 02-JUN-1995  
APPLICATION NUMBER: 83512  
FILING DATE: 05-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Resnick, David S  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 46522  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1810 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 4...1518  
OTHER INFORMATION:  
US-08-657-868B-3

Query Match 2.1%; Score 81.8; DB 3; Length 1810;  
Best Local Similarity 51.5%; Pred. No. 9.4e-12;  
Matches 222; Conservative 0; Mismatches 197; Indels 12; Gaps 1;  
Qy 1158 GGCAATGTAGATATCGTCGGAACAAACAGTTCAGTCTTCTTATTCAGGACGCTATCAA 1217  
Db 367 GGTAATTTGGGATTTAGTAGGACGACACGCTTTTCTTTATTCGCTGATGCGATCAA 426  
Qy 1218 TTCCCTCATTTGATTCAGCTGTCAAGCCGCAACACAGTGAATTTCCCGAGCTGCA 1277  
Db 427 TTCCCTGATTTTCATCCACACCCAAACAGAGATCTCTCAACTAATTTTGCCTAACCCC 483  
Qy 1278 ACTGCATGATACGCGATGGGATTTCTCAGCCAGCAGCCAGCTCATTCGATGCCCTC 1337  
Db 484 -----GACATGGTATGGGATTTTGGAGTAATCTTCTGAAAGCTTGTATCAAGTA 534  
Qy 1338 TTCTGGGCAATGTCAGGACATGGAAATCCCTCGCTCAATGCGTCAATGTTGATGGTGGGC 1397  
Db 535 ACATGGGTTATGAGCGATAGGGGTATTCTCTAAATCTTTCCGCCACATGGATGTTTGGC 594

Qy		1398	GTCCATACCTTCCGACTTGTCACGCAGCAGGGCAACTCGACCTTGGTCAAGTTTCGCTGG	1457
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Qy		1458	ANGACCCCTCAAGSAGAGCGGGCGCTGTATGGAAAGACGACAGGCTCTTGGCGGAAAG	1517
Db		655	TTAACCATGCAGAGCGGCTTAAGCACTTGACTAATGAAGAAGCTGCAGANAATCAGAAAGCAT	714
Qy		1518	AATCCCGACTTCCATCGACAAGACCCTCGGATGCCATTCAATCTCGAAGGTACCCGTAG	1577
Db		715	GATCCTGATTCCAATCAAGGGATTTATTCGATGCGTAGAGGGGATTTCCCAA AAA	774
Qy		1578	TGGGAGGTAA G	1588
Db		775	TGCAAAATTAAG	785

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RESULT 15
US-09-615-192A-121
; Sequence 121, Application US/09615192A
; Patent No. 6410718
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; TITLE OF INVENTION: Modification of Plant Lignin Content
; FILE REFERENCE: 11000.1003C40
; CURRENT APPLICATION NUMBER: US/09/615,192A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 08/975,316
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 08/713,000
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: US 09/169,789
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 121
; LENGTH: 1243
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-615-192A-121

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Query Match	2.08;	Score 78.8;	DB 4;	Length 1243;
Best Local Similarity	51.28;	Pred. No. 4.9e-11;		
Matches 219;	Conservative 0;	Mismatches 197;	Indels 12;	Gaps 1;
QY	1158	GGCAATGTAGATATCGTCGGAAACAACGGTTCACATCTCTTTCATTCAGGACGCTATTCAA	1217	
Db	475	GGAAACTTTGATCTGTGTGGGGAACAATTTCCACGTCTCTTCGTTCCGGATGCANTGAAA	534	
QY	1218	TTCCCTCGATTTGATTCACCGTGTCAAGCCGCAACCCAGACAGTGAATTCGCCAGGCTGCA	1277	
Db	535	TTCCCGACCGGATCCATGCTGTTCAGCCGAACCCGAACTCTAACATCCAGGAGATGG	594	
QY	1278	ACTGCACATGATACGGCATCGGATTTTCTCAGCCAGCAGGCCACAGCTCATTCGATGCCCTC	1337	
Db	595	AGAAATCATC-----GATTTCTTCTCCACACGACCCGAGAGTCTGTCCACGCTC	642	
QY	1338	TTCTCGGGCAATGTCAGGACATGGAATCCCTCGCTCAATGGTCTATGTTGATGGTGGGGC	1397	
Db	643	GCCTGGTTCTTCATGATGTGGGCATTCCTCAGGACTACAGGCACATGGAGGATTCGGT	702	
QY	1398	GTCCATACCTTCCGACTTGTACCGCAGAGGGGCAACTGGACCTTGCTCAGTTTCCTCGTGG	1457	
Db	703	GTGCAGGCTTTCACCTTCATCACACAGACGGGAACCGAATTCAGTTTAAATTCCTACTGG	762	
QY	1458	AAGACCCCTCCAAGGAAGACGGGCCCTTGGTATGGGAAGAGGCACAGGCTCTTTGTCGCGAAAG	1517	
Db	763	AAGCCCAACTTGGGGGTGAAGTCTTGCTGGAGGAGGCGGATTCCTCATTTGAGGATCG	822	
QY	1518	AAATCCGACTTCCATCGACACAGACCTCTCGGATGCCATTTGAATCTGGAAGGTACCCCTGAG	1577	

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Db      823 AACACAGGCGATCGCACCAAGSATCTTTGACTCGATCGCTGCTGSCAACTACCCGGAG 882
Qy      1578 TGGGAGGT 1585
Db      883 TGGGAGCT 890

Search completed: June 11, 2003, 22:21:02
Job time : 204 secs

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Search completed: June 11, 2003, 22:21:02  
Job time : 204 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model  
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(without alignments)  
11543.087 Million cell updates/sec

Title: US-09-674-195c-1  
Perfect score: 3862  
Sequence: 1 ggcactctgctgcgcgata.....aacaccttcacaaagatccc 3862

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 2054640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: gb.htg.\*  
3: gb.in.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*  
15: em.ba.\*  
16: em.fun.\*  
17: em.hum.\*  
18: em.in.\*  
19: em.mu.\*  
20: em.om.\*  
21: em.or.\*  
22: em.ov.\*  
23: em.pat.\*  
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25: em.pl.\*  
26: em.ro.\*  
27: em.sts.\*  
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37: em.htg.vrt.\*  
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39: em.htgo.hum.\*  
40: em.htgo.mus.\*  
41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	3848.4	99.6	3863	8	AF026268	AF026268 Ajellomyces
2	3359.2	87.0	4807	8	AY103480	AY103480 Ajellomyces
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6	636.2	16.5	4271	8	AF026268	AF026268 Ajellomyces
7	507.4	13.1	2969	8	AF026268	AF026268 Ajellomyces
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16	249.2	6.5	2794	6	AF026268	AF026268 Ajellomyces
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19	173.8	4.5	198677	1	AF026268	AF026268 Ajellomyces
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ALIGNMENTS

RESULT 1  
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LOCUS AF026268 3863 bp DNA linear PLN 29-MAR-1999  
DEFINITION Ajellomyces capsulatus M antigen gene, complete cds.  
ACCESSION AF026268  
VERSION AF026268.2 GI:4530620  
KEYWORDS  
SOURCE Ajellomyces capsulatus.  
ORGANISM Ajellomyces capsulatus.  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; Onygenaceae; Ajellomyces.  
REFERENCE 1 (bases 1 to 3863)  
AUTHORS Zancope-Oliveira, R.M., Reiss, E., Lott, T.J., Mayer, L.W. and  
Deepe, G.S. Jr.  
TITLE Molecular cloning, characterization, and expression of the M



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RESULT 2
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LOCUS      4807 bp DNA linear PLN 13-AUG-2002
DEFINITION Ajellomyces capsulatus catalase B (CATB) gene, complete cds.
ACCESSION AY103480
VERSION   AY103480.1 GI:21539318
KEYWORDS .
SOURCE    Ajellomyces capsulatus.
ORGANISM  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Onygenales; Onygenaceae; Ajellomyces.
REFERENCE Johnson, C. H. and McEwen, J. E.
            Characterization of the Histoplasma capsulatum gene for the
            externally located catalase B enzyme
            Unpublished
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            Johnson, C. H. and McEwen, J. E.
            Submitted (14-MAY-2002) Medical Research & D.W. Reynolds Dept. of
            Geriatrics, Central Arkansas Vet. Healthcare System & Univ. of
            Arkansas for Medical Sciences, 4300 W. 7th St. (VAMC151/LR), Little
            Rock, AR 72205, USA
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ORIGIN

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Query Match      87.08; Score 3359.2; DB 8; Length 4807;
Best Local Similarity 95.28; Pred. No. 0;
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U97574 LOCUS 3142 bp DNA linear PLN 16-MAR-2000  
 DEFINITION Aspergillus fumigatus catalase (catI) gene, complete cds.  
 ACCESSION U97574  
 VERSION U97574.1 GI:2431865  
 KEYWORDS  
 SOURCE Aspergillus fumigatus.  
 ORGANISM Aspergillus fumigatus  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
 REFERENCE 1 (bases 1 to 3142)  
 AUTHORS Calera, J.A., Paris, S., Monod, M., Hamilton, A.J., Debeauvais, J.P.,  
 Diaquin, M., Lopez-Medrano, R., Leal, F. and Latge, J.P.  
 TITLE Cloning and disruption of the antigenic catalase gene of  
 Aspergillus fumigatus  
 JOURNAL Infect. Immun. 65 (11), 4718-4724 (1997)



[illegible]



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QY	675	CAACGGAGCTGGTGGTCCCATCGAGGACCAACACACGCTCAAGGCTGGAATAGAGGCC	734	
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**RESULT 8**  
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**LOCUS**  
**DEFINITION**  
 A.niger catR gene, complete CDS.  
**VERSION**  
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**KEYWORDS**  
 catalase; catR gene.  
**SOURCE**  
 Aspergillus niger  
 Aspergillus niger  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
 Fowler.T.  
 Direct Submission  
 Submitted (12-MAY-1993) Timothy Fowler, Genencor Int. Inc., 180  
 Kimball Way, South San Francisco, CA, 94080, USA  
**REFERENCE**  
 2 (bases 1 to 3105)  
**AUTHORS**  
 Fowler.T., Rey,M.W., Vaha-Vahe,P., Power,S.D. and Berka,R.M.  
**TITLE**  
 The catR gene encoding a catalase from Aspergillus niger: primary  
 structure and elevated expression through increased gene copy  
 number and use of a strong promoter  
**JOURNAL**  
 Mol Microbiol. 9 (5), 989-998 (1993)  
**MEDLINE**  
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**PUBMED**  
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RESULT 9
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DEFINITION Aspergillus niger catalase (catr) gene, complete cds.
ACCESSION L15474
VERSION L15474.1 GI:403073
KEYWORDS catalase.
SOURCE Aspergillus niger DNA.
ORGANISM Aspergillus niger
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE
AUTHORS Fowler, T., Rev, M.W., Vaha-Vahe, P., Power, S.D. and Berka, R.M.
TITLE The catr gene encoding a catalase from Aspergillus niger: a
structure and elevated expression through increased gene copy
number and use of a strong promoter
MOL. Microbiol. 9 (5), 989-998 (1993)
JOURNAL 95020642
MEDLINE 7934925
PUBMED
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ORIGIN

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 Best Local Similarity 54.9%; Pred. No. 4.5e-84;

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 VERSION AX030039.1 GI:10190263  
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 ORGANISM Aspergillus niger  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
 REFERENCE 1 (bases 1 to 3108)  
 AUTHORS Vahne-Vahne, P., Berka, R.M. and Fowler, T.  
 TITLE Use of aspergillus niger catalase-r for hydrogen peroxide  
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				Tudzynski, P.			
				Submitted (23-JAN-1998) Tudzynski P., Institut fuer Botanik,			
				Westfaelische Wilhelms-Universitaet, Schlossgarten 3, Muenster,			
				D-48149, GERMANY			
				2 (bases 1 to 4616)			
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DEFINITION
ACCESSION AF243853
VERSION AF243853.1 GI:15022484
KEYWORDS
SOURCE
ORGANISM
Botryotinia fuckelliana.
Eukaryote; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Helotiales; Sclerotiniaceae; Botryotinia.
REFERENCE
1 (bases 1 to 2460)
Schouten, A., Vermeer, J. E. M. and van Kan, J. A. L.
Direct Submission
Submitted (10-NOV-2000). Laboratory of Phytopathology, WUR,
Binnenhaven 9, Wageningen 6709 PD, The Netherlands
FEATURES
Location/Qualifiers
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BASE COUNT 727 a 534 c 520 g 679 t
ORIGIN

Query Match
Best Local Similarity 9.2%; Score 355.2; DB 8; Length 2460;
Matches 1103; Conservative 0; Mismatches 778; Indels 201; Gaps 8;

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Db 116 ATTTTCTAGACCATGTTACATTAATGACACCAATACATACCTTCACTACCGATCGACGG 175
Qy 690 GTCCCATCGAGGACCAACACGCTGAAGCTGAAATAGAGCCCACTCTACTTACGG 749
Db 176 GGCCTATACAGAGGACCAACGATTTAAAGCTGTGCAAGAGGCGCCGACACTACTTGAAG 235
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Thu Jun 12 08:47:28 2003

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Job time : 9801 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 15:32:45 ; Search time 801 Seconds  
(without alignments)  
10857.949 Million cell

Title: US-09-674-195C-1

Perfect score: 3862  
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Scoring table: IDENTITY\_NUC

scoring table: IDENTITY=100  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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## SUMMARIES

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3	424.8	11.0	3108	14	AAQ46248	Aspergillus niger
4	424.8	11.0	3108	14	AAQ48459	catr gene. Asperg
5	279.4	7.2	1186	21	AAAF3196	Aspergillus oryzae
6	249.2	6.5	2794	17	AAAT42791	Scytalidium catala
7	240.2	6.2	1185	21	AAAF3317	Aspergillus oryzae
8	164	4.2	2037	24	ABK74731	Bacillus lichenifo
9	159.4	4.1	3466	20	AAZ88047	Catalase kat HPI1

E. coli DNA for ce  
Catalase kat HP11  
DNA encoding novel  
H. pylori catalase  
H. pylori catalase  
Salmonella typhi D  
Pseudomonas aerugi  
Pseudomonas gene i  
A. thaliana gene 1  
Rice catalase A (  
Pseudomonas sp ABC  
C. glutamicum SRT  
Arabidopsis thalia  
Arabidopsis thalia  
Arabidopsis thalia  
Arabidopsis thalia  
C. glutamicum codin  
C. glutamicum codin  
Helicobacter pylor  
Nucleotide sequenc  
Helicobacter pylor  
Helicobacter pylor  
Wheat catalase cDN  
Genomic Rice catal  
Arabidopsis thalia  
Arabidopsis thalia  
Arabidopsis thalia  
Arabidopsis thalia  
Clone of A. thalia  
Helicobacter CP2 a  
Helicobacter CP2 a  
Helicobacter CP2 a  
Bacillus thermogl  
Bacillus thermogl  
Bacillus thermogl  
Helicobacter pylor  
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Bacillus lichenifo  
V. vulnificans-1  
Eucalyptus grandis  
Bacillus clausii g

## ALIGNMENTS

RESULT 1  
AAZ35972  
ID AAZ35972 standard: DNA: 3862 BP.

XX  
AC  
AA735972.XX  
DT 09-FEB-2000 (first entry)

XX  
DE  
XX  
Histoplasma capsulatum M antigen gene  
SEO ID NO:1.

XX  
Histoplasma capsulatum: fungus: M antigen: vaccine: detection; kw

KW histoplasmosis: diagnosis: infection: antimicrobial; antibody; ss.

XX 05 Histoplasma capsulatum.

XX PN WQ9955874-A2.

XX  
PD  
04-NOV-1999.

XX 27-APR-1999: 99WO-US09151.

XX  
PR 30-APR-1998: 98US-0083676.XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Zancope-Oliveira RM, Lott TJ, Mayer LW, Reiss E, Deepe GS;  
PT

XX  
DR WPT: 2000-023360/02.

DR P-PSDB; AAY30130.  
XX

New isolated Histoplasma capsulatum nucleic acids, used to develop products for the diagnosis, prevention and treatment of histoplasmosis

xx  
xx  
xx  
CC  
CC  
CC  
CC  
CC  
CC  
CC  
CC  
CC  
CC  
xx  
xx  
SQ

Claim 1; Page 70-71; 75pp; English.

The present sequence represents the M antigen gene isolated from Histoplasma capsulatum (HC). HC polypeptides can be used for detecting antibodies for detecting a previous or current HC infection in a subject. They can also be injected into the skin of a subject to detect past exposure to HC by detecting swelling of the skin. The antibodies can be used for detecting current HC infection in a subject. HC nucleic acids and polypeptides can also be used for the treatment of HC histoplasmosis as well as in vaccines for the prevention of HC histoplasmosis.

Sequence 3862 BP; 984 A; 1011 C; 838 G; 1028 T; 1 other;

Query Match		100.0%;	Score 3861;	DB 21;	Length 3862;		
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Matches 3862;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
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QY	121	TTTTATTTTCAATCATCTCTCTGTGCGCAACATGAGGTATGCGAGCTCTGGACCTGG	180				
Db	121	TTTTATTTTCAATCATCTCTCTGTGCGCAACATGAGGTATGCGAGCTCTGGACCTGG	180				
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Db	661	ACAGTGGTCTTAAACAGGACGCTGGTGGTCCCATCGAGGACCAACACAGCTGAAGC	720				
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DB	781	TGATCATGAGGGTATGATGATACAAATATGTGACCTGTGTGCAATCCGCTAATTC	840
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DB	1021	CTGCTCGGATATCAGGATTTGCGACCTGCTGTATACCGATGAAGGCAATTTTGGTA	1080
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QY	1681	CTTTATATACGTTTCTTCTATATAGTGGGCTTCAATTTGGTGAATGAAGCAGATCAATC	1740
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QY	1741	CAAGTTTGTATTTGATTTAGATCCCAACCAAAATCATCCAGAGAACTTTGTTCTTT	1800
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3361 TCTCACATCAATCTATATTTGATCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 3420  
3421 GAGCAATAATGATAGATTAACAAATAATTAACAAATAATTAACAAATAATTAACAA 3480  
3421 GAGCAATAATGATAGATTAACAAATAATTAACAAATAATTAACAAATAATTAACAA 3480  
3481 TCAGATATATCTATCTATCTGTTGATGATACCTCAAAAATGCCAAGCTTGCCTGAT 3540  
3481 TCAGATATATCTATCTATCTGTTGATGATACCTCAAAAATGCCAAGCTTGCCTGAT 3540  
3541 TGAATATTTATGCTGTAATGTTAGGAGAGCGTACCATCCAAATACCAAGAAAACA 3600  
3541 TGAATATTTATGCTGTAATGTTAGGAGAGCGTACCATCCAAATACCAAGAAAACA 3600  
3601 TGTGTTAGCTTAAATCTCACTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3660  
3601 TGTGTTAGCTTAAATCTCACTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3660  
3661 TGACATCTGATAAAAATGCTGTTTCCGCTTCCAGCAGCATGTTATGACTTTTCAAT 3720  
3661 TGACATCTGATAAAAATGCTGTTTCCGCTTCCAGCAGCATGTTATGACTTTTCAAT 3720  
3721 ATAGATAAAACCTGACGATTTAGCCCTGTTGGGGAATAGGGGTTAGGGGGCGGAGC 3780  
3721 ATAGATAAAACCTGACGATTTAGCCCTGTTGGGGAATAGGGGTTAGGGGGCGGAGC 3780  
3781 TACATATCATCTCCCATATGACCAAAAACCTTAAATAGATATATATATATATATATAT 3840  
3781 TACATATCATCTCCCATATGACCAAAAACCTTAAATAGATATATATATATATATATAT 3840  
3841 ACAACACCTTCAAAAAGGATCC 3862  
3841 ACAACACCTTCAAAAAGGATCC 3862

RESULT 2  
AAQ46249  
ID AAQ46249 standard; DNA; 8528 BP.  
XX  
AC AAQ46249;  
XX  
XX  
DT 17-MAR-1994 (first entry)  
XX  
DE Construct EC2L (Contains catR and pyrG coding sequences).  
XX  
KW Aspergillus niger; catalase; catR; hydrogen peroxide; ss.

```

OS Synthetic.
XX Key Location/Qualifiers
FH misc_feature 1..8
FT /*tag= a
FT /label= Linker sequence.
FT 9..1957
FT 5'UTR
FT /*tag= b
FT /function= GlaxA promoter.
FT 1958..4370
FT CDS
FT /*tag= c
FT /label= catr coding region.
FT 4371..4432
FT 3'UTR
FT /*tag= d
FT 4433..4440
FT misc_feature
FT /*tag= e
FT /label= Linker sequence.
FT 4441..6093
FT polyA_site
FT /*tag= f
FT /label= glaxA polyadenylation and termination
FT signals
FT 6094..8510
FT CDS
FT /*tag= g
FT /label= pyrG gene.
FT 8511..8528
FT misc_feature
FT /*tag= h
FT /label= Linker sequence.
XX
XX WO9318166-A.
XX
XX 16-SEP-1993.
XX
XX 04-MAR-1993; 93WO-US02020.
XX
XX 04-MAR-1992; 92US-0845989.
XX 04-MAR-1992; 92US-0846181.
XX
XX (GENV ) GENENCOR INT INC.
XX
XX Berka RM, Fowler T, Rey MW;
XX WPI; 1993-303480/38.
XX
XX Aspergillus niger catr gene sequence - from which catr promoter
XX has been deleted and Aspergillus glucoamylase promoter gene has
XX been inserted
XX
XX Disclosure; Figure 3; 43pp; English.
XX
XX The Aspergillus niger catr gene was identified and isolated. The
XX native promoter of the gene was removed and replaced with the
XX Aspergillus glucoamylase promoter gene. This modification allows
XX increased expression of the catr gene without the need to supply
XX hydrogen peroxide to induce expression. Cells into which this
XX construct is inserted preferably have the glucose oxidase gene
XX (goxA) deleted. This deletion minimises the generation of
XX gluconate waste material and the use of waste treatment processes.
XX
XX Sequence 8528 BP; 1951 A; 2321 C; 2209 G; 2047 T; 0 other;
XX
XX Query Match 11.28; Score 433.4; DB 14; Length 8528;
XX Best Local Similarity 55.98; Pred. No. 7.6e-108;
XX Matches 1117; Conservative 0; Mismatches 666; Indels 214; Gaps 7;
XX
XX 672 TACACAGGACGTGGGTGGTCCCTGAGGACCAACACAGCCCTGAAGGCTGGAATAGAG 731
XX 2125 TGACTACCGACTTTGGCACTCCGATCTCCGACACGACAGCTCAAGCGGGCCCGG 2184
XX 732 GCCCAACTCTACTTGGAGATTTATCTCCGGCAGAAAGATTCAACACTTTGATCATGAGA 791
XX 2185 GTCTACCTCTGTTGGAGGACTTTATCTCCGTGAGAAGCTTCAGCGGTCGACCATGAGC 2244
XX 792 GGGTATGTAGATACA----AAATATGTGACCGGTGTTGCCAAATCCCGCTAATTTTAC 847

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Matches	1193;	Conservative	0;	Mismatches	762;	Indels	221;	Gaps	9;
QY	494	ATCGCGTCGCTCAAGCTTTATCTACGCGCTCGCGGGTGTGTTCTGTCAGAGCTGTCCCTAC	553						
DB	327	ATGCGTCAATTTCTGCTTTTGCCAGCTGTGCTGGTATCGGTGGGGTCAATGCCCGCTAC	386						
QY	554	ATGTCAGGGAGATGCCGTAGCGGTCAAGAGGCCCTCTGATCGCCGCCATGACATCTC	613						
DB	387	CTGTGCGGTGAATAGTGTTCACCGAGGAGCAGACAATGCTGSC-----GATACCAATT	440						
QY	614	TCCGACCCTAGGGACCACTTTCTTAGCAAGTTTTTACATTTGACGATGAACAGTCCGTGCTA	673						
DB	441	GAGGTCACGGAGCAGCCATTGACACACACCTGTATGTCAATGACCGGTAGCTACATG	500						
QY	674	ACAACGGACGTGGGTGGTCCCATCGAGGACCAACACAGCCTGAAGGTGGAAATAGAGC	733						
DB	501	ACTACCGACTTTGGCACTCCGATCTCCGACAGACCACTCTCAAGSCGGGCCCGTGGT	560						
QY	734	CCAACTCTACTTTAGGATTTTATCTCCGCCAGAGATTCAACACTTTGATCAATGAGAGG	793						
DB	561	CCTACCCCTGTTGGAGGACTTTATCTCCGTCAGAAGCTTCAGCGGTTCGACCATGAGCGT	620						
QY	794	GTATGTAGATACA-----AAATATGTGACCGTGTTCGAAATCCGCTAAATTTTACGC	849						
DB	621	GTAAGTACAGTAACGTGCTGGGGTGTGTAGTAACAAATAATTTGACCCAGTGGTTTCAATT	680						
QY	850	AGGTTCTGTAGCGCGCGCTCCATGCTCGAGGAGCTGGTCCCATGCGGTATTACATCTC	909						
DB	681	AGGTCGCCGAGCGGTGCTCCAGCCCGTGGTCCCGTGCATATGGTACTTTTCAATCTC	740						
QY	910	ATAATACTGGTTCGATATACACAGCCGCATCTCTTGAACGCGGAGAGAAAGCAGA-CA	968						
DB	741	ACGCCGACTGGTCGAAGCTCACGGCTCGCGATTCTTGAGTGCCAACTAGAGAGAGCC	800						
QY	969	CCAGTATTCTGGCGGTTTCTACAGTCGCTGTGTAGCAGAGGACGTGTGACTCTGCTCGC	1028						
DB	801	CCATGTTCTGCTCGCTCTCTACTGTGGTGGGTTTCCGGTGGTAGTGTGTGACACTCGCGT	860						
QY	1029	GATATCCAGGATTTGGACCCGCTGTGTATACCGATGAAGGCAATTTTGGTAGGCAATTAT	1088						
DB	861	GATGTTTACCGGTCACGCTTGTGGTGTCTACACTGACGAGGGTAACATATGTTA-----	912						
QY	1089	ATCGTGGTAGCTATCTATACACACACACAATAATGATACAAACCCAGAGACCTAGGC	1148						
DB	913	-----TCATTGATATGGTCAACCAACAATAATCAATACATGCTAAACAGATATGTC	962						
QY	1149	TGACTACTCGGCAATGTAGATATCGTCGGAACAACAGTTCCAGTCTTCTTATTCACGAC	1208						
DB	963	T-----CTACTAGACATCTGTCGSTATCAATTTGCGCCCTCTTCTATCCAGGC	1011						
QY	1209	GCATTTCATTTCCCTGATTGATTACCGTGTCAAGCGCGCAACACAGACGTGAATTTCCC	1268						
DB	1012	GCAATCCAGTTTCCCGATCTTGTCCACGCCATCAAGCCCAATGCCCAAAATGAGATCCCC	1071						
QY	1269	CAGGCTGCAACTGCATGATACGGCATGGGATTTCCCTACGACGAGCCAGCTCATTTG	1328						
DB	1072	CAGGCGGTACTGACACACATTTCCCGTTGGGACTCTTTCAGCCAGAGACCTGCCCCC	1131						
QY	1329	CATGCCCTTCTTGGCAATGTCAAGACATGGAATCCCTCGCTCAATTCGCTCATGTTGAT	1388						
DB	1132	CACAGTGCCCTTGTGCTGATGTCTGTGTACCGGTATTCCTCGTCTTTCCGCCACATGAAC	1191						
QY	1389	GGTGGGGCGTCCATACCTTCGGACTCTGTACCGACGAGGCACTCGACCTTGGTCAAG	1448						
DB	1192	GGCTACGGAGTCCACAGCTTCGGCTTGTCCCTGCCAATGGCACTTCCAAAGGTGGTCGA	1251						
QY	1449	TTTCCCTGGAGACCCCTCCAAGGAGAGCGGGCCGTGTATGGGAAGAGGCACAGGCTTT	1508						
DB	1252	ACACCTTGGAAGTCCCAACAGGGGTGTGCCAGTCTGGTGGGATGAAGCTCAGGCCGT	1311						
QY	1509	GGCGAAAGAATCCCGACTTCCATCTGCACAGACCTCTGGATGCCATTGAATCTGGAAGG	1568						
DB	1312	GCTGTTAGACAGTACTACACCCGCGGATCTGTACATGCGATGCGCAATGGCCAC	1371						

OY 2649 AAATCGCCCTCCTGAC 2664  
Db 2271 AGGTGGCTTCTGCGC 2286

RESULT 4  
AAQ48459  
ID AAQ48459 standard; DNA; 3108 BP.

XX AAQ48459;

XX 29-MAR-1994 (first entry)

XX catR gene.

XX catR gene; A. niger; catalase-R; hydrogen peroxide; oxygen; water;  
KW pH range; shelf life; beef liver catalase; contact lenses; ss.

XX Aspergillus niger.

XX Key Location/Qualifiers

FT CDS 327..2746

FT /\*tag= a

FT /product= Catalase-R

FT exon 327..620

FT /\*tag= b

FT /number= Exon 1

FT misc\_difference 339..341

FT /\*tag= c

FT /codon= seq:TGC aa:Trp

FT intron 621..682

FT /\*tag= d

FT /number= Intron 1

FT exon 683..909

FT /\*tag= e

FT /number= Exon 2

FT misc\_difference 713..715

FT /\*tag= f

FT /codon= seq:GCC aa:none given

FT misc\_difference 797..800

FT /\*tag= g

FT /codon= seq:AGCC aa:Thr

FT intron 910..970

FT /\*tag= h

FT /number= Intron 2

FT exon 971..1386

FT /\*tag= i

FT /number= Exon 3

FT intron 1387..1440

FT /\*tag= j

FT /number= Intron 3

FT exon 1441..1605

FT /\*tag= k

FT /number= Exon 4

FT intron 1606..1654

FT /\*tag= l

FT /number= Intron 4

FT exon 1655..2743

FT /\*tag= m

FT /number= Exon 5

XX WO9317721-A.

XX PN

XX PD 16-SEP-1993.

XX 04-MAR-1993; 93WO-US02018.

XX 04-MAR-1992; 92US-0845990.

XX (GENV ) GENENCOR INT INC.

XX PI Berka RM, Fowler T, Vaha-Vahe P;

XX

DR WPI; 1993-303156/38.  
DR P-PSDB; AAR41753.

XX Cleaning and disinfecting contact lenses - using hydrogen  
FT peroxide soln. and decomposing residue on lenses with reduced  
PT amt. of Aspergillus niger catalase R

XX Disclosure; Fig 5; 22pp; English.

XX This sequence represents the catR gene of A. niger and encodes  
CC the catalase-R protein. This enzyme catalyses the conversion of  
CC hydrogen peroxide to oxygen and water. Catalase-R is a soluble  
CC cytoplasmic enzyme which is stable over a wide pH range, has an  
CC extended shelf life and is resistant to deactivation in high  
CC concentrations of hydrogen peroxide. Catalase-R is more effective  
CC than beef liver catalase for neutralisation of concentrated (eg. 3%)  
CC hydrogen peroxide solutions. This catalase may be used in the  
CC cleaning and disinfecting of contact lenses.

XX SQ Sequence 3108 BP; 674 A; 955 C; 708 G; 769 T; 2 other;

Query Match 11.0%; Score 424.8; DB 14; Length 3108;  
Best Local Similarity 54.8%; Pred. No. 9.5e-106;

Matches 1193; Conservative 0; Mismatches 762; Indels 221; Gaps 9;

OY 494 ATGCGGTGCTCAAGCTTATCTCGCTCGCGGGGTGTTGTTCTGAGGCTGTCCTAC 553  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 554 ATGTCAGGGAGATGCTAGCGGTCAAGAGCCCTCGATGCCGCCATGACACTCTC 613  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 614 TCCGACCTACGGACCAAGTTCTTAGCAAGTTTACATTTGACATGACAGTCGGTGCTA 673  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 674 ACACGGAGCTGGGTGCTCCATCGAGGACCAACACACGCTGAAGCTGGAATAGAGGC 733  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 734 CCAACTCTACTTGAGGATTTATCTTCGCCAGAGATTCAACACTTTGATCAGAGG 793  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 801 CCTATGTTCTGCTGCTTCTCTACTGTGGTGTCCCGGTGTTGACACTGCGGT 860  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 1029 GATATCCAGGATTTGCGACCGCTCTGTATACCGATGAAGGCAATTTGGTAAGCATTTAT 1088  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 861 GATGTTACGGTCAAGCTTGTGCTGTTCTACACTGACGAGGGTAACATATGTTA 912  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 1089 ATCGTGGTATCATACTATAACAGCACAAATAATGAATACAAACCCAGGACCTAGGC 1148  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 913 -----TCTTGATATGTTCCACCAACAATAATTCATATGCTAACAGATATGTC 962  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 1149 TGACTACTCGGCAATAGATATCGTGGAAACAACGTTCCAGTCTTCTTCTTCCAGGAC 1208  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 963.T-----CTACTAGACATCGTCGGTATCAATTTCCGCCCTTCTTCTATCCAGGAC 1011  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY	1209	GCATTTCAATCCCTGATTGATTACGCTGTCAAGCGCAACAGACAGTGAATTC	1266
Db	1012	GGCATCCAGTCCCGGATCTTGCCACGCCATCAGCCCATGCCACATGAGATCCCC	1071
QY	1269	CAGGCTGCAACTGCACATGATACGCATGGGATTTCCTCAGCCAGCAGCCAGCTCAT	1328
Db	1072	CAGCGCGCTACTGCAACACATTCGCGTTGGGACTTCTTCAGCCAGCAGACACTGC	1131
QY	1329	CATGCCCTCTTCTGGGCAATGTCAAGGACATGGAATCCCTCGCTCAATGCGTCATG	1388
Db	1132	CACAGTGCCTTGTGCTGATCTCTGGTAACGGTAATCTCTGTTCTTCCGCCACATGA	1191
QY	1389	GGGTGGGCGGTCCATACCTTCGCACTTGTTCACGACGAGGCAACTCGACTTGGTCA	1448
Db	1192	GGCTACGGAGTCCACAGCTTCGCTCGCTGCCAATGGCACTTCCAAAGTGGTCCGA	1251
QY	1449	TTTCGCTGGAAGACCTTCAAGGAAGAGCGGCTGTATGGGAAGGACACAGGCTTT	1508
Db	1252	ACACCTTGAAGTCCCAACAGGTTTGCCAGTCTGGTGTGGGATGAAGCTCAGCGCGT	1311
QY	1509	GGCGGAAGATCCCGACTTCCATCGACAAAGACCTCTGGGATGCCATTTGAATCGA	1568
Db	1312	GCTGTGTAAGAACGTGACTACCAACCGCAGGATCTGTACAATSCGATGCCAATGC	1371
QY	1569	TACCTCGAGTGGGAGGTAAAGATATGATTCCTCCCAATCATTTAGTCTGCAGTGT	1628
Db	1372	TACCGAAATACGAGTCAAGCA	1394
QY	1629	TGCTCTGCTGGTTCCTTTTTCGCTTTTCTATATCTTCAACTAAGACTGACTTTAT	1688
Db	1395	-----ATCCCTTGATGTCTATCGATAGGC-----TTT	1423
QY	1689	ACGTTTACTCATATAGCTGGCTTTCATTTGGTGAATGAAGCAGATCAATCCAGTTG	1748
Db	1424	TGCTGCAATCCCTAGTCCAGCCAGATCATGGATGAGCTGACATGCTTCGTTTCG	1483
QY	1749	ATTTGCACTATATAGATCCCAAAATCATCCCAAGAACTTGTCTTTCACCCCAA	1808
Db	1484	GCTTCGACCTTCTGGATCCCAACCAAGTTGTCCTCCGAGGAGTTGTCCCTTAC	1543
QY	1809	TCGGAAATATGGTCTTGAACCGAAACCCAAAAGTATTTTCCCAAACTGACGATCA	1868
Db	1544	TCGGAATGATGGAGCTCAATGCCAACCCCACTACTTTCCTGAAGTTGAACAGGTG	1603
QY	1869	TGGTTGGTCACCCCTATATATTTGGAATATGATATACATGTATAGTATGAAGCTA	1928
Db	1504	GTGTATGTATCCCAATTCAT-----CAATGCCA	1633
QY	1929	TATCTAAATATATTTCCACAGTTCCAAACAGGTGATGTAGTTCGGGAATCGATTCAG	1988
Db	1634	GACATATCTAATCTGCAAGTTCCAAACCGGTGACGTGCTCTGCGATTTGACTTCAC	1693
QY	1989	GATGACCTTTGTTTCAGGCGCGTTGACTCTTACCTTGACACTCAATTTGAATCGCAT	2048
Db	1694	GAGACACCCCTGCTGCAAGGCGGTCTCTTCTACCTCGACACTCAGTTGACCCGTAC	1753
QY	2049	GGAGTCCCAACTTCGAGCAACTCGGATCAACAGACCCCGCATCCCATTCATAACAC	2108
Db	1754	GGGGTCCCAACTTCGAGCAATCCCCGTAACCGTCTCTGCAAGCCCGTTCAACAAC	1813
QY	2109	ATTCGGGACGGTGGTGAAGTACTTCTCACCTACCATGTCAACTTCCATCTTGACCA	2168
Db	1814	AAACCGTAGG-----	1823
QY	2169	ATCGATTCTGATAGAGTATTACATCCCGCTCGACAGGACAAATGTTTCATCCCTTA	2228
Db	1824	-----GCTTCGGCCAGCAGCAGATCCCCACCA	1850
QY	2229	ACACGGCGCATATACACCACTCAATGAGCAACGGATTCCCAACAGACCAACCGGA	2288
Db	1851	ACAACCTGGGCGCTACACCCCAACAGCATGAGCAAGGTTACCCCATGCAAGCCACGA	1910
QY	2289	CCCATAAACAGGATTCTTTCACCCCGACTGGCGGTATGGTAAATGGACCACTAGTCGGG	2348

CC in a first filamentous fungal (FF) cell relative to expression of the			CC same genes in one or more second filamentous fungal cells. Monitoring		
CC the global expression of genes from FF cells allows the production			CC potential of the microorganisms to be improved. New genes may be		
CC discovered, possible functions of unknown open reading frames can be			CC identified, and gene copy number variation and stability can be		
CC monitored. The expression of genes can be used to study how FF cells			CC adapt to changes in culture conditions, environmental stress, spore		
CC morphogenesis, recombination, metabolic or catabolic pathway			CC engineering. Using ESTs provides several advantages over genomic or		
CC random cDNA clones including elimination of redundancy as one spot on an			CC array equals one gene or open reading frame, and organisation of the		
CC microarrays based on function of the gene products to facilitate			CC analysis of the results. AAF07478 to AAF11247 represents ESTs from		
CC Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus			CC niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and		
CC AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are			CC all specifically claimed in the present invention.		
XX			XX		
SQ Sequence 1186 BP; 252 A; 350 C; 289 G; 294 T; 1 other;			SQ		
Query Match			7.2%; Score 279.4; DB 21; Length 1186;		
Best Local Similarity			59.6%; Pred. No. 5.4e-66;		
Matches 604; Conservative 0; Mismatches 262; Indels 148; Gaps 2;					
Qy	572	ACGGGTCAGAAAGGCCCCCTCGATCGCGCATGACACTCTCTCCGACCCCTACGGACACG 631			
Db	80	ACCGGTGAGGTTGAAGTCGCGACAGAGNACCGACGATGCCACCCCGGACAGAGAA 139			
Qy	632	TTTCTTAGCAAGTTTACATTTGACGATGAACAGTCGGTGCTAACACGAGCGTGGTGT 691			
Db	140	TTCTTTGCCAGTACTATATGGCGCAATGACACATTCCTGACCTCCGACGTCGGCGG 199			
Qy	692	CCCATCGACACCCACACCCCTGAAGGCTGGAATAGAGGCCCACTCTACTTGGAGGT 751			
Db	200	CCTATTGAGGATCAGAACGCCCTCAAGTCGGAGACCGCGGCCGACATTCCTGGAGGT 259			
Qy	752	TTTATCTTCGCCAGAGATTCACACTTTTGATCATGAGAGGTGTGTAGATACAAATA 811			
Db	260	TTCATCTTCGCAGAGAAGATCCAGCGCTTCGATCACGAAGT----- 301			
Qy	812	TGTGACCGTGTGGAAATCCGCTAATTTACCGAGGTTCTTCCGAGCGCGCTCCA 871			
Db	302	-----GTTCCCTGAACGTGCGAGTCCA 321			
Qy	872	TGCTCGAGGAGCTGTGCCATGCGGTATTACATCTCTATAAATCACTGGTCAATATCAC 931			
Db	322	CGCTCGCGGTGTGGTGCCTATGCTTTCACCTCGTACGGTGACTACTTAACATCAC 381			
Qy	932	AGCGGCATCTCTTTGAACGCGGCAAGGAAGCAGACACAGTATTCGTGGGTTTCTAC 991			
Db	382	TGCTGCCCTCGTTCTTGGAGCTGAGGGCAAGGAGACTCCGGTTTTCGTGGGATTTCTGAC 441			
Qy	992	AGTCGCTGGTAGCAGAGCAGTGTGACTCTCTCGGATATCCACGATTTGCGACCG 1051			
Db	442	TGTTCCGGGTAGCCGTGTAGTTCGGATTGGCTGGGATGTTCTAGCTTTGGGACTCG 501			
Qy	1052	TCCTGTATACCGATGAAGCAATTTTGGTAAGCATTTATCTGTGTAGTCACTATAAC 1111			
Db	502	TTTCTACACTGATGAGGTACT----- 524			
Qy	1112	AGCACAAACAAATATGAATACAAACCCAGGACCTAGGCTGACTTCGGCAATGTAGATAT 1171			
Db	525	-----TCGATAT 531			
Qy	1172	CGTCGGAACACAGTTCCAGTCTTCTTCACTCAGACGCTATTCAATTCCTGATTTGAT 1231			
Db	532	TGTTGGCAACAACTATCCCGTCTTCTCATCCAGGACGCTATCTTTCCCTGATCTCAT 591			
Qy	1232	TCACGCTGTCAAGCCCAACACAGACAGTGAATTTCCAGGCTGCAACTGCACATGATAC 1291			
Db	592	CCACGCTGTCAAGCCCTCGTGGTGGACATGAGATCCCTCAGGCTGCCACTGCCCATGCTC 651			
RESULT 6			AAAT42791		
ID	AAAT42791 standard; DNA; 2794 BP.		XX	AAAT42791;	
AC	1..2821		XX	02-FEB-1997 (first entry)	
DT	Scytalidium catalase gene.		DE	Catalase; hydrogen peroxide; pasteurisation; bleaching; ss.	
KW	Scytalidium thermophilum.		OS	Scytalidium thermophilum.	
Key	Location/Qualifiers		FT	Key	
FT	exon		FT	exon	
FT	/tag= a		FT	/tag= a	
FT	/codon_start= 1..3		FT	/codon_start= 1..3	
FT	283..413		FT	283..413	
FT	/tag= b		FT	/tag= b	
FT	414..617		FT	414..617	
FT	/tag= c		FT	/tag= c	
FT	618..696		FT	618..696	
FT	/tag= d		FT	/tag= d	
FT	697..717		FT	697..717	
FT	/tag= e		FT	/tag= e	
FT	718..793		FT	718..793	
FT	/tag= f		FT	/tag= f	
FT	794..955		FT	794..955	
FT	/tag= g		FT	/tag= g	
FT	956..1108		FT	956..1108	
FT	/tag= h		FT	/tag= h	
FT	1109..1165		FT	1109..1165	
FT	/tag= i		FT	/tag= i	
FT	1166..1218		FT	1166..1218	
FT	/tag= j		FT	/tag= j	
FT	1219..1788		FT	1219..1788	
FT	/tag= k		FT	/tag= k	
FT	1789..1842		FT	1789..1842	
FT	/tag= l		FT	/tag= l	
FT	1843..2670		FT	1843..2670	
FT	/tag= m		FT	/tag= m	
FT	2671..2764		FT	2671..2764	
FT	/tag= n		FT	/tag= n	
FT	2765..2794		FT	2765..2794	
FT	/tag= o		FT	/tag= o	
FT	complement (133..146)		FT	complement (133..146)	
FT	/tag= p		FT	/tag= p	
FT	/note= "forward primer PmeS5"		FT	/note= "forward primer PmeS5"	
FT	1285..1304		FT	1285..1304	
FT	/tag= q		FT	/tag= q	
FT	/note= "reverse primer St3.2not"		FT	/note= "reverse primer St3.2not"	





Db 600 GGCACCTTCGGACAGAGCTGAAGAAGCTCGATGGACTGAAGTTGGCTTCCTGGCTTCG 659  
 QY 2669 GAGACGGTAGTCTACGATCGGAGCAGCTCCGGGCGCGCTTTAACAGCGCCACACAC 2728  
 Db 660 GTTGAGACCCCTGCTCCATCGAGGCGAGCCTCTGAGCTCAGCAAGCAGCTTTCTGAGGAC 719  
 QY 2729 AAAGTAGATATCGTCTAGTGGCTCATCGCTTGATGCCCAACGCGGCTGAACATGACC 2788  
 Db 720 GCGTTGATGTGTCTGCTGCTG-----CGAGCGCTGCTCGGATGGCTTGATCAGACT 773  
 QY 2789 TATTCGGGCGCGAGCGCTCGATCTCGATGCGGCTGATGCGCTGCTGCTGCGGCGG 2839  
 Db 774 TACTCCGATCGGATGCCATCCAGTTCGATGCTGTGATCGTGGCGCGCG 824

RESULT 8

ABK74731

ID ABK74731 standard; DNA; 2037 BP.

AC ABK74731;

DT 13-AUG-2002 (first entry)

DE Bacillus licheniformis genomic sequence tag (GST) #2022.

KW Differential gene expression; genomic sequenced tag; GST;  
 KW altered culture condition; environmental stress;  
 KW physiological provocation; ds.

OS Bacillus licheniformis.

XX WO200229113-A2.

XX 11-APR-2002.

XX 05-OCT-2001; 2001WO-US31437.

XX 06-OCT-2000; 2000US-0680598.

XX 27-MAR-2001; 2001US-279526P.

XX (NOVO ) NOVOZYMES BIOTECH INC.

XX (NOVO ) NOVOZYMES AS.

XX Berka R, Clausen IG;

XX WPI; 2002-416684/44.

XX Monitoring differential expression of several genes in first Bacillus  
 cell relative to expression of same genes in one or more second  
 PT Bacillus cells, by using substrate containing Bacillus genomic  
 PT sequenced tag array -

XX Claim 4: SEQ ID NO 2022; 200pp; English.

XX The invention describes a method of monitoring differential expression of  
 genes in a first Bacillus cell relative to expression of the genes in  
 other Bacillus cells, comprising hybridising labelled nucleic acid probes  
 CC isolated from Bacillus cells to a substrate containing array of Bacillus  
 CC genomic sequenced tags (GST), examining the array, and determining  
 CC relative gene expression by an observed hybridisation reporter signal of  
 CC a spot in the array. The method is useful for measuring the expression of  
 CC genes in a first Bacillus cell relative to expression of the same genes  
 CC in one or more second Bacillus cells. The method is useful for monitoring  
 CC global expression of several genes from a Bacillus cell, discovering new  
 CC genes, identifying possible functions of unknown open reading frames and  
 CC monitoring gene copy number variation and stability. Monitoring changes  
 CC in expression of genes may be used to provide a representation of the way  
 CC in which Bacillus cells adapt to changes in culture conditions,  
 CC environmental stress or other physiological provocation. Extensive  
 CC follow-up characterisation is unnecessary, when one spot on an array  
 CC equals one gene or one open reading frame, since sequence information is  
 CC available. This sequence represents a genomic sequence tag (GST) used in  
 CC the method of the invention.

CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

SQ Sequence 2037 BP; 561 A; 500 C; 550 G; 426 T; 0 other;

Query Match 4.2%; Score 164; DB 24; Length 2037;  
 Best Local Similarity 61.4%; Pred. No. 4.2e-34;  
 Matches 263; Conservative 0; Mismatches 165; Indels 0; Gaps 0;

QY 1158 GGCATGTAGATATCGTCGGAACAACGTTCCAGTCTCTTTCATTCAGGAGCTATTCAA 1217  
 Db 396 GGGAACTATGATCTTGTGGCAACAACATCCCGCTTTTCTTCATTCAGGATGCCATCAAG 455  
 QY 1218 TTCCCTGATTGATTCACGCTGTCAAGCCGCAACAGACAGTGAATTCCTCCAGGCTGCA 1277  
 Db 456 TTCCCTGACCTGTGTCACGCTTTTAAACCGGAACCAACGAATGCCGAGGCTTCT 515  
 QY 1278 ACTGCACATGATACGGCATGGATTTCTCAGCCAGCAGCCAGCTCATTTGCATGCCCTC 1337  
 Db 516 ACGCGCAGATACGTTTGGGACTTTGTGCGCAACAATGAAGAAACGGCCCATGATC 575  
 QY 1338 TTCTGGCAATGTACAGACATGGAATCCCTCGCTCAATGCTCATGTGATGGTGGGC 1397  
 Db 576 ATGTGAGCAATGTCTGACAGGCGATTCGCGGAAGCTACAGGATGTGGAAGCTTCGGC 635  
 QY 1398 GTCCATACCTTCGACTTGTACCGAGGAGGCACTCGACCTTGTGTCAGTTTCGCTGG 1457  
 Db 636 GTTCATACGTTACAGTTTGTAAACGAAGAGGCGCACTTGTGTTAAATTTCACTGG 695  
 QY 1458 AAGACCTCCCAAGGAAGAGCGGCTGTGATGGAAGAGCAGAGCTCTTGGCGGAAAG 1517  
 Db 696 AAGCCGCTCTCGGCTCCATTCGCTGCTGGAGAGAGCGAGCAATTCGCGGANA 755  
 QY 1518 AATCCGACTTCCATCGACAAAGACCTCTGGATGCCATTTGAATCTGGAAGGTACCTGAG 1577  
 Db 756 GATCCGACTATCACCGCGCGATCTGTGGGAAGCGATCGAAGAGCGGATGAAGTGGAG 815  
 QY 1578 TGGGAGGT 1585  
 Db 816 TATGAGCT 823

RESULT 9

AAZ88047

ID AAZ88047 standard; DNA; 3466 BP.

AC AAZ88047;

DT 19-APR-2000 (first entry)

DE Catalase kat HP11 gene.

XX Catalase; hydrogen peroxide; contact lens; disinfecting solution; ds.

XX Bacillus subtilis.

XX Escherichia coli.

XX CN1219588-A.

XX 16-JUN-1999.

XX 11-DEC-1997; 97CN-0120386.

XX 11-DEC-1997; 97CN-0120386.

XX (BIOT-) BIOTECHNIQUE DEV CENT.

XX Zhang L, Huang Q, Luo Z;

XX WPI; 1999-494879/42.

XX

[illegible]

二

[illegible]

Db 880 AAACCACTGGCAGGTAAAGCCCTCAGTCTGTTGGATGAAGCAAAAACCTACCGGACGT 939  
 QY 1518 AATCCCGACTTCCATCGACAAGACCTCTGGGATGCCATTGAATCTGGAAGGTACCCGTGAG 1577  
 Db 940 GACCCGGACTTCCACCGCGCGGAGTGTGGGAAGCCATTGAAGCAGGCGATTTCCGGAA 999  
 QY 1578 TGGGA 1582  
 Db 1000 TACGA 1004

RESULT 11

AAZ88404  
 ID AAZ88404 standard; cDNA; 3466 BP.  
 XX  
 AC AAZ88404;  
 XX  
 DT 05-MAY-2000 (first entry)  
 XX  
 DE Catalase kat HP11 gene sequence SEQ ID NO:10.  
 XX  
 KW Catalase; genetic engineering; hydrogen peroxide decomposition;  
 KW contact lens; disinfectant; ss.  
 XX  
 OS Escherichia coli.  
 XX  
 PN US6022721-A.  
 XX  
 PD 08-FEB-2000.  
 XX  
 PF 20-FEB-1998; 98US-0027166.  
 XX  
 PR 03-JAN-1997; 97TW-0100018.  
 PR 11-DEC-1997; 97CN-0120386.  
 XX  
 PA (BIOT-) DEV CENT BIOTECHNOLOGY.  
 XX  
 PI Hwong C, Lo C, Chang LE;  
 XX  
 DR WPI; 2000-160378/14.  
 XX

Isolated catalase gene derived from Bacillus thermoglucosidius useful for decomposing hydrogen peroxide in residual disinfectant remaining on a contact lens -

Example 4; Fig 8; 30pp; English.

The present invention describes a catalase isolated from Bacillus thermoglucosidius. A composition containing a B. thermoglucosidius catalase is used to decompose hydrogen peroxide present in residual disinfectant remaining on a contact lens to avoid undesired injury to users. The catalase enzyme can also be used to treat textile substances which have been bleached with hydrogen peroxide. The catalase is derived from a non-mammalian source and reducing the need to use bovine liver catalases so the risk of cross infection from cows to humans is reduced. The production procedure is simple and has low cost with high yield of enzyme. The present sequence represents the catalase kat HP11 gene from an example from the present invention.

Sequence 3466 BP; 920 A; 890 C; 815 G; 841 T; 0 other;

Query Match 4.0%; Score 156.2; DB 21; Length 3466;  
 Best Local Similarity 60.5%; Pred. No. 8.2e-32;  
 Matches 257; Conservative 0; Mismatches 168; Indels 0; Gaps 0;

QY 1158 GGCAATGTAGATATCTCGAACAACAGTTCAGTCTTCTTCAATCAGGACGTAFTCAA 1217  
 Db 1400 GGTATTTGACCTCGTGGCAATAACACGCCAATCTTCTTATCCAGGATCGCATAAA 1459  
 QY 1218 TTCCCTGATTGATTCACGCTGTCAAGCGCAACAGACAGTGAATTCCTCCAGGCTGA 1277  
 Db 1460 TTCCCGGATTTGTTTCACTGGGTAAACTAGACCCCACTGGCAATTCACAGGGCAA 1519

QY 1278 ACTGCACATGATACGGCATGGGATTTCTCAGCCAGCAGCCAGCTCATTCATGCCCTC 1337  
 Db 1520 AGTGCCACGATATCTTCTGGGATTTATGTTTCTGCAACCTGAACCTCTGCACAAGTG 1579  
 QY 1338 TTCTGGCAATGTACAGGACATGGATCCCTCGCTCATGTCGTATGTTGATGGGTGGGC 1397  
 Db 1580 ATGTGGCGATGTGGGATCGCGGATCCCGCGAGTTACCGCACCATGGAAGGCTTCGGT 1639  
 QY 1398 GTCCATACCTTCGACTTGTCAACGACGAGGGCAACTCGACTTGGTCAGTTTCGGTGG 1457  
 Db 1640 ATTCACACTTCCGCTGATTAATGCCGAGGGAAGGACAGTTTGACGTTTCCACTGG 1699  
 QY 1458 AAGACCTTCCAAAGGAAGAGCGGCTGTATGGAAGAGGACAGGCTCTTGGCGGAAAG 1517  
 Db 1700 AAACCACTGGCAGGTAAAGCTCTACTGTTGGATGAAGCAAAAACATCCCGGACGT 1759  
 QY 1518 AATCCGACTTCCATCGACAAGACCTCTGGGATGCCATTGANTCTGAAGGTACCTGAG 1577  
 Db 1760 GACCGGACTTCCACCGCGGAGTTGTGGAGCCATTGAAGCAGGCCATTTTCCGGAA 1819  
 QY 1578 TGGGA 1582  
 Db 1820 TACGA 1824

RESULT 12

AAZ92713  
 ID AAZ92713 standard; cDNA; 3299 BP.  
 XX  
 AC AAZ92713;  
 XX  
 DT 13-FEB-2002 (first entry)  
 XX  
 DE DNA encoding novel human diagnostic protein #28517.  
 XX  
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200175067-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 30-MAR-2001; 2001WO-US08631.  
 XX  
 PR 31-MAR-2000; 2000US-0540217.  
 PR 23-AUG-2000; 2000US-0649167.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Drmanac RT, Liu C, Tang YT;  
 XX  
 DR WPI; 2001-639362/73.  
 DR P-PSDB; ABG28526.  
 XX

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -

Claim 1; SEQ ID No 28517; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical







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OW nucleic - nucleic search, using sw model

Run on: June 11, 2003, 18:10:29 ; Search time 2548 Seconds  
(without alignments)  
10062.003 Million cell updates/sec

Title: US-09-674-195C-1  
Perfect score: 3862  
Sequence: 1 ggaatcctgctggtccgata.....aacaccttcaaaagatgcc 3862

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7602234 seqs, 3319262570 residues

Total number of hits satisfying chosen parameters: 15204468

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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  - 2: /cgn2.6/ptodata/2/pna/US06\_NEW\_COMB.seq.\*
  - 3: /cgn2.6/ptodata/2/pna/US07\_NEW\_COMB.seq.\*
  - 4: /cgn2.6/ptodata/2/pna/US08\_NEW\_COMB.seq.\*
  - 5: /cgn2.6/ptodata/2/pna/US09\_NEW\_COMB.seq.\*
  - 6: /cgn2.6/ptodata/2/pna/US09\_NEW\_COMB.seq2.\*
  - 7: /cgn2.6/ptodata/2/pna/US09\_NEW\_COMB.seq3.\*
  - 8: /cgn2.6/ptodata/2/pna/US10\_NEW\_COMB.seq.\*
  - 9: /cgn2.6/ptodata/2/pna/US10\_NEW\_COMB.seq2.\*
  - 10: /cgn2.6/ptodata/2/pna/US60\_NEW\_COMB.seq.\*
  - 11: /cgn2.6/ptodata/2/pna/US60\_NEW\_COMB.seq2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3861	100.0	3862	5	US-09-674-195C-1
2	3861	100.0	3862	6	US-09-674-195B-1
3	396	10.3	1739	8	US-10-369-493-36590
4	345.6	8.9	2258	8	US-10-369-493-27243
5	259.8	6.7	1146	7	US-09-675-784A-1693
6	249.2	6.5	2794	10	US-60-459-902-29
7	180	4.7	2274	8	US-10-156-761-347
8	180	4.7	9025608	8	US-10-156-761-1
9	178.6	4.6	2133	9	US-10-282-122A-31325
10	178.4	4.6	2071	8	US-10-369-493-42972
11	173.8	4.5	2319	8	US-10-369-493-47146
12	173.6	4.5	2247	9	US-10-282-122A-19563
13	172.8	4.5	2163	8	US-10-282-122A-25910
14	172.2	4.5	2283	8	US-10-417-886-3735
15	172	4.5	2052	8	US-10-369-493-44226
16	170.4	4.4	2256	9	US-10-282-122A-23604
17	168.8	4.4	2061	8	US-10-369-493-47050
18	167.4	4.3	2105	9	US-10-282-122A-8801
19	167.2	4.3	2313	8	US-10-446-203-701
20	164	4.2	1923	8	US-10-369-493-31575
21	162.6	4.2	2109	8	US-10-369-493-35598
22	162.4	4.2	933	8	US-10-369-493-33235

23	161	4.2	2128	8	US-10-369-493-34178	Sequence 34178, A
24	161	4.2	2148	8	US-10-431-652-2704	Sequence 2704, Ap
25	159.4	4.1	1995	9	US-10-282-122A-9519	Sequence 9519, Ap
26	159.4	4.1	2097	8	US-10-369-493-41486	Sequence 41486, A
27	159.4	4.1	2118	8	US-10-369-493-33952	Sequence 33952, A
28	158.4	4.1	2136	8	US-10-369-493-40960	Sequence 40960, A
29	157.8	4.1	2136	8	US-10-369-493-24541	Sequence 24541, A
30	157.8	4.1	2262	9	US-10-282-122A-6694	Sequence 6694, Ap
31	156.2	4.0	717	8	US-10-369-493-40088	Sequence 40088, A
32	156	4.0	2008	9	US-10-282-122A-36732	Sequence 36732, A
33	156	4.0	2349	8	US-10-425-114-28431	Sequence 28431, A
34	154.6	4.0	1713	9	US-10-282-122A-33173	Sequence 33173, A
35	154.6	4.0	2103	8	US-10-369-493-39039	Sequence 39039, A
36	154.6	4.0	2103	8	US-10-369-493-39406	Sequence 39406, A
37	154.4	4.0	2253	9	US-10-282-122A-39396	Sequence 39396, A
38	153	4.0	2106	8	US-10-369-493-40077	Sequence 40077, A
39	152.8	4.0	2019	8	US-10-369-493-38377	Sequence 38377, A
40	152.8	4.0	2019	8	US-10-369-493-38860	Sequence 38860, A
41	152.8	4.0	2091	8	US-10-369-493-31272	Sequence 31272, A
42	152.8	4.0	2097	8	US-10-369-493-28513	Sequence 28513, A
43	152.8	4.0	2109	8	US-10-369-493-35195	Sequence 35195, A
44	152.8	4.0	2121	9	US-10-282-122A-13322	Sequence 13322, A
45	152.8	4.0	2245	8	US-10-369-493-27469	Sequence 27469, A

ALIGNMENTS

RESULT 1  
US-09-674-195C-1  
; Sequence 1, Application US/09674195C  
; GENERAL INFORMATION:  
; APPLICANT: Rosely M. Zancoppe-Oliveira  
; APPLICANT: Timothy J. Lott  
; APPLICANT: Leonard W. Mayer  
; APPLICANT: Errol Reiss  
; APPLICANT: George S. Despe  
; TITLE OF INVENTION: NUCLEIC ACIDS OF THE M ANTIGEN GENE OF  
; TITLE OF INVENTION: HISTOPLASMA CAPSULATUM, ANTIGENS, VACCINES AND ANTIBODIES,  
; TITLE OF INVENTION: METHODS AND KITS FOR DETECTING HISTOPLASMOIS  
; FILE REFERENCE: 14114.0325U2  
; CURRENT APPLICATION NUMBER: US/09/674,195C  
; CURRENT FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: PCT/US99/09151  
; PRIOR FILING DATE: 1999-04-27  
; PRIOR APPLICATION NUMBER: 60/083,676  
; PRIOR FILING DATE: 1998-04-30  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 3862  
; TYPE: DNA  
; ORGANISM: Histoplasma capsulatum  
; FEATURE:  
; NAME/KEY: misc-feature  
; LOCATION: 3258  
; OTHER INFORMATION: n = g, a, c or t(u)  
US-09-674-195C-1  
Query Match 100.0%; Score 3861; DB 5; Length 3862;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3862; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGATCCTGCTGCTCGGATAACTTTGCTTTATTCGAAGGTCCTCGCGAATGCCAGGTGCC 60  
Db 1 GGATCCTGCTGCTCGGATAACTTTGCTTTATTCGAAGGTCCTCGCGAATGCCAGGTGCC 60  
QY 61 ATCGATCATATTTTGAAGTTTATCACCCTCAATGCTTCACCCCATGACGACCTTTTAT 120  
Db 61 ATCGATCATATTTTGAAGTTTATCACCCTCAATGCTTCACCCCATGACGACCTTTTAT 120  
QY 121 TTTTATTTTCATTCATCTTCTCTGTGGCAAAACATGACGATGCGAGTCTCGACCCCTGG 180  
|||||

Db	121	TTTTATTTTCATTTTCATCTTCTGTGTGGCAAAACATGCAAGTATGCGAGCTCTGGACCCCTGG	180
QY	181	GGTGTGGCCCTTGATCATATGGTTTATTTATAGCCGCCCGAAGCCCTGGCCTGTTAAA	240
Db	181	GGTGTGGCCCTTGATCATATGGTTTATTTATAGCCGCCCGAAGCCCTGGCCTGTTAAA	240
QY	241	TTTTGGACCTCTCTCCGCCCATTTTTCAAACTCTGTGTGCTCGTTTCCATTTCCCCCT	300
Db	241	TTTTGGACCTCTCTCCGCCCATTTTTCAAACTCTGTGTGCTCGTTTCCATTTCCCCCT	300
QY	301	TCCCATTTGGGTTTCCCTATAGCCACATCGCTGCCACTCAAGAAGGTCCTCAAGTCAAT	360
Db	301	TCCCATTTGGGTTTCCCTATAGCCACATCGCTGCCACTCAAGAAGGTCCTCAAGTCAAT	360
QY	361	TTGGTCCCTACCTCTCCAACACTATCTGCATATGAATATATATATATATATCTAAGTGC	420
Db	361	TTGGTCCCTACCTCTCCAACACTATCTGCATATGAATATATATATATATCTAAGTGC	420
QY	421	ATTGATTTATTTGCTCTTTCAGCATCTTTTGTCTCGAGCAAGCTTACTCCACGTTCAAT	480
Db	421	ATTGATTTATTTGCTCTTTCAGCATCTTTTGTCTCGAGCAAGCTTACTCCACGTTCAAT	480
QY	481	TCAGGGGTAAAAATGCGGTGCTCAAGCTTATATCTCGCTCGGGGTGTTGTTCTGCG	540
Db	481	TCAGGGGTAAAAATGCGGTGCTCAAGCTTATATCTCGCTCGGGGTGTTGTTCTGCG	540
QY	541	AGCCTGCTCCCTACATGTCAGGGAGATGCTTAGCGGTGAGAAAGGCCCTCGATCGCG	600
Db	541	AGCCTGCTCCCTACATGTCAGGGAGATGCTTAGCGGTGAGAAAGGCCCTCGATCGCG	600
QY	601	CCATGACACTCTCTCCGACCTACGAGCACGTTTCTTAGCAAGTTTACATTGACGATGA	660
Db	601	CCATGACACTCTCTCCGACCTACGAGCACGTTTCTTAGCAAGTTTACATTGACGATGA	660
QY	661	ACAGTCGGTGTAAACAGGACGTGGGTGCTCCCATCGAGACCAACACAGCCTGAAGGC	720
Db	661	ACAGTCGGTGTAAACAGGACGTGGGTGCTCCCATCGAGACCAACACAGCCTGAAGGC	720
QY	721	TGGAATATAGGGCCCACTCTACTGTGAGGATTTTATCTTCGCCAGAAAGATTCAACACTT	780
Db	721	TGGAATATAGGGCCCACTCTACTGTGAGGATTTTATCTTCGCCAGAAAGATTCAACACTT	780
QY	781	TGATCATGAGAGGATGTAGATACAAAATATGTGACCGTTTGCAAAATCCGCTAAATCA	840
Db	781	TGATCATGAGAGGATGTAGATACAAAATATGTGACCGTTTGCAAAATCCGCTAAATCA	840
QY	841	ATTTTAGCAGGTTCTCTGAGCGGCCCTCCATGCTCGAGGAGCTGTGTCGCCATGGGTAT	900
Db	841	ATTTTAGCAGGTTCTCTGAGCGGCCCTCCATGCTCGAGGAGCTGTGTCGCCATGGGTAT	900
QY	901	TCATCCTATATATACGTGTCAATATACAGCCGCATCTTCTTGAACGCGCGCAGGAA	960
Db	901	TCATCCTATATATACGTGTCAATATACAGCCGCATCTTCTTGAACGCGCGCAGGAA	960
QY	961	AGCAGACACAGTATTCTGTCGGTTTTCTACAGTCGCTGTATACCGATGAAGCAATTTTGGTA	1020
Db	961	AGCAGACACAGTATTCTGTCGGTTTTCTACAGTCGCTGTATACCGATGAAGCAATTTTGGTA	1020
QY	1021	CTGCTCGGATATCCAGGATTTGGACCCGCTGTGTATACCGATGAAGCAATTTTGGTA	1080
Db	1021	CTGCTCGGATATCCAGGATTTGGACCCGCTGTGTATACCGATGAAGCAATTTTGGTA	1080
QY	1081	AGCATATATCGTGGTAGTCAATCATACAGCACAAATATGAATACAAACCCAGG	1140
Db	1081	AGCATATATCGTGGTAGTCAATCATACAGCACAAATATGAATACAAACCCAGG	1140
QY	1141	ACGTAGGCTACTCTCGCAATGTAGATATCGTCGGAAACAACTTCCAGTCTTCTTCA	1200
Db	1141	ACGTAGGCTACTCTCGCAATGTAGATATCGTCGGAAACAACTTCCAGTCTTCTTCA	1200
QY	1201	TTCAAGACGCTATTCAATTTCCCTGATTTGATTCAGCTGTCAAGCGCAACACAGAGTG	1260
Db	1201	TTCAAGACGCTATTCAATTTCCCTGATTTGATTCAGCTGTCAAGCGCAACACAGAGTG	1260

QY	1261	AAATTCCCAGGCTGCAACTGCACATGATACGGCATGGGATTTCTCTCAGCCAGCAGCCCA	1320
Db	1261	AAATTTCCCAGGCTGCAACTGCACATGATACGGCATGGGATTTCTCTCAGCCAGCAGCCCA	1320
QY	1321	GCTCATTTGCATGCCCTCTCTTGGGCAATGTCAGGACATGGAATCCCTCGCTCAATCGCTC	1380
Db	1321	GCTCATTTGCATGCCCTCTCTTGGGCAATGTCAGGACATGGAATCCCTCGCTCAATCGCTC	1380
QY	1381	ATGTTGATGGGTGGGGCGTCCATACCTTCCGACTTGTCAACGACGAGGCGCACTGCACCT	1440
Db	1381	ATGTTGATGGGTGGGGCGTCCATACCTTCCGACTTGTCAACGACGAGGCGCACTGCACCT	1440
QY	1441	TGGTCAAGTTTCGCTGGGAAGACCTTCCAAGGAAGAGCGGCGCTGGTATGGGAAGAGGCAC	1500
Db	1441	TGGTCAAGTTTCGCTGGGAAGACCTTCCAAGGAAGAGCGGCGCTGGTATGGGAAGAGGCAC	1500
QY	1501	AGGCTCTTTGGGGAAAGAAATCCCGACTTCCATCGAAGACCTCTGGGATGCCATTTGAAT	1560
Db	1501	AGGCTCTTTGGGGAAAGAAATCCCGACTTCCATCGAAGACCTCTGGGATGCCATTTGAAT	1560
QY	1561	CTGGGAAGTACCCCTAGTGGAGGTAAGATATGATTTCCCCCAAAATCATTAGTTCCTGACAG	1620
Db	1561	CTGGGAAGTACCCCTAGTGGAGGTAAGATATGATTTCCCCCAAAATCATTAGTTCCTGACAG	1620
QY	1621	TGTTTCTCTGCTCTGCTGGTTCCTTTTTCGCTCTTTCTATATCTTCAACTTAAGACTTGA	1680
Db	1621	TGTTTCTCTGCTCTGCTGGTTCCTTTTTCGCTCTTTCTATATCTTCAACTTAAGACTTGA	1680
QY	1681	CTTTATATACGTTTTACTCATATAGCTGGGCTTTCAATTTGGTGAATGAAGACAGATCAATC	1740
Db	1681	CTTTATATACGTTTTACTCATATAGCTGGGCTTTCAATTTGGTGAATGAAGACAGATCAATC	1740
QY	1741	CAAGTTTGATTTGATCTATTAGATCCCAACCAATATCCAGAAAGAACTTGTTCCTTT	1800
Db	1741	CAAGTTTGATTTGATCTATTAGATCCCAACCAATATCCAGAAAGAACTTGTTCCTTT	1800
QY	1801	CACCCCAATCGGAAAATGCTTTGAACCGAAACCCAAAGAACTTATTTGCGGAAACTGA	1860
Db	1801	CACCCCAATCGGAAAATGCTTTGAACCGAAACCCAAAGAACTTATTTGCGGAAACTGA	1860
QY	1861	GCAGATCATGTTGGTCCACCCCTATATATTTGGAAATGAAATACATGTATAGCTAGAT	1920
Db	1861	GCAGATCATGTTGGTCCACCCCTATATATTTGGAAATGAAATACATGTATAGCTAGAT	1920
QY	1921	GAGCGGTATATCAAATATATTTCCACAGTTCACACAGGTCATGTAGTTCGCGGAATCG	1980
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QY	1981	ATTTCAGGATGACCTTTGCTTCAGGCGCGTGTACTCTACTCTGACACTCAATTTGA	2040
Db	1981	ATTTCAGGATGACCTTTGCTTCAGGCGCGTGTACTCTACTCTGACACTCAATTTGA	2040
QY	2041	ATCGCCATGGAGTCCCAACTTTCGAGCAACTGCCGATCAACAGACCCCGATCCCATTC	2100
Db	2041	ATCGCCATGGAGTCCCAACTTTCGAGCAACTGCCGATCAACAGACCCCGATCCCATTC	2100
QY	2101	ATAACAACTCGGACGGTGTGTGAAGCTTCTCACTACCATGTCAACTTCGCATC	2160
Db	2101	ATAACAACTCGGACGGTGTGTGAAGCTTCTCACTACCATGTCAACTTCGCATC	2160
QY	2161	TTGACCCAACTCGATTTGTATAGATTTAACTCCCGTCTGCACAGGACAAATGTTTCA	2220
Db	2161	TTGACCCAACTCGATTTGTATAGATTTAACTCCCGTCTGCACAGGACAAATGTTTCA	2220
QY	2221	CCCTCTAAACACGGCCGATATACACCAACTCAATGAGCAAGGATTTCCACCAACAAGC	2280
Db	2221	CCCTCTAAACACGGCCGATATACACCAACTCAATGAGCAAGGATTTCCACCAACAAGC	2280
QY	2281	CAACGGACCCATAACAGAGATTTCTCACCGACCTGGCGGTATGGTAAATGGACCACT	2340
Db	2281	CAACGGACCCATAACAGAGATTTCTCACCGACCTGGCGGTATGGTAAATGGACCACT	2340

[illegible]

Db	3421	GAGCAAAATGATGATAGATTACAAATAATTGCACACCCCAATAGGCTTCCCTCAGGATA	3480
Qy	3481	TCAGATATTATCATCATGTTGTAATGATACCTCAAAAATGCCACAAGCTTGCTTGATAT	3540
Db	3481	TCAGATATTATCATCATGTTGTAATGATACCTCAAAAATGCCACAAGCTTGCTTGATAT	3540
Qy	3541	TGAATATTTATATGCTGCTAAATGTAGGGAAGACGGTACCATCCAAATAACCCAGAAAAACA	3600
Db	3541	TGAATATTTATATGCTGCTAAATGTAGGGAAGACGGTACCATCCAAATAACCCAGAAAAACA	3600
Qy	3601	TGTTTTAGCTTAAAACTCTCACTAAGGTCGGTCGTGCTATTTCGAATTGGCTGGCGCAAGC	3660
Db	3601	TGTTTTAGCTTAAAACTCTCACTAAGGTCGGTCGTGCTATTTCGAATTGGCTGGCGCAAGC	3660
Qy	3661	TGACTATCTGATAAAAAATGCTGTATTCTCGCTTTCACGACGCATGTTATGACTTTCGAAT	3720
Db	3661	TGACTATCTGATAAAAAATGCTGTATTCTCGCTTTCACGACGCATGTTATGACTTTCGAAT	3720
Qy	3721	ATAGATAAAACCTGAACGATTTTAGCCCTCTTGGGGAAATAGGGGTAGGGGGGGAGC	3780
Db	3721	ATAGATAAAACCTGAACGATTTTAGCCCTCTTGGGGAAATAGGGGTAGGGGGGGAGC	3780
Qy	3781	TACATATCATTTCCCATATGACCAAAAACTAAATAGATATATATATATATATATATAT	3840
Db	3781	TACATATCATTTCCCATATGACCAAAAACTAAATAGATATATATATATATATATATATAT	3840
Qy	3841	ACAACACCTTCAAAAAGATCC	3862
Db	3841	ACAACACCTTCAAAAAGATCC	3862

## RESULT 2

```

US-09-674-195B-1
; Sequence 1, Application US/09674195B
; GENERAL INFORMATION:
; APPLICANT: Rosely M. Zancope-Oliveira
; APPLICANT: Timothy J. Lott
; APPLICANT: Leonard W. Mayer
; APPLICANT: Errol Reiss
; APPLICANT: George S. Deepe
; TITLE OF INVENTION: NUCLEIC ACIDS OF THE M ANTIGEN GENE OF
; TITLE OF INVENTION: HISTOPLASMA CAPSULATUM, ANTIGENS, VACCINES, AND ANTIBODIES,
; TITLE OF INVENTION: METHODS AND KITS FOR DETECTING HISTOPLASMOSIS
; FILE REFERENCE: 14114.0325U2
; CURRENT APPLICATION NUMBER: US/09/674,195B
; CURRENT FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: PCT/US99/09151
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,676
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3862
; TYPE: DNA
; ORGANISM: Histoplasma capsulatum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3258
; OTHER INFORMATION: n = g, a, c or t(u)
US-09-674-195B-1

```

	Query Match	100.0%;	Score 3861;	DB 6;	Length 3862;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 3862;	Conservative	0;	Mismatches	0;
				Indels	Gaps
				0;	0
QY	1	GGATCCTGCTGCTCGGATAACTTTTGCTTTATCTCAAGGGTCTCGCGAATGCCAGGTGCC	60		
Db	1	GGATCCTGCTGCTCGGATTAACCTTTTGCTTTATCCAAAGGTCTCGCGAATGCCAGGTGCC	60		
QY	61	ATCGCATCTATATTTTGAAGTTTATCACCTCAATGGCTTACCCCATGAGCGACCTTTTAT	120		

Db 61 ATCGATCTATATTTGAAGTTTATCACTCAATGAGTTTACCCCATGACGACCTTTTAT 120  
QY 121 TTTTATTTTATTCATCATCTTCTCTGTTGGCAACATGAGGTATCGAGCTCTGGACCTGG 180  
Db 121 TTTTATTTTATTCATCATCTTCTCTGTTGGCAACATGAGGTATCGAGCTCTGGACCTGG 180  
QY 181 GGTGTGGCCCTTGATGATATGTTTATTTATAGCCGCCCGGAAGCCCTGGCTGTAA 240  
Db 181 GGTGTGGCCCTTGATGATATGTTTATTTATAGCCGCCCGGAAGCCCTGGCTGTAA 240  
QY 241 TTTTGGACCTTCCFCCCGCCATCTTTCCAAACTTCTGTGGTCTGGTTCCTCCATTTCC 300  
Db 241 TTTTGGACCTTCCFCCCGCCATCTTTCCAAACTTCTGTGGTCTGGTTCCTCCATTTCC 300  
QY 301 TCCCCATTTGGGTTCCTATAGGCCACTCGCTGCTCCACTCAAGAGGGTCCCACTCAAT 360  
Db 301 TCCCCATTTGGGTTCCTATAGGCCACTCGCTGCTCCACTCAAGAGGGTCCCACTCAAT 360  
QY 361 TTGGTCCCTACCTCTCCAACTATCTGCATATGTAATATATATATATATATATATAT 420  
Db 361 TTGGTCCCTACCTCTCCAACTATCTGCATATGTAATATATATATATATATATATAT 420  
QY 421 ATTGATTAATTTCTCTTTCAGCATCTTTTCTGCTCGAGCAAGCTTACTCCAGCTCAAT 480  
Db 421 ATTGATTAATTTCTCTTTCAGCATCTTTTCTGCTCGAGCAAGCTTACTCCAGCTCAAT 480  
QY 481 TCAGGGGTAAATGCGGTCTGCTCAAGTTATACTCGCTCGGGGTGTGTTCG 540  
Db 481 TCAGGGGTAAATGCGGTCTGCTCAAGTTATACTCGCTCGGGGTGTGTTCG 540  
QY 541 AGCCTGTCCCTACATGTGAGGGAGATGCTAGGGTTCAGAAAGCCCTCGATCGCG 600  
Db 541 AGCCTGTCCCTACATGTGAGGGAGATGCTAGGGTTCAGAAAGCCCTCGATCGCG 600  
QY 601 CCATGACACTCTCTCCGACCTACGGACAGTTTCTTAGCAAGTTTACATTGACGATGA 660  
Db 601 CCATGACACTCTCTCCGACCTACGGACAGTTTCTTAGCAAGTTTACATTGACGATGA 660  
QY 661 ACAGTGGTGTAAACAGGACGTGGGTGGTCCCATCGAGACCAACACAGCCCTGAAGG 720  
Db 661 ACAGTGGTGTAAACAGGACGTGGGTGGTCCCATCGAGACCAACACAGCCCTGAAGG 720  
QY 721 TGGAAATAGAGCCCACTACTGAGGATTTTATCTCGCCGAGAGATTCAACACTT 780  
Db 721 TGGAAATAGAGCCCACTACTGAGGATTTTATCTCGCCGAGAGATTCAACACTT 780  
QY 781 TGATCATGAGAGGTATGTAGATCAAAATATGTGACCGTGTGCCAATCGCTAATCA 840  
Db 781 TGATCATGAGAGGTATGTAGATCAAAATATGTGACCGTGTGCCAATCGCTAATCA 840  
QY 841 ATTTTACGAGGTTCTGAGCGCCGCTCCATGCTCGAGGAGTGTGTGCCCATGGCGTAT 900  
Db 841 ATTTTACGAGGTTCTGAGCGCCGCTCCATGCTCGAGGAGTGTGTGCCCATGGCGTAT 900  
QY 901 TCACATCTTATAAATGCTCGAATATACAGCCGATCCTCTTGAAGCGGCGAGAA 960  
Db 901 TCACATCTTATAAATGCTCGAATATACAGCCGATCCTCTTGAAGCGGCGAGAA 960  
QY 961 AGCAGACACAGTATTCGTGGTCTTCTACAGTCTGCTAGCAGAGGAGTGTGACT 1020  
Db 961 AGCAGACACAGTATTCGTGGTCTTCTACAGTCTGCTAGCAGAGGAGTGTGACT 1020  
QY 1021 CTGCTCGGATATCCAGGATTTTGGACCGCTGTATACCGATGAAGCAATTTTGGTA 1080  
Db 1021 CTGCTCGGATATCCAGGATTTTGGACCGCTGTATACCGATGAAGCAATTTTGGTA 1080  
QY 1081 AGCATTATATCGTGGTAGTCTATCTATACAGCACAACAAATATGAATACAAACCCAG 1140  
Db 1081 AGCATTATATCGTGGTAGTCTATCTATACAGCACAACAAATATGAATACAAACCCAG 1140  
QY 1141 ACCTAGGCTACTCTGGCAATGTAGATATCGTCGGAACACAGTTCAGTCTCTTCA 1200  
Db 1141 ACCTAGGCTACTCTGGCAATGTAGATATCGTCGGAACACAGTTCAGTCTCTTCA 1200

QY 1201 TTCAGGACGCTATTCAATTCCTGTATTTGATTCAGCTGTCAAGCCGCAACAGACAGTG 1260  
Db 1201 TTCAGGACGCTATTCAATTCCTGTATTTGATTCAGCTGTCAAGCCGCAACAGACAGTG 1260  
QY 1261 AAATTTCCCAAGCTCGCAACTGACATGATACGGCATGGATTTCTCAGCCAGCAGCCCA 1320  
Db 1261 AAATTTCCCAAGCTCGCAACTGACATGATACGGCATGGATTTCTCAGCCAGCAGCCCA 1320  
QY 1321 GCTCATTTGCATGCCCTCTTCTGGGCAATGTCAGGACATGGAATCCCTGCTCAATGGGTC 1380  
Db 1321 GCTCATTTGCATGCCCTCTTCTGGGCAATGTCAGGACATGGAATCCCTGCTCAATGGGTC 1380  
QY 1381 ATGTTGATGGGTGGGGGCTCCATACCTTCGACTTTGTCACGAGAGGGCAACTCGACCT 1440  
Db 1381 ATGTTGATGGGTGGGGGCTCCATACCTTCGACTTTGTCACGAGAGGGCAACTCGACCT 1440  
QY 1441 TGGTCAAGTTTCGCTGGAGACCTCCAGAGAAAGAGGGGCTGGTATGGGAAGAGCAC 1500  
Db 1441 TGGTCAAGTTTCGCTGGAGACCTCCAGAGAAAGAGGGGCTGGTATGGGAAGAGCAC 1500  
QY 1501 AGGCTCTTGGCGGAAAGAAATCCCGACTTCCATCGACAAGACCTCTGGSATGCCATTCAT 1560  
Db 1501 AGGCTCTTGGCGGAAAGAAATCCCGACTTCCATCGACAAGACCTCTGGSATGCCATTCAT 1560  
QY 1561 CTGGAAGGTACCCTGAGTGGGAGTAAATATGATTTCCCAATCAATTAATTTCTGACAG 1620  
Db 1561 CTGGAAGGTACCCTGAGTGGGAGTAAATATGATTTCCCAATCAATTAATTTCTGACAG 1620  
QY 1621 TGTTCCTCTCTGTGCTGGTCTTTCGCTCTTTTCTTATATCTTCACTAAGACTGA 1680  
Db 1621 TGTTCCTCTCTGTGCTGGTCTTTCGCTCTTTTCTTATATCTTCACTAAGACTGA 1680  
QY 1681 CTTTATATAGCTTTTACTCATATAGTGGGCTTTCAATTTGGTGAATTAAGAGCATCAATC 1740  
Db 1681 CTTTATATAGCTTTTACTCATATAGTGGGCTTTCAATTTGGTGAATTAAGAGCATCAATC 1740  
QY 1741 CAAGTTTGAATTCGATCTATTAGATCCCAAAATCATCCCAAGAAACTTTGTCCTTT 1800  
Db 1741 CAAGTTTGAATTCGATCTATTAGATCCCAAAATCATCCCAAGAAACTTTGTCCTTT 1800  
QY 1801 CACCCCAATCGGAAATAATGGTCTTGACCGAAACCCCAAAAGTTATTTTCCGGAACCTGA 1860  
Db 1801 CACCCCAATCGGAAATAATGGTCTTGACCGAAACCCCAAAAGTTATTTTCCGGAACCTGA 1860  
QY 1861 GCAGATCATGGTGGTTCACCCCTATATATTTGGAAATGAATACATGTATAGTAGAT 1920  
Db 1861 GCAGATCATGGTGGTTCACCCCTATATATTTGGAAATGAATACATGTATAGTAGAT 1920  
QY 1921 GAAGCTATATCTAAATATATTTCCACAGTTTCCACAGTTTCCACAGGTCATCTAGTTCGCGGAATCG 1980  
Db 1921 GAAGCTATATCTAAATATATTTCCACAGTTTCCACAGGTCATCTAGTTCGCGGAATCG 1980  
QY 1981 ATTTACGAGTACGACCTTTGCTTCAAGGCGGCTTGTACTCTTACCTTGACACTCAATTTGA 2040  
Db 1981 ATTTACGAGTACGACCTTTGCTTCAAGGCGGCTTGTACTCTTACCTTGACACTCAATTTGA 2040  
QY 2041 ATCGCATGGAGGTCCCACTTCGAGCAACTGCCGATCAACAGACCCCGCATCCCATTC 2100  
Db 2041 ATCGCATGGAGGTCCCACTTCGAGCAACTGCCGATCAACAGACCCCGCATCCCATTC 2100  
QY 2101 ATAACAACAACTCGGACGCTGTGTAGTACTTTCTCACCTAGCATGTCAACTTCCATC 2160  
Db 2101 ATAACAACAACTCGGACGCTGTGTAGTACTTTCTCACCTAGCATGTCAACTTCCATC 2160  
QY 2161 TTGACCCCAATCGATTTGTATAGATTAATTAACATCCCGTCTGACAGGACAAATTTTCAT 2220  
Db 2161 TTGACCCCAATCGATTTGTATAGATTAATTAACATCCCGTCTGACAGGACAAATTTTCAT 2220  
QY 2221 CCCTCTAAACAGGCGGCGATATACACCACTCAATGAGCAACGGATTTCCACAAACAGC 2280  
Db 2221 CCCTCTAAACAGGCGGCGATATACACCACTCAATGAGCAACGGATTTCCACAAACAGC 2280

2281 CAACGGACCCATACAGAGGATCTTCAACGGACCTGGCGGTATGGTAATAGGACCACT 2340  
2281 CAACGGACCCATACAGAGGATCTTCAACGGACCTGGCGGTATGGTAATAGGACCACT 2340  
2341 AGTGGGGAGCTAGCCGGAGCTTCAACGAGCTGTGTCTCCCAACCGGCTCTCTTCTACAA 2400  
2341 AGTGGGGAGCTAGCCGGAGCTTCAACGAGCTGTGTCTCCCAACCGGCTCTCTTCTACAA 2400  
2401 CTCACCTACGGTCTTTCGAGAGCAATCTCTGTCACAGCCCATCGGCTTTCGAAACCTCCCA 2460  
2401 CTCACCTACGGTCTTTCGAGAGCAATCTCTGTCACAGCCCATCGGCTTTCGAAACCTCCCA 2460  
2461 CGTGGGAGTGAACCGGTGCTAAGACGTCATCATCCAGCTGAACCGCTGCGACAACGA 2520  
2461 CGTGGGAGTGAACCGGTGCTAAGACGTCATCATCCAGCTGAACCGCTGCGACAACGA 2520  
2521 CCTCCGCCCGCGCTGCGGCTAGCTATCGGCGTGGAAACCCCATCCCGGAGCCCAACCTT 2580  
2521 CCTCCGCCCGCGCTGCGGCTAGCTATCGGCGTGGAAACCCCATCCCGGAGCCCAACCTT 2580  
2581 CTACCAACACAGGCAACCGTCCCATCGGACCTTCGGGACGAAATCTCTGCGGCTCGA 2640  
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2641 CGGGCTGAACATCGCCCTCTGACAGAGACGAGTGTAGCTTACGATCGCGGAGCAGCT 2700  
2641 CGGGCTGAACATCGCCCTCTGACAGAGACGAGTGTAGCTTACGATCGCGGAGCAGCT 2700  
2701 CGGGCGCGGTTTAAACAGCGCCCAACAAAGTAGATATCGTCTAGTGGGCTCATCGCT 2760  
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2821 CGTGATCGTGGCGGCTGCTACAGAGCCCTCAACGCAATACCCCAAGAGGTGCGCC 2880  
2821 CGTGATCGTGGCGGCTGCTACAGAGCCCTCAACGCAATACCCCAAGAGGTGCGCC 2880  
2881 GCTCAGATATTACGGATGCAATACCGGTATGGAAGCCGCTGGCGGCTGGGTGACGG 2940  
2881 GCTCAGATATTACGGATGCAATACCGGTATGGAAGCCGCTGGCGGCTGGGTGACGG 2940  
2941 TAGCAATGAAGCCCTTCGTGACGCTCTTATGGCGCTGGTGGGATGCGTCAATGGGCT 3000  
2941 TAGCAATGAAGCCCTTCGTGACGCTCTTATGGCGCTGGTGGGATGCGTCAATGGGCT 3000  
3001 GGACCGCCGGTGTGTATATTTCCACAGATGAGTGAGGCTAGCTTAGAGTGTCTT 3060  
3001 GGACCGCCGGTGTGTATATTTCCACAGATGAGTGAGGCTAGCTTAGAGTGTCTT 3060  
3061 GGACGGATTACGGCATATCGTCTTGAATCGGTTCCGCTTGGATAGAGCTTGTATG 3120  
3061 GGACGGATTACGGCATATCGTCTTGAATCGGTTCCGCTTGGATAGAGCTTGTATG 3120  
3121 AGGTTTGGGCGCAATATGGGTTTACTACCCCGCCCGCCCGCCCGCCCGCCCGCCCG 3180  
3121 AGGTTTGGGCGCAATATGGGTTTACTACCCCGCCCGCCCGCCCGCCCGCCCGCCCG 3180  
3181 CTGTTTTTCCATCTTGGTGGATATATTCAGATATACGTAATATTCGTTTACGAA 3240  
3181 CTGTTTTTCCATCTTGGTGGATATATTCAGATATACGTAATATTCGTTTACGAA 3240  
3241 GCCGGTGTCAAGCTTCANGAGGCTTAATTAATTTGAAGAGGAGGTGAAGTGAATCTTG 3300  
3241 GCCGGTGTCAAGCTTCANGAGGCTTAATTAATTTGAAGAGGAGGTGAAGTGAATCTTG 3300  
3301 GTGTAACTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTC 3360  
3301 GTGTAACTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTC 3360  
3361 TCTCACATTCATCTATATTGATCTTGTCTTGTAGCTGTGTTAAATATAAGCCCAAGA 3420

3361 TCTCACATTCATCTATATTGATCTTGTCTTGTAGCTGTGTTAAATATAAGCCCAAGA 3420  
3421 GAGACAAATAATGATAGATTAACAATAATTCACACCCCATAGGCTTCCCTCAGGATA 3480  
3421 GAGACAAATAATGATAGATTAACAATAATTCACACCCCATAGGCTTCCCTCAGGATA 3480  
3481 TCAGATATTATCTATCATCTGTTGTAATGATACCTCAAAAATGCCAAGCTTGCCTGATAT 3540  
3481 TCAGATATTATCTATCATCTGTTGTAATGATACCTCAAAAATGCCAAGCTTGCCTGATAT 3540  
3541 TGAATATTTATGCTGTAATGTAAGGAGAGCTACCATCCAATAACCAAGAAACACA 3600  
3541 TGAATATTTATGCTGTAATGTAAGGAGAGCTACCATCCAATAACCAAGAAACACA 3600  
3601 TGTTTTAGCTTAAATCTCACTAAGCTCGTGTCTATTGAAATGGCTGCGGCAAGC 3660  
3601 TGTTTTAGCTTAAATCTCACTAAGCTCGTGTCTATTGAAATGGCTGCGGCAAGC 3660  
3661 TGACTATCTGATAAAAATGCTGTATTTCCGCTTCACGAGCATGTTATGACTTTCGAAT 3720  
3661 TGACTATCTGATAAAAATGCTGTATTTCCGCTTCACGAGCATGTTATGACTTTCGAAT 3720  
3721 ATAGATAAAACCTGACGAGTTCACCCCTGTTGGGGGAAATAGGGTGGGGGCGAGC 3780  
3721 ATAGATAAAACCTGACGAGTTCACCCCTGTTGGGGGAAATAGGGTGGGGGCGAGC 3780  
3781 TACATATCATCTCCATATGACCAAACTAAATAGATATATATATATATATATATATAT 3840  
3781 TACATATCATCTCCATATGACCAAACTAAATAGATATATATATATATATATATATAT 3840  
3841 ACAACACCTTCAAAAAGGATCC 3862  
3841 ACAACACCTTCAAAAAGGATCC 3862

RESULT 3  
US-10-369-493-36590  
; Sequence 36590, Application US/10369493  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; PRIOR FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 36590  
; LENGTH: 1739  
; TYPE: DNA  
; ORGANISM: Aspergillus nidulans  
US-10-369-493-36590

Query Match 10.3%; Score 396; DB 8; Length 1739;  
Best Local Similarity 56.1%; Pred. No. 3.3e-93;  
Matches 1035; Conservative 0; Mismatches 600; Indels 209; Gaps 7;  
QY 615 CGGACCTACGACCAAGTTCTTACCAAGTTTACATGACGATGAACAGCTGGGTGCTAA 674  
DB 101 CGAGGCCACTGAGGAATTTCTGTCGAGTACTCTTGACGACACGACGCTGCTACCTGA 160  
QY 675 CAACGACCTGGGTGCTGCCATCAGAGCAACACAGCCTGAAGCTGGAATAGAGGCC 734  
DB 161 CGACTGACCTGCGGCGCCCAATAGGACCAAGAGTCTCAAGCGCGGTGCGCGGCT 220  
QY 735 CAACCTACTGTAGGATTTTATCTCCGCCAAGAGTCAACACTTTGATCATGAGAGG 794

Db 221 CTACCCCTGCTGGAGACTTTATCTTCCTCGTCAGAGATCCAGGATTCGACCCAGCGGG 280  
 QY 795 TATGTAGATCAAAATATGTACCGTGTTCGAAATCCGCTAAATCAATTTTACGAGGTT 854  
 Db 281 TGAGTACTGAGGACTCTTCAATGTCGATTGAA-ACGTTGGATGCTGACTGCGCAGGTC 339  
 QY 855 CCTGAGCGCGCTCCATGCTCAGAGAGCTGGTGCCTATGCGGATATTCACATCTTATAAT 914  
 Db 340 CCGAGGCTGCCGTCCATGCTCGGGGTGCAGGTGCCACGGGTCTCTACCTCGTACGCG 399  
 QY 915 AACTGGTTCGAATATCAGCGCATCTTCTTGAACGCGGAGGAGGAGGAGCAGACAGTA 974  
 Db 400 GACTTCTCCAAATCAGCGCGCTCTCTCTCTGCTGAGGGTAAAGAGAGACCCCGTC 459  
 QY 975 TTCTGGGTTTCTACAGTCGCTGTAGCAGGCGAGTGTGACTCTCTGCTCGCATATC 1034  
 Db 460 TTCTGCGGTTCTGACCGCTGCGGCGAGTCTGCGAGTCTGACCTGCGCGCGCATGTC 519  
 QY 1035 CAGGATTTGCGACCGCTCTGTATACCGATGAGCAATTTGGTAAGCATATATCGTG 1094  
 Db 520 CAGGTTTCGCCACCGCTTTTACACTGACGAGGCGCACTTT----- 561  
 QY 1095 GTAGTCATCTANTACAGCACAAATATGAATACAAACCCAGGACTAGGCTGACTA 1154  
 Db 562 ----- 561  
 QY 1155 CTCGGCAATGTAGATATCTCGGAACACGTTTCAGTCTTCTTCATTTCAGAGCGCTATT 1214  
 Db 562 -----GATATGCTCGGTAAACAAATTCCTCGTCTTTTTCATCCAGGATGCCATC 609  
 QY 1215 CAATTCCTCGATTGATTACGCTGTCAAGCGCGCAACAGCAGTGAATTTCCCGAGCT 1274  
 Db 610 CAGTTTCCCGAGCTGATCCAGCGCTCAAGCCAGGCGGATCGTGAATCCCGAGGCT 669  
 QY 1275 GCAACTGACATGATACGCGATGGATTTCTCAGCAGCAGCAGCAGCAGTCAATTCATGCC 1334  
 Db 670 GCCAGCGCATGACGCGCTGGGATTTCTCAGCCAGCAGCAGCAGCAGTCTTCACACC 729  
 QY 1335 CTCCTTCTGGCAATGTACGAGCATGGAATCCCTCGCTCAATGCGTCATGTTGATGGGTG 1394  
 Db 730 CTGCTCTGGGCATGGCGGTCACGGTATCCCGGTTCTGTCGCCAGCTGATGGGTTC 789  
 QY 1395 GCGCTCCATCTCCGACTTGTCAAGCAGCAGGCGCACTGAGCTTTGGTCAAGTTTCG 1454  
 Db 790 GGTGTGCACATTTCCGCTCGTCACGAGGATGGCTCCACCAAGCTCGTCAAGTTCCAC 849  
 QY 1455 TGAAGACCTTCCAGGAAGAGCGGCGCTGTATGGGAAGAGCAGCAGCTTTGGCGGA 1514  
 Db 850 TGAAGACCTTCCAGGTTTGGCAAGTATGGTCTGGGAGGAGCTCAGCAATTTCTGGC 909  
 QY 1515 AAGATCCGACTTCCATCGACAAGCCTCTGGGATGCCATTAATCTGGAAGGTACCCCT 1574  
 Db 910 AAGACCCCGACTACATGCGCCAGGATCTGTGAGTGCATGAGCTGCGCGGTACCCCT 969  
 QY 1575 GAGTGGGAGGTAAAGATATGATCCCCCAATCATTTAGTCTGACAGTGTCTCTGCTCT 1634  
 Db 970 GAGTGGGAGGTATGTTACCCCT----- 991  
 QY 1635 GTGCTGCTCTTTCTGCTTTTCTATATCTTCAACTAAGACTGACTTTATATAGTTT 1694  
 Db 992 -----TATTTCTACTACATAGCAAGATGTTTAC 1020  
 QY 1695 TACTCATATAGCTGGGCTTTCATTTGTTGAATGACGAGATCAATCCAAAGTTTGTTCG 1754  
 Db 1021 TGACCGGACAGCTTAACGTGCAATCATGGACGAGGAGGACAGTTCGCTTTGGCTTCG 1080  
 QY 1755 ATCTATTAGATCCCAAAATCATCCAGAGAACTTCTCTTTCACCCCAATCGGNA 1814  
 Db 1081 ACCTTTTCGACCTACCAAGATTGTCCTTGAGATACGCTCCATTTGACCCCGCTGGCA 1140  
 QY 1815 AATGCTCTTGACCCAAACCAAAAGTTATTTTCCGAAACTGAGCAGATCATGGTTG 1874  
 Db 1141 AGATACCTCAACCCCAACCCCGCACTACTTTTGGCGAGACTGAGCAGGTCATGGTAG 1200

QY 1875 GTCCACCCCTATATATTTTGAATATGAATACATGTATAGTAAAGCGTATATCTA 1934  
 Db 1201 GCTTCTCTCTCCCTTC-----TGATCCCTCTCTTTGCCGTTTCTTAAC 1245  
 QY 1935 ATATATTTCCACAGTTTCCAAACCGAGGTATGTATTCGCGGAATCGATTTCACGAGTAC 1994  
 Db 1246 AGTA-----ACAGTTCCAAACCCGCGCACGTCGTGGTGGTGTGACTTCACCGAGAT 1298  
 QY 1995 CTTTGTCTTACGCGCGCTTACTCTTACCTTGACACTCAATTTGAATGCCATGGAGGT 2054  
 Db 1299 CCGCTTCTCAGTAGGCGGCGGACAACTTTTTTGTCTTTTACCTAA----- 1351  
 QY 2055 CCCAACTTCGAGCAACTGCCGATCAACAGACCCCGCATCCCATTCCTAATAACAATTCG 2114  
 Db 1352 GCTGACTGAAAGCAGGAGCTTTTTCAGCTACCTTGACACCCAGCTCAACCGCAATGGT 1411  
 QY 2115 GACGGTGTGTAAAGTACTTCTCAGCTACCATGTCTCACTTCCATCTTGACCCCAATCGAT 2174  
 Db 1412 GCGCGAATTTGAGCAGTTGCCCTCAACCGCGCGGTGCTATTTCAC----- 1462  
 QY 2175 TTGTATAGATTTAATCATCCCGTCTGACAGGACAAATTTTCATCCCTTAAACACGG 2234  
 Db 1463 -----AACAAACACGTCGACGTCGTGSCCAGATGTTTCATTCGCTGAACCCG 1511  
 QY 2235 CCGCATATACACCACTCAATGAGCAACCGATTCGCAACAAAGCAACCGGACCCATA 2294  
 Db 1512 ATGGTACAGCCCAACACCGCTGAAGGATCAACCTCAACAGGCGCAACCGACTGCGG 1571  
 QY 2295 ACAGAGATTTCTCACGACCTGGCGTATGTAATGAGCAGCTAGTGGCGGACTCA 2354  
 Db 1572 GTGCGGATTTTACTGCTCTGACGCTACTGCCAAGCGCATCTGTGCGTGCACAGA 1631  
 QY 2355 GCCGAGCTTCAAGAGCTGTGTCACACCGGCTCTTCTACAACTCACTCAGCGTCT 2414  
 Db 1632 GTCCACCTTCGAGATGCTGTGTCAGCCCGGCTTTCTGGAACTCTCTTCTCCG 1691  
 QY 2415 TCGAGAAGCAATTTCTCGTCAAGCCATCGCTTCGAAACTCC 2458  
 Db 1692 CCGAGAAGCAGTTCGTGGTCAAGCCATTCGCTTCGCCACCGC 1735

## RESULT 4

US-10-369-493-27243  
 ; Sequence 27243, Application US/10369493  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Hinkle, Gregory J.  
 ; APPLICANT: Slater, Steven C.  
 ; APPLICANT: Goldman, Barry S.  
 ; APPLICANT: Chen, Xianfeng  
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
 ; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
 ; FILE REFERENCE: 38-10(52052)B  
 ; CURRENT APPLICATION NUMBER: US/10/369,493  
 ; CURRENT FILING DATE: 2003-02-28  
 ; PRIOR APPLICATION NUMBER: US 60/366,039  
 ; PRIOR FILING DATE: 2002-02-21  
 ; NUMBER OF SEQ ID NOS: 47374  
 ; SEQ ID NO 27243  
 ; LENGTH: 2258  
 ; TYPE: DNA  
 ; ORGANISM: Neurospora crassa  
 US-10-369-493-27243

Query Match 8.9%; Score 345.6; DB 8; Length 2258;  
 Best Local Similarity 52.7%; Pred. No. 7.2e-80;  
 Matches 1230; Conservative 0; Mismatches 779; Indels 327; Gaps 9;

QY 629 CAGTTTCTTACCAAGTTTATACATTGACGATGAACAGTTCGGTGTGTAACAACGAGCGTGGT 688  
 Db 106 CAGAGTTGAAGGAGTTGAGGTTGAGGCAACGCGCAATTCATGACAACAGATTTTCGGC 165

QY 689 GGTCCCATCGAGGACCAACACAGCCTGAAGGCTGGAATAGAGGCCCAACTCTACTTGAG 748  
 DB 166 GGCAACATTTGAGGAACAGCTTACGTCTGAAGCTGGTGGCCGGGCTCGACATTTGCTGAG 225  
 QY 749 GATTTCATCTCCGCCAGAGATTCACACATTTGATCATGAGAGGCTATGTAGATACAAA 808  
 DB 226 GACTTCATCTCCGTCAGAGCTCCAGCACTTCGACCATGAGCGGTATGTCTCCCTGCG 285  
 QY 809 ATATG-----TGACCGGTGTGCAATVCCGCTAAATTCATTTT--ACGAGGTTCCTGAGC 861  
 DB 286 CATGGCCCAATTAGCATCAAGAATCCTAGCTAACGAAAGTTTGATACCAGATTTCCGAGA 345  
 QY 862 GCGCCCTCATCTCGAGAGCTGGTCCCATGCGGTATTCACATCTCTATATATCTGCT 921  
 DB 346 GAGTCGTTCATGCGCGGTGGTGGTCCCGCTGATCTTCCACAGTATGTATGCGGACTGGT 405  
 QY 922 CGAATATCACAGCGCATCTTCTTTGAACGCGGCGAGGAAAGACAGACAGATTTTCGTGC 981  
 DB 406 CCAACATACCGCGGCTCTCTCCCTGGGCGCAAGGACAAAGCAACACCGGTCTTCGTCC 465  
 QY 982 GGTTCCTACAGTCGTGTAGAGAGGAGGTGTGACTCTGCTCGGATATCCAGGAT 1041  
 DB 466 GCTTCCTACCGTTCGCGGTTCAGGGGTTCGCGGACACTGCGCGTATGTTCAGGGCT 525  
 QY 1042 TTGGACCGCTGTATACGATGAAGGCAATTTTGGTAAGCATATATCTGTGTATCA 1101  
 DB 526 TCGCCAGGATTTGTTTGACCA-----CGTACACACCTTCCCTTC 569  
 QY 1102 TACTCATACAGCACACAATAATGATACAAACCCAGGACCTTAGCTGACTCTCGGCA 1161  
 DB 570 ACCTCTTCAGCAGGGGTTAACTTGACTCCAGCTATACCGACGAG-----GGCA 618  
 QY 1162 ATGTAGATATCGTGGAAACAAGTTCCTAGCTCTTCTCATTCAGGAGCTATTCATTTCC 1221  
 DB 619 ACTTTGATATCGTGGGCAACAACATCTCCGCTCTTTTCATTCAGGATGCCATCCGCTTC 678  
 QY 1222 CTGATTTGATTACGCTGTCAAGCGCAACAGACAGTGAATTTCCCGAGGTCGAAGTG 1281  
 DB 679 CCGACCTTATTCACCTCGTCAAGGCTAGCCCGCAACATGAGTTTCCCAAGCGCCACCG 738  
 QY 1282 CACATGATACGGATGGATTTCTCAGCAGCAGCGCCAGCTCATTTGCATGCCCTCTCT 1341  
 DB 739 CCCAGCATCGCTTGGGACTTCTCAGCTCCGAGCCCTCCGCTCTCCACACCCCTCTCT 798  
 QY 1342 GGGCAATTCAGGACATGGAATCCTCGCTCAATGCTCATGTGATGGTGGGCGGCTCC 1401  
 DB 799 GGGCATGCTTGGCAACGGTATTCCTCCGCGAGCTACCGTCTCATATGATGGTTTCCG 858  
 QY 1402 ATACCTCCGACTTGTACCGACAGGCGCACTCGACCTTGGTCAAGTTTCGTGGGAAGA 1461  
 DB 859 ATACCTTCGCTGTGACCGGAGCGCAAGTCCAAAGCTCGTCAAGTGGCATTTGGAAGA 918  
 QY 1462 CCCCTCAAGGAGAGCGGCGCTGTATGGGAAGGACAGGCTTTCGGGGAAGAATC 1521  
 DB 919 GGAACAGGGAAGGCGGCTCTGCTTGGGAGGAGGCTCAAGTCTCGCGGCAAGACG 978  
 QY 1522 CCGACTTCATCGCAACAGCTCTGGGATGCCATTTGAATCTGGAAGTACCCCTGAGTGG 1581  
 DB 979 CCGACTTCACCGCTCAGGATCTCTGGGAGCTATCGAGTCCGGAACGCCCTTCATGGG 1038  
 QY 1582 AGGTAAGATATGATTTCCCCCAATCATTTAGTTCTGACAGTGTCTCTGCTCTGCGTT 1641  
 DB 1039 ----- 1038  
 QY 1642 GCTCTTTCTCTTTCTATATCTTCAACTAAGACTGACTTTATATACGTTTACTCAT 1701  
 DB 1039 ----- 1038  
 QY 1702 ATAGCTGGCTTTCAATTTGGTGAATGAAGCAGATCAATCCAAGTTTGAATTTGATCTAT 1761  
 DB 1039 --AGCTCGCGTTTACGTTATTTGACGAGGACAAAGGCCAGGCTTACGGCTTTCGACTTCT 1096  
 QY 1762 AGATCCCAACAAATATATCCCAAGAGAACTTGTCTTCTTTCACCCCAATCGGNAATGGT 1821

DB 1097 TGATCCCAACAGTTCCTTCCCGAGGAGTTCCGCCCTCTCCAGGTTCTGGTGAGATGAC 1156  
 QY 1822 CTTGAAACCGAAACCCAAAGATTATTTTGGCGAAACTGAGCAGATCATGTTGGTCCACC 1881  
 DB 1157 CCTCAACCGAACCTTATGAATCTACTTTCGCGGAGACGAGCATC----- 1202  
 QY 1882 CCCTATATATTTGGAATATGAATACATATAGTATAGTAGATGAAGCGTATATCTAAATAT 1941  
 DB 1203 ----- 1202  
 QY 1942 TTCCACAGTTTCCAAACAGGTCATGTAGTTCGCGGAATCGATTTTCAGCGGATGACCTTTGC 2001  
 DB 1203 -----TCCTTCAGCGCGGCACATTTGTCGCGCGTCSACTTCCACGAGGATCCCGCTGC 1257  
 QY 2002 TTCAGGCGCGCTTCTACTCTTACCTTCACACTCAATTTGAATTCGCACTGAGGTTCCTCAACT 2061  
 DB 1258 TGCAGGTGCTCTCTACAGTCTCTACAGTCTCTACAGTCTCTACAGTCTCTACAGTCTCT 1317  
 QY 2062 TCGAGCAACTCCGATCAACAGACCCCGCATCTCCATTTCCATTAACAACAATCGGAGCGTG 2121  
 DB 1318 TTGAGCAGTCTCCCATCAACCGCTGTCTCTGGCGTCCACACAACACCGCGACGCT- 1376  
 QY 2122 CTGGTAGCTACTTCTACCTACCTACCTCACTTCCATCTTGACCAATCGATTTGTATA 2181  
 DB 1377 ----- 1376  
 QY 2182 GAGTATTAACTCCCGTCTGCACAGGACAAATTTTCATCCCTCTTAACACAGCGCGCAT 2241  
 DB 1377 -----CAAGCGCAGCTTGGATCCCAAGAACATCCACCACTA 1414  
 QY 2242 TACACCACTCAATGAGCAACGATTCCTCAACAGCAACGCAACCGGACCCATACAGNG 2301  
 DB 1415 CAGCCCGCTTACCTTCAACAGGGTACCTCTGCCAGGCCAACAGACGCTGGCGCGGG 1474  
 QY 2302 ATTCTTACCGCACCTGGCGTATGTTAAATGGACACTAGTTCGCGAGCTCAGCGCCGAG 2361  
 DB 1475 CTTCTTACCTACCCCGCGCGCACCGCTCTGGCGTCTGACCGCGAGCTCAGCGCCAC 1534  
 QY 2362 CTTCAACAGCTCTGGTCCCAACCGCTCTTCTTCAACATCACHTCACTGCTTCGAGAA 2421  
 DB 1535 CTTTGAAGCACTACACCCAGCCCGCTCTTCTTCACTGCTCACCCCGCTCGAGCA 1594  
 QY 2422 GCATTTCTCTCAAGGCTTCCGAAACTTCCCAACTTCCGAGTGGAGTGAACCGTGGC 2481  
 DB 1595 GCAGTTCTCATCAAGCGATCCGCTTCGAGGCGACCGCTCACCAAGCAGCGCTCA 1654  
 QY 2482 TAAGACGCTCATCATCAGCTGAACCGCTGACACAGCTCTGCGCGCGCGCTCGCGT 2541  
 DB 1655 GAAGACGTTCTCGAGCAGCTTAAACAAGATCTCCAAAGAGCTGGCGAAGCGCTGGCGT 1714  
 QY 2542 AGCTATCGGCGTGAACCCCATCCCGGAGACCCACCTTCTACCACAACAGGCAACCGT 2601  
 DB 1715 TGGCTTCGGCTCGAGGCGCGCGAGCCCGACCGCTACTACTACCAACAATGTACCCGG 1774  
 QY 2602 CCCATTCGCGCTTCGGCAGCAATCTCTGCGGCTGACGGGCTGAAATCGCCCTCTCT 2661  
 DB 1775 CGCGTTTCTCATCTTCAAGAGAGCTCTCCACCATCGCCACCTCCCGCTCGCGCTCT 1834  
 QY 2662 ---GACAAGAGAGCGGTAGTCTACGATTCGCGGAGCAGCTCCGGCGCGCTTTAACAG 2718  
 DB 1835 CTCACCAACCAAGGCGGCTCCCTCGACAAAGGCAAGGCGCTCAAGGAGCAGCTCGAGAA 1894  
 QY 2719 CGCCACAACAAGTAGATATCTCTAGTGGGCTCATTCGCTTGTATCCCCAACGCGCGT 2778  
 DB 1895 GGACGGCTCAAGGTCACTGCTGCGGAGTACCTTTCGACGCGGTTCGACGAGACCTA 1954  
 QY 2779 GACATGACCTATTCGGCGCGCAGGCTGCTGATCTTCGATGCTGCTGCTCGCGG 2838  
 DB 1955 CTCGCTCGCGACGCCACCGCTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2014  
 QY 2839 CCTGCTCAGCAGCGCTCAA-----CGCAATACCCAAAGAGTTCGCGCTCAGGATAT 2892

Db 2015 CTTACGGCGGAAGGCGCCATGAGCCCTCTTTCCCTGCTGCGGCTCCTAGCCAGATTCT 2074  
QY 2893 TACGGATGATACGCGTATGGAAGCCCGTTGGCGCGTGGAGCGGTAGCAATG 2948  
Db 2075 TACTGATGGTTACCGTGGGGTAAGCCCGTTGTCGCGTGGCGGCGCAAGAAG 2130

RESULT 5  
US-09-675-784A-1693  
; Sequence 1693, Application US/09675784A  
; GENERAL INFORMATION:  
; APPLICANT: HARE, ROBERTA S.  
; APPLICANT: SHAW, KAREN J.  
; APPLICANT: SHIMER JR., GEORGE H.  
; APPLICANT: KESSLER, MARCO  
; APPLICANT: NOLLING, JORK  
; APPLICANT: ZENG, QIANDONG  
; APPLICANT: GREENE, JONATHAN R.  
; TITLE OF INVENTION: ASPERGILLUS FUMIGATUS NUCLEIC ACIDS AND POLYPEPTIDES,  
; FILE REFERENCE: 2976-4020US1  
; CURRENT APPLICATION NUMBER: US/09/675,784A  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR FILING DATE: 60/156,338  
; NUMBER OF SEQ ID NOS: 13925  
; SEQ ID NO 1693  
; LENGTH: 1146  
; TYPE: DNA  
; ORGANISM: Aspergillus fumigatus  
US-09-675-784A-1693

Query Match 6.7%; Score 259.8; DB 7; Length 1146;  
Best Local Similarity 58.3%; Pred. No. 2.2e-57;  
Matches 594; Conservative 0; Mismatches 277; Indels 148; Gaps 2;  
QY 564 AGATGCCCTAGCGGTGAGAAAGCCCGCTCGATCGCGCGCATGACACTCTCTCCGACCTA 623  
Db 131 ATATGACCGGCGAGCTCAACCGCTGTGATGAGATATCCGATGGCGAGCTGCCGACGCA 190  
QY 624 CGGACCACTTCTTAGCAAGTTTACATGACGATGACAGTGGTGGTCTTAACACGAGC 683  
Db 191 CAGAGGAATCTGTGCCAGTATTATCTCAACGACAATGATGCGCTTCATGACGTCGCGC 250  
QY 684 TGGGTGGTCCATCGAGGACCAACAGCCCTGAAGGCTGGAATAGAGGCCCACTAC 743  
Db 251 TGGGCGGCCCTATCGAAGATCAGATAGTCTCAGTGGCGGAGCGGTGGTCCACCTGC 310  
QY 744 TTGAGGATTTATCTTCGCGCAGAGATTCACACTTTGATCATGAGAGGGTATGTAGAT 803  
Db 311 TCGAAGATTTATCTTCGCTCAAAGATACAGCGTTTCGACCATGACGGTCTC----- 363  
QY 804 ACAAAATATGTGACCGGTGTGCAATCCGCTAATTCATTTACGCGAGGTCTCTGAGCGC 863  
Db 364 -----CCCGAGCGT 372  
QY 864 GCGTCCATGCTCAGGAGGTGTGCCATGGCTATTTCACATCCCTATATAATATGCTG 923  
Db 373 GCGTCCATGCTCAGGAGGTGTGCCGCGCCATGGAGTCTTCACTTCATATGCGACTTCTCG 432  
QY 924 AATATCAGCGCATCTTCTTGAACGCGCGGAGGAAAGACACACAGTATTCGTGGCG 983  
Db 433 AACATCACTCGGCTTCTTCTTGGCCAGGAAAGGCAAGCAACCCCTGATTTGTCGCG 492  
QY 984 TTTTCTACATCGCTGTAGCAGGCGAGTGTGTGACTCTGCTCGCATATCCACGATTT 1043  
Db 493 TTCTCAGCGTGCAGGAGCAGAGGTAGTTCGATCTGCGCGCTGATGTTACGTTTT 552  
QY 1044 GCGACCGCTGTATACCGATGAGGCAATTTGGTGAAGCAATATATCGTGTAGTCATA 1103  
Db 553 GCCACTCGTTCTTATACCGCAGGAGCAAT-----583  
QY 1104 CTCATAACGACCAACAAATATGAATACAAACCCAGGACCTAGGCTGACTACTCGGCAAT 1163

Db 584 -----583  
QY 1164 GTAGATATCGTCGGAACAACGCTTCCAGTCTTCTTTCATTTCAGGAGCGTATTCAATTCCT 1223  
Db 584 -TCGATATCGTTGGAAACAATATCCCTGTATTTCTATCCAGGATGCTATCTCTTCC 642  
QY 1224 GATTGTATTCAGCTGTCAAGCCGCAACGACAGTGAATTCGCCAGGCTGCAACGCA 1283  
Db 643 GATCTGATCCAGCGCTCAAGCCGAGAGGTGACACAGAGATCCCTCAGGCTGCCACTGCT 702  
QY 1284 CATGATAGCGCATGGATTTCTCAGCCAGAGCCAGCTCATTTGATGCGCTCTTCTGG 1343  
Db 703 CATGACTCGGCTGGGACTTCTTTCAGCCAGCAGCAAGCAGATGACACACTCTCTGG 762  
QY 1344 GCAATGTCAGACATGGAATCCCTCGCTCAATGCTGATGTTGATGGTGGGGGCTCCAT 1403  
Db 763 GCTATGCTCGGCATGGCATTTCTTCCGACATGTTGATGGTTCGGTGTGCAT 822  
QY 1404 ACCTTCGACTGTACCGAGGAGGCAACTTCGACCTTGGTCAAGTTTTCGCTGGAAGACC 1463  
Db 823 ACCTTCGATTCGTGACAGATGACGGTGCATCCAGCTCGTCAAAATTTCACTGGAAGTCT 882  
QY 1464 CTCGAAGGAAGAGCGGCTGGTATGGAAGAGCGACAGGCTCTTGGCGGAAAGATCCC 1523  
Db 883 TTGAGGCGCAAGCGCATGGTCTGGAAGAGCCGACAGACCTCTGGAAGAAATCCT 942  
QY 1524 GACTTCCATCGACAAGACCTCTGGGATGCCATTTGAAATCTGGAAGGATACCCTGAGTGGGA 1582  
Db 943 GACTTTCATGCTCAGGATTTGCAGATGCAATCGAGGCTGAGGCTATCCGGAGTGGGA 1001

RESULT 6  
US-60-459-902-29  
; Sequence 29, Application US/60459902  
; GENERAL INFORMATION:  
; APPLICANT: Novozymes Biotech, Inc.  
; APPLICANT: Connolly, Mariah  
; APPLICANT: Brody, Howard  
; TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficien  
; FILE REFERENCE: 10345-000-US  
; CURRENT APPLICATION NUMBER: US/60/459,902  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 29  
; LENGTH: 2794  
; TYPE: DNA  
; ORGANISM: Scytalidium thermophilum  
US-60-459-902-29

Query Match 6.5%; Score 249.2; DB 10; Length 2794;  
Best Local Similarity 48.0%; Pred. No. 2.1e-54;  
Matches 1087; Conservative 0; Mismatches 1048; Indels 129; Gaps 8;  
QY 849 CAGGTTCTGAGCGCGCTCCATGCTCGAGAGCTGGTGGCCATGGGCTATTTCATCC 908  
Db 411 CAGGTTCCGAAAGGCGGCTCCATGCTCGAGCGCTGGAGCAGACGCGACCTTCAGAGT 470  
QY 909 TATAATACTGTCGAATATACACCGCATCTTCTTGAACGCGGCGAGGAAGCAGACA 968  
Db 471 TAGCGCGCTGGAGTAACATACCCTGCGCTCTTCTGAAACGCGACTTGAAGAGCAGACG 530  
QY 969 CCAGTATTCTGCGGTTTTCTACAGTCTGCTAGCAGAGCAGTGTGACTCTGCTCGC 1028  
Db 531 CCGGTGTTGTCGCGTTCTCGACCGTTCTGGGTCTCGAGGAGCGCAGACCGCGAGA 590  
QY 1029 GATATCCAGGATTTGCGACCGCTGTATACCATGAAGCAATTTTGGTAAAGCATAT 1088  
Db 591 GACGTTCAAGTTTTCGCGACGCGGTTTGTAAAGTTTGTGTTTTCATTCTGTTCCGCTCT 650  
QY 1089 ATCGTGTAGTCATACTACTATAACAGCAC-----1116

Db 651 GTAGAGGAGGTTAGATATGAGCTAACGTGTGTGTGTGAATGACTGATGAAG 710  
 Oy 1117 -----AACAAATATGATATACAAACCCAGAGCCTGACTACTGCGCAAT 1163  
 Db 711 CAACCTTGTACGTCCAGAGCATGTCCTTCTATCTGTGGAGCCATGTGTCTAT 770  
 Oy 1164 GT-----AGATATCGTGGAAACAAAGCTTCCATCTCTTCATTC 1203  
 Db 771 GTGACGTTGCTAATCTGTGATATGTCGAAACAAACATCCGCTATCTCTATTC 830  
 Oy 1204 AAGAGGCTATTCATATCCCTGATTTGATTCACGCTGTCAAGCCGACAGCACTGAAA 1263  
 Db 831 AAGATGCAATCCAGTTCTCTGACCTTATACCTGCTCAAGCCGCTGCCAGCAACGA 890  
 Oy 1264 TTCCCGAGGCTGCAATGCAATGATAGCGCATGGGATTTCTCTACCCAGCAGCCGACT 1323  
 Db 891 TTCCCGAGGCTGCAATGATAGCGCATGGGATTTCTCTACCCAGCAGCCGACT 950  
 Oy 1324 CATTCATGCGCTCTCTGTGGCAATGTCAAGATGCAATCCCTGCTCATATGCTCATG 1383  
 Db 951 CCATGCTAAGCAATGAGCAAGAGAGCCGCACTGGGGTGACATGCCAGGAGTACACAA 1010  
 Oy 1384 TTGATGGGTGGGGCTGTACATACCTTGTCCGACTTGTCCAGCAGAGGCACTGACCTTGG 1443  
 Db 1011 GCGTTCGATGACCTCTGTGTGACCAAGGAGTACAACTCCAGGAGACTCGAAGAG 1070  
 Oy 1444 TCAGATTTCCGCTGGAAAGACCTTCCAAAGAAAGAGCGGCTGATATGGAAAGGCGCAC 1503  
 Db 1071 ATTGCGCAATATGATGACACAGAACTGACAGATGTAGACACAGTTGCTTGGGCAATGT 1130  
 Oy 1504 CTCTGGCGGAAAGAAATCCGACTTCCATGCAACAACTGAGATGGCATTTGAATCTG 1563  
 Db 1131 CCGGCGACGGAATCCCTCGAGCTACCGCATATGTAGCTTGGCTGGGTGAGATGAC 1190  
 Oy 1564 GAAGATACCTGAGTGGAGATAGATATGATTCGCCCAATATTAATTTCTACAGTGT 1623  
 Db 1191 GTGAATCCATTTCTAACCTCAAGCCAGATGGCTTCGCGCTCCACAGCTCCGGTTGT 1250  
 Oy 1624 TTCTCTGCTGTGCGTGTGCTTTGCTTTTCTATATCTTCAATCAAGACTGACTT 1683  
 Db 1251 CAAGATGACGGCTGTCCAGATGTGATCAAGTGGCATTTCAAGTCCAGCCAGGAAAGC 1310  
 Oy 1684 TATATAGCTTTTACTCATATAGTGGCTTTCATTTGATGATGAAAGCATCAATCCAA 1743  
 Db 1311 GAGCTATGCTGGGAAGAGGCGAGGTCTTTCGCAAGATGCCACTTCCACCGTCA 1370  
 Oy 1744 GTTGTATTTGATCTATTTAGTCCACCAAAATCATCCAGAAACTTGTCTCTTCC 1803  
 Db 1371 GGACCTTGGGATGCTATTTAGTCCGGGA-----CGAACCAAGATGGATGTCTCGT 1424  
 Oy 1804 CCCAATGGGAAAAATGCTTGAACCCAAACCCAAAAGTTATTTTGGCCAAACTGAGCA 1863  
 Db 1425 CCAGATTTTCATGATGCTCCAGGCGCAAGCCTTTGGCTTGAATTTGGTGGACCCGACAA 1484  
 Oy 1864 GATCATGTTGTGTCACCCCTATATATTTGGAATATGAAATACATGTTACTGATGAA 1923  
 Db 1485 GATCATCCCGGAGAGTACGCCCCCTTACAGAAAGTGGGCTTGAAGCTGATGCGAA 1544  
 Oy 1924 GGTATATCTAATATATTTCCAC-----AGTTCCACAGAGTCTATGATTCG 1972  
 Db 1545 TCCGACCAACTACTTCCCGGAGAGACGAGCATATTTCCAAACCCGGTCAATATGCTCG 1604  
 Oy 1973 CGGAATCGATTTCAAGATGACCCCTTGTGAGGGCGCTGTGACTCTTACTTGAAC 2032  
 Db 1605 CGGCAATCGACTTCAGGAGAGATCCCTGCTACAGGAGAGCCCTTTTGTGATCTGAC 1664  
 Oy 2033 TCAATTTGATTCGCAATGAGTCCCAACTTGGAACTGCGGATCAAGACAGACCCGAT 2092  
 Db 1665 GAGCTGAAACGGAAAGGCGGCCCACTTTGAGAGCTGCCATCAACATGCCCCGGGT 1724  
 Oy 2093 CCATTCATTAACAAATCGGAGGCTGCTGTAAGTACTTCTACCTACCAATGTCA 2152

Db 1725 GCCGATTCAACAAATATTCGACGCGCGCCGAGATGTTCTATCCAGGACAAAGTA 1784  
 Oy 2153 CTTCACATCTTGACCAATGATTTGTATAGATTTAAATCCCGCTGTCAAGAGCA 2212  
 Db 1785 TCCGTGTAAGTCCCTC-----TTTTGCTGTGATGCTGTGTGGCTTGTGCA----- 1833  
 Oy 2213 ATGTTATCCCTTAAACAGCGCGCATATACACCCACTCAATGACAAAGATTTCCA 2272  
 Db 1834 -----CAGACGAGTACACTCCCAACACCTTGAAACAGTGTATTCG 1875  
 Oy 2273 CAACAGCCAAACCGGAGCCCAATTAACAGAGATTTCTACCCGACCTGGGCTATGTAAT 2332  
 Db 1876 CGGCAACCCCAACAAATAGCCGAGCGAGATTTCTTCAACAGCGCTGTGCGGTAC 1935  
 Oy 2333 GGACCACTAGTGCAGAGCTACAGCCGAGCTCAACAGCTGTGATCCCAACCGCTCTC 2392  
 Db 1936 GGTCCCTGTGCTGTGAGTGTGTCCAATTCACACACACACAGCTGAGCCGCTCTTC 1995  
 Oy 2393 TTCTACAACTGCTACAGGCTTTCGAGAAAGCAATTCCTGTCAAAGCTGAGGCTTCGA 2452  
 Db 1996 TTCTTCAACTCTCTACCTCCGTCGCAACAGTTCTCTGTCACAGCTGAGCTTCGA 2055  
 Oy 2453 AACTCCACGTTGCGAGTGAACCGGTGTAAGAGCTCATATCATCTGAAACCGGCTC 2512  
 Db 2056 ATCAAGCTTTGAAATGAGGAAAGTCAAGAAAGAGTGTCTACCCAGCTCAACCGGCTC 2115  
 Oy 2513 GACAAAGCACTGCGCCGCGCTGCTAGCTATGCGGCTGCAACCCCAATCCCGGAC 2572  
 Db 2116 AGCCATGACGTGGCGCTGCGTGGCCGCTCTATCGGCTTCCGCGGCGCCGAGCGGAC 2175  
 Oy 2573 CCACCTTCTACCAACAAAGGCAACGCTCCCATCGGACCTTGGGACGAATCTCTG 2632  
 Db 2176 GACACATCTACCAACAAAGAGAGCTGCGCTGCTCAATGCTTGAAGGCGGCTTGG 2235  
 Oy 2633 CGGCTGACGCGGCTGAAATGCTCCCTCTGACAAAGAGAGAGCTTACGATGCGC 2692  
 Db 2236 CCTACATC-----AAGACTCTCGGCTGCGGATCTGCTACACAGAGGATCGAAGCGC 2292  
 Oy 2693 GAGCAGCTCCGCGCGCGCTTTAAAGCGCCAAACAAAGTAAATGATGCTCTGTG 2752  
 Db 2293 CTGGATCAAGCGCCGAGCTGCGACCGCTGTGAAGAGAGCGGCTTGTGTCAAGCTT 2352  
 Oy 2753 TCATGCTGTATCCCAACGCGCGTGAACATGATATTCGCGCGCGAGGCTGATC 2812  
 Db 2353 GTGGCTGAAACGCTGCGCGAGGCGGTAGACAGAGTACGAGCGGATCCACGGGT 2412  
 Oy 2813 TTGATGCGGTGATGCTGCGCGGCTG-----CTACAGCGCCCTCA 2857  
 Db 2413 TTGAGCGGCTTGTGTGTGTGAGCGGCGGCGGCTGTTGCCAGCACCGCTGCTG 2472  
 Oy 2858 AGCCATTAACCAAGAGTGGCGGCTGAGATTAATACGATGATACGCTATGGAAG 2917  
 Db 2473 CCGTGTCTCCGAGCGGCGAGCCGCTTGCAGATCTTGTGAGCGGATGAGGGAAG 2532  
 Oy 2918 CCGTGGGCGCGCTGCTGAGAGGCTGACCAATGAAGCCCTTGTGAGCTCTTATGCGCT 2977  
 Db 2533 CCGGTGGGTGTGTGTGTGGAAGTGCAGAGAGTGTGAGATCCGCGGATGTCCGGA 2592  
 Oy 2978 GGTGGGATGCTGAGATGGCTGAGACCGCCGCGGTGATAT 3021  
 Db 2593 GAGCGGAGCGGGGTATTTGAGAGAGTCTGAGATGTTTGT 2636

RESULT 7  
 US-10-156-761-347  
 ; Sequence 347, Application US/10156761

; GENERAL INFORMATION:  
 ; APPLICANT: OMDA, SATOSHI  
 ; APPLICANT: IKEDA, HARUO  
 ; APPLICANT: ISHIKAWA, JUN  
 ; APPLICANT: HORIKAWA, HIROSHI  
 ; APPLICANT: SHIBA, TADAYOSHI  
 ; APPLICANT: SAKAKI, YOSHIYUKI

APPLICANT: HATORI, MASAHIRA  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-262  
CURRENT APPLICATION NUMBER: US/10/156,761  
CURRENT FILING DATE: 2002-05-29  
PRIOR APPLICATION NUMBER: JP 2001-204089  
PRIOR FILING DATE: 2001-05-30  
PRIOR APPLICATION NUMBER: JP 2001-272697  
PRIOR FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 15109  
SEQ ID NO 347  
LENGTH: 2274  
TYPE: DNA  
ORGANISM: Streptomyces avermitilis  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(2274)  
US-10-156-761-347

Query Match 4.7%; Score 180; DB 8; Length 2274;  
Best Local Similarity 63.8%; Pred. No. 3.3e-36;  
Matches 273; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

QY 1158 GGCAATGATATATCGTGGAAACAAGTTCAGTCTTCTCATTCAGAGCGCTATTCAA 1217  
DB 586 GGGCTCTGACCTGGTGGTAACAACATCCGGTCTTTTTCATCCAGAGCGATCAAG 645  
QY 1218 TTCCCGATTGATTCAGCGCTGTCAAGCCGACACAGAGTGAATTCGCCAGCGTCA 1277  
DB 646 TTCCCGAGATCATCCAGCGGCAAGCCGACCCGAGACGGAGATCCCGAGGCGAG 705  
QY 1278 ACTGACATGATACGCGATGGGATTTCCTCAGCCGACGAGCCAGTCAATTCATGCTC 1337  
DB 706 ACCGCGACGACAGCTTCTGGAGCTTCGTCACTGACACCGAAGCAGCACACCAACC 765  
QY 1338 TTCTGGGCAATGTCAGACATGGAATCCCTGCTCAATGCTCATGTTGATGGTGGGC 1397  
DB 766 CTGTGAACATGTCGACCGGGGCAATCCCGCTGCTGACGAATGATGAGGCTTGGC 825  
QY 1398 GTCCATACCTTCGCACTGTGACCGAGAGGGCAATCGACCTGCTCACTGCTGCTG 1457  
DB 826 GTCCACACGTTCCGCTGTGACAGCGGCGCCGACGAGCTGTGATGTTCCACTGG 885  
QY 1458 AAGACCTTCAGAGAGAGCGGCTGTGATGAGAGAGCAGGCTCTTGGCGAAG 1517  
DB 886 AAGCCCAATTTGGCGTCACTCCCTGTGTGGAGAGGCGCATCACCACGCGCTC 945  
QY 1518 AATCCGACTTCATCGACAGAGCTCTGSGATCCCTTGAATCTGGAAGTACCTGAG 1577  
DB 946 GACCCGAGCTTCACCGCGGAGCTCGCGACGCTGAGGCGCGCCACCGCGCAG 1005  
QY 1578 TGGAGGT 1585  
DB 1006 TGGAGCT 1013

## RESULT 8

US-10-156-761-1  
Sequence 1, Application US/10156761  
GENERAL INFORMATION:  
APPLICANT: OMURA, SATOSHI  
APPLICANT: IKEDA, HARUO  
APPLICANT: ISHIKAWA, JUN  
APPLICANT: HORIKAWA, HIROSHI  
APPLICANT: SHIBA, TADAYOSHI  
APPLICANT: SAKAKI, YOSHIYUKI  
APPLICANT: HATORI, MASAHIRA  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-262  
CURRENT APPLICATION NUMBER: US/10/156,761  
CURRENT FILING DATE: 2002-05-29  
PRIOR APPLICATION NUMBER: JP 2001-204089  
PRIOR FILING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: JP 2001-272697  
PRIOR FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 15109  
SEQ ID NO 1  
LENGTH: 9025608  
TYPE: DNA  
ORGANISM: Streptomyces avermitilis  
FEATURE:  
NAME/KEY: misc-feature  
LOCATION: (4187715)  
OTHER INFORMATION: a, t, c, g, other or unknown  
US-10-156-761-1

Query Match 4.7%; Score 180; DB 8; Length 9025608;  
Best Local Similarity 63.8%; Pred. No. 1.8e-34;  
Matches 273; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

QY 1158 GGCAATGATATATCGTGGAAACAAGTTCAGTCTTCTCATTCAGAGCGCTATTCAA 1217  
DB 407179 GGGCTCTGACCTGGTGGTAACAACATCCGGTCTTTTTCATCCAGAGCGATCAAG 407238  
QY 1218 TTCCCGATTGATTCAGCGCTGTCAAGCCGACACAGAGTGAATTCGCCAGCGTCA 1277  
DB 407239 TTCCCGAGATCATCCAGCGGCAAGCCGACCGGAGATCCCGAGGCGAG 407298  
QY 1278 ACTGACATGATACGCGATGGGATTTCCTCAGCCAGAGCCAGCTCATTCAGTCCCTC 1337  
DB 407299 AGCCGCGACGACAGTTCCTGGACTTCCTGACCTGACACCGAAGGAGCGACAC 407358  
QY 1338 TTCTGGGCAATGTCAGACATGGAATCCCTGCTCAATGCTCATGTTGATGGTGGGC 1397  
DB 407359 CTGTGAACATGTCAGCGGCGGCAATCCCGCTGCTGACGAATGATGAGGCTTGGC 407418  
QY 1398 GTCCATACCTTCGCACTGTGACCGAGAGGGCAATCGACCTGCTCACTGCTGCTG 1457  
DB 407419 GTCCACAGTTCGCTGTGACAGCGGCGCCGACGAGCGCTGTGATGTTCCACTGG 407478  
QY 1458 AAGACCTTCAGAGAGAGCGGCTGTGATGAGAGAGCAGGCTCTTGGCGAAG 1517  
DB 407479 AAGCCCAATTTGGCGTCACTCCCTGTGTGGAGAGCGCATCACCACGCGCTC 407538  
QY 1518 AATCCGACTTCATCGACAGACCTCTGSGATCCCTTGAATCTGGAAGTACCTGAG 1577  
DB 407539 GACCCGAGCTTCACCGCGGAGCTCGCGACGCTGAGGCGCGCCACCGCGCAG 407598  
QY 1578 TGGAGGT 1585  
DB 407599 TGGAGCT 407606

## RESULT 9

US-10-282-122A-31325  
Sequence 31325, Application US/10282122A  
GENERAL INFORMATION:  
APPLICANT: Wang, Liangsu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Kari  
APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
APPLICANT: Xu, H.  
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: ELITRA.034A  
CURRENT APPLICATION NUMBER: US/10/282,122A  
CURRENT FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
Remaining Prior Application data removed - See file wrapper or PALM.  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 31325  
LENGTH: 2133  
TYPE: DNA  
ORGANISM: Pseudomonas putida  
US-10-282-122A-31325

Query Match 4.6%; Score 178.6; DB 9; Length 2133;  
Best Local Similarity 63.8%; Pred. No. 7.4e-36;  
Matches 271; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

QY 1158 GGCATGATGATTCCTCGGAACAGTCCAGTCTCTTCATTCAGACGCTATTCAA 1217  
DB 472 GGCATGATGATTCCTCGGAACAGTCCAGTCTCTTCATTCAGACGCTATTCAA 531  
QY 1218 TTCCCGATTTGATTCACGCTGTCAAGCCGCAACAGCAAGTAAATCCCGAGCTGCA 1277  
DB 532 TTCCCGATTTGATTCACGCTGTCAAGCCGCAACAGCAAGTAAATCCCGAGCTGCA 591  
QY 1278 ACTGCACATGATACGGGATGATTCCTCAGCCAGCAGCCAGCTTCATTCAGTCCCTC 1337  
DB 592 TCGCGATGATGATTCCTCAGCCAGCAGCTTCATTCAGTCCCTC 651  
QY 1338 TTCTGGGATGATTCAGGATGATTCCTCAGCCAGCAGCTTCATTCAGTCCCTC 1397  
DB 652 ATGTGGGATGATTCAGGATGATTCCTCAGCCAGCAGCTTCATTCAGTCCCTC 711  
QY 1398 GTCCATACCTTCGATTCAGGATGATTCCTCAGCCAGCAGCTTCATTCAGTCCCTC 1457  
DB 712 GTCCATACCTTCGATTCAGGATGATTCCTCAGCCAGCAGCTTCATTCAGTCCCTC 771  
QY 1458 AAGACCTTCAGGATGATTCCTCAGCCAGCAGCTTCATTCAGTCCCTC 1517  
DB 772 AAGACCTTCAGGATGATTCCTCAGCCAGCAGCTTCATTCAGTCCCTC 831  
QY 1518 AATCCGATTCAGGATGATTCCTCAGCCAGCAGCTTCATTCAGTCCCTC 1577  
DB 832 GACACGATTCAGGATGATTCCTCAGCCAGCAGCTTCATTCAGTCCCTC 891  
QY 1578 TGGGA 1582  
DB 892 TGGGA 896

RESULT 10  
US-10-369-493-42972  
; Sequence 42972, Application US/10369493  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
FILE REFERENCE: 38-10(52052)B  
CURRENT APPLICATION NUMBER: US/10/369,493  
CURRENT FILING DATE: 2003-02-28  
PRIOR APPLICATION NUMBER: US 60/360,039  
PRIOR FILING DATE: 2002-02-21  
NUMBER OF SEQ ID NOS: 47374  
SEQ ID NO 42972  
LENGTH: 2071  
TYPE: DNA  
ORGANISM: Myxococcus xanthus  
US-10-369-493-42972

Query Match 4.6%; Score 178.4; DB 8; Length 2071;  
Best Local Similarity 63.6%; Pred. No. 8.2e-36;  
Matches 272; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

QY 1158 GGCATGATGATTCCTCGGAACAGTCCAGTCTCTTCATTCAGACGCTATTCAA 1217  
DB 400 GGCATGATGATTCCTCGGAACAGTCCAGTCTCTTCATTCAGACGCTATTCAA 459  
QY 1218 TTCCCGATTTGATTCACGCTGTCAAGCCGCAACAGCAAGTAAATCCCGAGCTGCA 1277  
DB 460 TTCCCGATTTGATTCACGCTGTCAAGCCGCAACAGCAAGTAAATCCCGAGCTGCA 519  
QY 1278 ACTGCACATGATACGGGATGATTCCTCAGCCAGCAGCTTCATTCAGTCCCTC 1337  
DB 520 TCGCGATGATGATTCCTCAGCCAGCAGCTTCATTCAGTCCCTC 579  
QY 1338 TTCTGGGATGATTCAGGATGATTCCTCAGCCAGCAGCTTCATTCAGTCCCTC 1397  
DB 580 ATGTGGGATGATTCAGGATGATTCCTCAGCCAGCAGCTTCATTCAGTCCCTC 639  
QY 1398 GTCCATACCTTCGATTCAGGATGATTCCTCAGCCAGCAGCTTCATTCAGTCCCTC 1457  
DB 640 GTCCATACCTTCGATTCAGGATGATTCCTCAGCCAGCAGCTTCATTCAGTCCCTC 699  
QY 1458 AAGACCTTCAGGATGATTCCTCAGCCAGCAGCTTCATTCAGTCCCTC 1517  
DB 700 AAGACCTTCAGGATGATTCCTCAGCCAGCAGCTTCATTCAGTCCCTC 759  
QY 1518 AATCCGATTCAGGATGATTCCTCAGCCAGCAGCTTCATTCAGTCCCTC 1577  
DB 760 AATCCGATTCAGGATGATTCCTCAGCCAGCAGCTTCATTCAGTCCCTC 819  
QY 1578 TGGGAGT 1585  
DB 820 TGGGAGT 827

RESULT 11  
US-10-369-493-47146  
; Sequence 47146, Application US/10369493  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 47146  
; LENGTH: 2319  
; TYPE: DNA  
; ORGANISM: Deinococcus radiodurans  
US-10-369-493-47146

```

: PRIOR APPLICATION NUMBER: 60/267, 636
: PRIOR FILING DATE: 2001-02-09
: PRIOR APPLICATION NUMBER: 60/269, 308
: PRIOR FILING DATE: 2001-02-16
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 78614
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 19563
: LENGTH: 2247
: TYPE: DNA
: ORGANISM: Enterobacter cloacae
US-10-282-122A-19563

Query Match      4.5%; Score 173.6; DB 9; Length 2247;
Best Local Similarity 62.9%; Pred. No. 1.6e-34;
Matches 269; Conservative 0; Mismatches 159; Indels 0; Gaps 0;

QY      1158  GGCNATGTAGATATACGTGCGAAACAAAGTTCAGTCTTTCATTCAGAGCGATATCA 1217
Db      568  GGTATTTTCATCTGTGTGGGCATATACACCCCGGTGTTCTTCATTCAGAGCGCATATA 627

QY      1218  TTCCTGATTTGATTCACGCTGTCAAGCCGCAACCAACAGACAGTAAATTCCCAAGCTGCA 1277
Db      628  TTCTCTGACTTTGTTCATGCGGTAAACCCGAGGCCACTGTGGGCATACCGCAGGGACAA 687

QY      1278  ACTGCACATATATACGGCATGGGANTTTCCTCAGCAGACAGCCAGCTCATGTGCCTC 1337
Db      688  AGCGCGCAGACACCTTCTGGGACTACGTCTCACTCAGCGACTGAAACCTTACACAAAGTG 747

QY      1338  TTCCTGGCAATGTCAAGACATGGAATCCCTCGCTCAATGCGTATGTTGAGGTGGGG 1397
Db      748  ATGCGGCGCATGTGACAGCCGCGGATTCGCGCAGCATGACAGATGAAAGGGTTTGT 807

QY      1398  GTCCATACCTTCCGACTGTGCACCGACGAGAGGSCAATCGACTTGGTCAAGTTCCGTGG 1457
Db      808  ATCCATACCTTCCGCTGTGATCAATGCGGAGGGAAGCCAGTTTGGCGCTTCACTGG 867

QY      1458  AAGACCTCCCAAGAAAGCGGGCGCTGTATGGGAAGAGGACACAGGCTTTGGCGGAAG 1517
Db      868  AAGCGGTGGCGGGAAGCGCTGTGTGTGGGAGAGGCGCAGAAAGCTGACCGGAGCC 927

QY      1518  AATCCGACTTCATGACAAAGACCTCTGGAGTGCATTGAATCTGGAAAGTACCTGAG 1577
Db      928  GATCCGGAATTCATGCGCCGCGAGCTGTGGAGTCCATTGAACGGCGCATTTCCCGGAA 987

QY      1578  TGGAGGT 1585
Db      988  TAGGAGCT 995

RESULT 13
US-10-282-122A-25910
: Sequence 25910. Application US/10282122A
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
: TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
: FILE REFERENCE: ELIIRA.034A
: CURRENT APPLICATION NUMBER: US/10/282.122A
: PRIOR APPLICATION NUMBER: 2003-02-20
: PRIOR FILING DATE: 2000-03-21
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: 60/206, 848

```

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;; PRIOR FILING DATE: 2000-05-23
;; PRIOR APPLICATION NUMBER: 60/207,127
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: 60/230,335
;; PRIOR FILING DATE: 2000-09-06
;; PRIOR APPLICATION NUMBER: 60/230,347
;; PRIOR FILING DATE: 2000-09-09
;; PRIOR APPLICATION NUMBER: 60/242,578
;; PRIOR FILING DATE: 2000-10-23
;; PRIOR APPLICATION NUMBER: 60/253,625
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/267,636
;; PRIOR FILING DATE: 2001-02-09
;; PRIOR APPLICATION NUMBER: 60/269,308
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 78614
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 25910
;; LENGTH: 2163
;; TYPE: DNA
;; ORGANISM: Mycobacterium avium
US-10-282-122A-25910
```

```
Query Match
Best Local Similarity 4.58; Score 172.8; DB 9; Length 2163;
Matches 270; Conservative 0; Mismatches 162; Indels 0; Gaps 0;
```

```
Db 1154 ACTGGCAATGTAGATATCGTCGGAACAACGTTCCAGTCTTCTTATTCAGAGCGCAT 1213
471 ACAAGGCAATATACGACTGTGTGGCAACACTTCCCGGTCTTCATTCAGAGCGCAT 530
1214 TCAATTCCTGATTTATTCACGCTGTCAAGCCGCAACAGAGTGAATTTCCCAAGC 1273
531 CAAGTTCCTGATTTATTCACGCTGTCAAGCCGCAACAGAGTGAATTTCCCAAGC 1273
1274 TGAACCTGCATGATATACGCGCATGGATTTCTTCTTCCAGCCAGCCAGCTCATTCATGC 1333
591 GCAGTGTGCGACGACGCGCTGTGGACTTGTCTCTACACCCGAGACGTTGACGCC 650
1334 CCTTCTTGTGGCAATGTGAGACATGAAATCCTGCTCAATCGTATGATGATGGGTG 1393
651 CATCATGTGGGTGTGAGTGTGACGCGGCGCTGCGCGAGCTACCGATATCGAGGGTT 710
1394 GGGCGTCCATCTTCCGACTTGTACACGAGGCACTGAGCTTGTGCAAGTTTCG 1453
711 CGGGTGTGACACTTTCGGCTGTGAAAGCCCGCGGCGAGGACTTTCGTGAAGTTCCA 770
1454 CTGGAAGACCTCCCAAGAGAGCGGCGCTGTATGGGAAGGACAGAGCTTGTGGCGG 1513
771 CTGGAACCCCGACTGCGCTGCATCTGTGATCTGGAGCAATGCCAAGATCGCGCG 830
1514 AAGAAATCCCGACTTCCATGCAACAGACCTCTGGGATGCAATTAATCTGGAAGTACCC 1573
831 CAAGAACCCCGATTAACACCCGCGGACCTGTGGAGGCCATCAATCCGCGCATACCC 890
1574 TGAGTGGAGGT 1585
891 GGAGTGGAGCT 902
Db
```

```
RESULT 14
US-10-417-886-3735
;; Sequence 3735, Application US/10417886
;; GENERAL INFORMATION:
;; APPLICANT: Keith G. Weinstein et al.
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROBACTER
;; FILE REFERENCE: 107196.135
;; CURRENT APPLICATION NUMBER: US/10/417,886
;; CURRENT FILING DATE: 2003-04-17
```

```
;; PRIOR APPLICATION NUMBER: US/09/252,691C
;; PRIOR FILING DATE: 1999-02-18
;; PRIOR APPLICATION NUMBER: US 60/094,145
;; PRIOR FILING DATE: 1998-07-24
;; PRIOR APPLICATION NUMBER: US 60/074,787
;; PRIOR FILING DATE: 1998-02-18
;; NUMBER OF SEQ ID NOS: 11326
;; SEQ ID NO 3735
;; LENGTH: 2283
;; TYPE: DNA
;; ORGANISM: Enterobacter cloacae
US-10-417-886-3735
```

```
Query Match
Best Local Similarity 62.48; Score 172.2; DB 8; Length 2283;
Matches 270; Conservative 0; Mismatches 163; Indels 0; Gaps 0;
```

```
Db 1158 GGCATGTAGATATCGTCGGAACAACGTTCCAGTCTTCTTATTCAGAGCGCAT 1217
601 GGCATTTTGTACCTGTGCGGAATTAACACCCGTTTCTTCTTATTCAGAGCGCAT 660
1218 TTCCGATTTGATTCACGCTGTCAAGCCGCAACAGACAGTGAATTTCCCGAGCTGCA 1277
661 TTCCGATTTGATTCACGCTGTCAAGCCGCAACAGACAGTGAATTTCCCGAGCTGCA 1277
1278 ACTGCACATGATAGGCGCATGGATTTCTTCCAGCAGAGCCAGCTCATTCGATCCCTC 1337
721 AGTGGCGATGACCTTCTGTGGACTACGTTCTCCCTCAACCCGAAACCTTCACAACTG 780
1338 TTCTGGCAATGTAGAGACATGAAATCCCGCTCAATCGTATGATGGGGGGC 1397
781 ATGTGGCGATGTGTGACCGGGGATCCACGAGCTATTCGACCATGAAAGCTTTGGT 840
1398 GTCCATCTTCCGACTGTGACCGAGGCGCACTGACCTGTGCAAGTTTCGCTGG 1457
841 ATCATATCTTCCGCTGTGATTAACGCTGAAGGTAAAGCGATTTGCTTCACCTG 900
1458 AAGACCTCCAGAAAGACGCGGCTGTATGGGAAGAGGACAGGCTTTGGCGAAG 1517
901 AAGACCTCCAGAAAGACGCGGCTGTATGGGAAGAGGACAGGCTTTGGCGAAG 1517
1518 AATCCGACTTCCATGCAACAGACCTCTGGATGCAATTAATCTGGAAGTACCTGAG 1577
961 GATCCGACTTCCATGCAACAGACCTCTGGATGCAATTAATCTGGAAGTACCTGAG 1577
1578 TGGAGGTAAAT 1590
1021 TACGAGCTGGGT 1033
Db
```

```
RESULT 15
US-10-369-493-44226
;; Sequence 44226, Application US/10369493
;; GENERAL INFORMATION:
;; APPLICANT: Cao, Yongwei
;; APPLICANT: Hinkle, Gregory J.
;; APPLICANT: Slater, Steven C.
;; APPLICANT: Goldman, Barry S.
;; APPLICANT: Chen, Xiandeng
;; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
;; FILE REFERENCE: 38-10(52052)B
;; CURRENT APPLICATION NUMBER: US/10/369,493
;; PRIOR FILING DATE: 2003-02-28
;; PRIOR APPLICATION NUMBER: US 60/360,039
;; NUMBER OF SEQ ID NOS: 47374
;; SEQ ID NO 44226
;; LENGTH: 2052
;; TYPE: DNA
;; ORGANISM: Rhodospseudomonas palustris
US-10-369-493-44226
```

us-09-674-195c-1.rnpa

Thu Jun 12 08:47:33 2003

```

Query Match      4.5%; Score 172; DB 8; Length 2052;
Best Local Similarity 62.6%; Pred. No. 4e-34;
Matches 268; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

OY 1158 GGCATATGATATCGTGGAAACACAGTTCAGTCTTCTCATTCAGAGCTATTCAA 1217
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 400 GGCATATGATATCGTGGAAACACAGTTCAGTCTTCTCATTCAGAGCTATTCAA 459
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1218 TTCCCTGATTGATTCACGCTGTCAAGCCGACACAGATGAAATCCCAAGCTGCA 1277
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 460 TTCCCGACCTGATCCATTGCTGAGAGAGAGCCGCGGCGTTCCGAGGCGCA 519
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1278 ACTGCACATGATACGGCATGGGATTTCTCAGCCAGAGCCAGCTCATTTGCATGCCCTC 1337
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 520 TCGGCCACAGACATTTCTGGGACTTCACTACGCTGACGCCGAAAGCATGCACATGGTG 579
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1338 TTCTGGGCAATGTCAAGACATGGAATCCCTGCTCAATGCGTCATGTTGATGGTGGGC 1397
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 580 ATGTGGGTGATGTGGACCGCCGCAATCCCGCTGCTCGTTTCATGGAAGGCTTCGGC 639
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1398 GTCCATACCTTCCGACTGTCAACGACAGAGGCAACTGACCTGTCAAGTTTCGCTGG 1457
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 640 GTCCACACTTCGCGCTGTCATGCGGAGGCGAATCACTCTGTGAAGTTCACTGG 699
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1458 AAGACCTCCAGAGAGAGCGGCTGTGTATGGGAAGGACAGGCTTGGCGGAAG 1517
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 700 AAGCCCAAGCTCGGAGATGCACTGCTGTGTGAGAGGCGGTAGATCAAGGGCGCC 759
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1518 AATCCGACTTCATCGACAAAGACCTGTGGATGCCATTGAATCTGGAAGTACCCTGAG 1577
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 760 GATCCTGACTTCATCGCGGGGATCTGTGAGCCGAATCTGACCGGCAATTTCCGGA 819
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1578 TGGGAGT 1585
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 820 TGGGAGT 827
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

Search completed: June 12, 2003, 01:18:29  
 Job time : 2586 secs

GenCore version 5.1.6  
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## OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 22:21:06 ; Search time 348.269 Seconds

(without alignments)  
1921.975 Million cell updates/sec

Title: US-09-674-195C-14

Perfect score: 23  
Sequence: 1 dcaagtcgagcgttcacgcatg 23Scoring table: IDENTITY\_NWC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenBank1.\*  
1: gb\_ba.\*  
2: gb\_hcg.\*  
3: gb\_in.\*  
4: gb\_cm.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vl.\*  
15: em\_ba.\*  
16: em\_fun.\*  
17: em\_hum.\*  
18: em\_in.\*  
19: em\_mu.\*  
20: em\_om.\*  
21: em\_or.\*  
22: em\_ov.\*  
23: em\_pat.\*  
24: em\_ph.\*  
25: em\_pl.\*  
26: em\_ro.\*  
27: em\_sts.\*  
28: em\_un.\*  
29: em\_vl.\*  
30: em\_hcg\_hum.\*  
31: em\_hcg\_inv.\*  
32: em\_hcg\_other.\*  
33: em\_hcg\_mus.\*  
34: em\_hcg\_pin.\*  
35: em\_hcg\_rod.\*  
36: em\_hcg\_mam.\*  
37: em\_hcg\_vrt.\*  
38: em\_sy.\*  
39: em\_hngo\_hum.\*  
40: em\_hngo\_mus.\*  
41: em\_hngo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	22	95.7	1704	8	HCC18SRRN	275306 H. capsulatu
2	22	95.7	1704	8	HCF18SRRN	275307 H. capsulatu
3	22	95.7	1713	8	HC18SR	X58572 H. capsulatu
4	22	95.7	1726	8	AF320009	AF320009 Ajellomyc
5	20.4	88.7	494	8	AB030916	AB030916 Aspergill
6	20.4	88.7	786	8	AF088252	AF088252 Teloschis
7	20.4	88.7	969	8	AF113712	AF113712 Dibaels b
8	20.4	88.7	990	8	AF107345	AF107345 Dibaels b
9	20.4	88.7	1031	8	AF203458	AF203458 Cyclocaneus
10	20.4	88.7	1054	8	AB030917	AB030917 Aspergill
11	20.4	88.7	1479	8	AEU45438	U45438 Amylocarpus
12	20.4	88.7	1648	8	SC072712	U72712 Stipula cer
13	20.4	88.7	1673	8	AN18SR	X78538 A. niger (1s
14	20.4	88.7	1678	8	PY133996	Y13996 Paecilomyce
15	20.4	88.7	1686	8	AF113713	AF113713 Dibaels b
16	20.4	88.7	1687	8	AF184749	AF184749 Bunodopho
17	20.4	88.7	1692	8	AF113710	AF113710 Stipula p
18	20.4	88.7	1696	8	AF113711	AF113711 Stipula p
19	20.4	88.7	1701	8	AF085473	AF085473 Dibaels b
20	20.4	88.7	1721	8	AF242259	AF242259 Acrosporm
21	20.4	88.7	1732	8	AB008408	AB008408 Aspergill
22	20.4	88.7	1733	8	AB008397	AB008397 Aspergill
23	20.4	88.7	1733	8	AB008413	AB008413 Aspergill
24	20.4	88.7	1733	8	D63695	D63695 Aspergillus
25	20.4	88.7	1733	8	D63697	D63697 Aspergillus
26	20.4	88.7	1734	8	AB006716	AB006716 Talaromy
27	20.4	88.7	1737	8	AB033479	AB033479 Leveillob
28	20.4	88.7	1746	8	AF053726	AF053726 Kirschaete
29	20.4	88.7	1770	8	AB002079	AB002079 Aspergill
30	20.4	88.7	1771	8	AB002066	AB002066 Aspergill
31	20.4	88.7	1772	8	AF053729	AF053729 Helicascu
32	20.4	88.7	1774	8	AB003947	AB003947 Talaromy
33	20.4	88.7	1776	8	AB003948	AB003946 Penicill
34	20.4	88.7	1777	8	AB003808	AB003808 Aspergill
35	20.4	88.7	1989	8	CSP301706	AJ301706 Capnobotr
36	20.4	88.7	2150	8	AB003945	AB003945 Penicill
37	20.4	88.7	2734	8	AR0421692	AJ421692 Anaptychl
38	20.4	88.7	3717	8	PPE21689	AJ421689 Physconia
39	19.4	84.3	1759	8	AB005561	AB005561 Kockovaei
40	19	82.6	913	8	AF006722	AF006722 Antennari
41	18.8	81.7	144	8	AB046947	AB046947 Endophyte
42	18.8	81.7	144	8	AB046948	AB046948 Endophyte
43	18.8	81.7	144	8	AB046949	AB046949 Endophyte
44	18.8	81.7	192	8	AF062662	AF062662 Endophyte
45	18.8	81.7	192	8	AF062664	AF062664 Endophyte

## ALIGNMENTS

RESULT 1  
LOCUS HCC18SRRN 1704 bp DNA linear PLN 10-DEC-1999  
DEFINITION H. capsulatum ssp. duboisii 18S rRNA gene.  
ACCESSION 275306  
VERSION 275306.1 GI:1419549  
KEYWORDS 18S ribosomal RNA; 18S rRNA gene; small subunit ribosomal RNA.  
SOURCE  
ORGANISM  
Ajellomyces capsulatus.  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; Onygenaceae; Ajellomyces.  
REFERENCE  
1 (bases 1 to 1704)  
Okeke, C.N., Kappe, R., Zakikhani, S., Nolte, O. and Sonntag, H.G.  
Ribosomal genes of Histoplasma capsulatum var. duboisii and var.  
farciminosum



REFERENCE 2 (bases 1 to 1726)  
 AUTHORS Kasuga, T., White, T.J. and Taylor, J.W.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-NOV-2000) Roche Molecular Systems, 1145 Atlantic Ave., Alameda, CA 94501, USA  
 FEATURES  
 source  
 1. 1726  
 /organism="Afellowmyces capsulatus"  
 /strain="ATCC26032: G217b"  
 /db\_xref="ATCC:26032"  
 /db\_xref="taxon:5037"  
 /note="class 2 North American population"  
 <1. >1726  
 /product="18S ribosomal RNA"  
 BASE COUNT 440 a 371 c 475 g 440 t  
 ORIGIN  
 Query Match 95.7%; Score 22; DB 8; Length 1726;  
 Best Local Similarity 100.0%; Pred. No. 1.7;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 2 CGAAGTCGAGCTTTCAGCATG 23  
 ||||||||||||||||||||  
 Db 153 CGAAGTCGAGCTTTCAGCATG 132  
 ||||||||||||||||||||  
 RESULT 5  
 AB030916/c 494 bp DNA linear PLN 19-AUG-1999  
 LOCUS Aspergillus niger gene for 18S rRNA, partial sequence.  
 DEFINITION AB030916  
 ACCESSION AB030916.1 GI:5738920  
 VERSION 18S rRNA: 18S ribosomal RNA.  
 KEYWORDS Aspergillus niger (strain:IEF1) DNA.  
 SOURCE Aspergillus niger  
 ORGANISM Aspergillus niger  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
 REFERENCE 1 (bases 1 to 494)  
 AUTHORS Shintani, T. and Matsumoto, Y.  
 TITLE Aspergillus niger gene for 18S rRNA, partial sequence  
 JOURNAL Published Only in Database (1999)  
 REFERENCE 2 (bases 1 to 494)  
 AUTHORS Shintani, T. and Matsumoto, Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (10-AUG-1999) Tomoyoshi Shintani, Industrial Research Center of Ehime Prefecture, Laboratory of Food Process, 487-2 Kumeikubo, Matsuyama, Ehime 791-1101, Japan  
 (E-mail:shintani@itl.pref.ehime.jp, URL:www.itl.pref.ehime.jp, Tel:81-89-976-7612, Fax:81-89-976-7313)  
 FEATURES  
 source  
 1. 494  
 /organism="Aspergillus niger"  
 /strain="IEF1"  
 /db\_xref="taxon:5061"  
 <1. >494  
 /product="18S ribosomal RNA"  
 BASE COUNT 141 a 100 c 121 g 131 t 1 others  
 ORIGIN  
 Query Match 88.7%; Score 20.4; DB 8; Length 494;  
 Best Local Similarity 95.5%; Pred. No. 11;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 2 CGAAGTCGAGCTTTCAGCATG 23  
 ||||||||||||||||||||  
 Db 171 CGAAGTCGAGCTTTCAGCATG 150  
 ||||||||||||||||||||  
 RESULT 6  
 AF088252 786 bp DNA linear PLN 17-JUN-1999  
 LOCUS Teloschistes cf. chrysophthalmus Feige and Mies ESS-6640 18S  
 DEFINITION ribosomal RNA, partial sequence.

ACCESSION AF088252  
 VERSION AF088252.1 GI:4731142  
 KEYWORDS Teloschistes cf. chrysophthalmus Feige and Mies ESS-6640.  
 SOURCE Teloschistes cf. chrysophthalmus Feige and Mies ESS-6640  
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes; Lecanorales; Teloschistaceae; Teloschistaceae; Teloschistes.  
 REFERENCE 1 (bases 1 to 786)  
 AUTHORS Steenroos, S.K. and Depriest, P.T.  
 TITLE SSU rDNA phylogeny of cladoniiform lichens  
 JOURNAL Am. J. Bot. 85, 1548-1559 (1998)  
 REFERENCE 2 (bases 1 to 786)  
 AUTHORS Depriest, P.T., Ivanova, N. and Gargas, A.  
 TITLE Direct Submission  
 JOURNAL Submitted (31-AUG-1998) Department of Botany, NHB-166, Smithsonian Institution, National Museum of Natural History, 10th & Constitution Avenue NW, Washington, DC 20560-0166, USA  
 FEATURES  
 source  
 1. 786  
 /organism="Teloschistes cf. chrysophthalmus Feige and Mies ESS-6640"  
 /specimen\_voucher="Feige & Mies ESS-6640 (US)"  
 /db\_xref="taxon:88650"  
 /country="Cape Verde: Santo Antao, 1988"  
 <1. >786  
 /product="18S ribosomal RNA"  
 /note="small subunit ribosomal RNA"  
 BASE COUNT 208 a 161 c 198 g 219 t  
 ORIGIN  
 Query Match 88.7%; Score 20.4; DB 8; Length 786;  
 Best Local Similarity 95.5%; Pred. No. 11;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 2 CGAAGTCGAGCTTTCAGCATG 23  
 ||||||||||||||||||||  
 Db 134 CGAAGTCGAGCTTTCAGCATG 113  
 ||||||||||||||||||||  
 RESULT 7  
 AF113712 969 bp DNA linear PLN 06-DEC-1999  
 LOCUS Dibaels baecomyces small subunit ribosomal RNA gene, partial sequence.  
 DEFINITION AF113712  
 ACCESSION AF113712.1 GI:6502558  
 VERSION Dibaels baecomyces.  
 KEYWORDS Dibaels baecomyces.  
 SOURCE Dibaels baecomyces.  
 ORGANISM Dibaels baecomyces.  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes; Lecanoromycetes; Incertae sedis; Icmadophiliaceae; Dibaels.  
 REFERENCE 1 (bases 1 to 969)  
 AUTHORS Platt, J.L. and Spatafora, J.W.  
 TITLE Evolutionary relationships of nonsexual lichenized fungi: molecular phylogenetic hypotheses for the genera Siphula and Thamnia from SSU and LSU rDNA analyses  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 969)  
 AUTHORS Platt, J.L. and Spatafora, J.W.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-DEC-1998) Department of Botany & Plant Pathology, Oregon State University, 2082 Cordley Hall, Corvallis, OR 97331-2902, USA  
 FEATURES  
 source  
 1. 969  
 /organism="Dibaels baecomyces"  
 /db\_xref="taxon:83478"  
 <1. >969  
 /product="small subunit ribosomal RNA"  
 BASE COUNT 268 a 189 c 243 g 268 t 1 others  
 ORIGIN  
 Query Match 88.7%; Score 20.4; DB 8; Length 969;

Best Local Similarity 95.5%; Pred. No. 11;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTCAGCATG 23  
Db 128 CGAAGTCGAGGCTTTCAGCATG 107

RESULT 8  
AF107345/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AF107345  
Dibaeis baecomyces small subunit ribosomal RNA gene, partial  
sequence.  
AF107345  
AF107345.1 GI:6318520  
Dibaeis baecomyces.  
Dibaeis baecomyces  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;  
Lecanoromycetes incertae sedis; Icmadophiliaceae; Dibaeis.  
1 (bases 1 to 990)  
Platt, J.L., Camacho, F.J. and Spatafore, J.W.  
Evolution of the lichen symbiosis within the Lecotiales: molecular  
phylogenetic hypotheses for dibaeis and Baecomyces  
Unpublished  
2 (bases 1 to 990)  
Platt, J.L. and Spatafore, J.W.  
Direct Submission  
Submitted (18-NOV-1998) Botany & Plant Pathology, Oregon State  
University, 2082 Cordley Hall, Corvallis, OR 97331, USA  
Location/Qualifiers  
1..990  
/organism="Dibaeis baecomyces"  
/isolate="OSC56400"  
/db\_xref="taxon:83478"  
<1..>990  
/product="small subunit ribosomal RNA"

BASE COUNT 269 a 189 c 248 g 264 t

ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 990;  
Best Local Similarity 95.5%; Pred. No. 11;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTCAGCATG 23  
Db 117 CGAAGTCGAGGCTTTCAGCATG 96

RESULT 9  
AF203458/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AF203458  
Cyclaneusma minus small subunit ribosomal RNA gene, partial  
sequence.  
AF203458  
AF203458.1 GI:9622908  
Cyclaneusma minus.  
Cyclaneusma minus.  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;  
Rhytismatales; Rhytismataceae; Cyclaneusma.  
1 (bases 1 to 1031)  
Gerhardt, D.S., Platt, J.L., Stone, J.K., Spatafore, J.W.,  
Holst-Jensen, A., Hamelin, R.C. and Kohn, L.M.  
Phylogenetics of Helotiales and Rhytismatales based on partial  
small subunit nuclear ribosomal DNA sequences  
Mycologia 93 (5), 915-933 (2001)  
2 (bases 1 to 1031)  
Gerhardt, D.S., Platt, J.L., Stone, J.K., Spatafore, J.W.,  
Holst-Jensen, A., Hamelin, R.C. and Kohn, L.M.  
Direct Submission  
Submitted (12-NOV-1999) Department of Botany and Plant Pathology,  
Oregon State University, 2082 Cordley Hall, Corvallis, OR

FEATURES 97331-2902, USA  
Location/Qualifiers  
source 1..1031  
/organism="Cyclaneusma minus"  
/strain="93197"  
/specific\_host="Pinus sylvestris"  
/db\_xref="taxon:64355"  
<1..>1031  
/product="small subunit ribosomal RNA"

BASE COUNT 275 a 203 c 264 g 289 t

ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 1031;  
Best Local Similarity 95.5%; Pred. No. 12;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTCAGCATG 23  
Db 117 CGAAGTCGAGGCTTTCAGCATG 96

RESULT 10  
AB030917/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AB030917  
Aspergillus niger var. awamori gene for 18S rRNA, partial sequence.  
AB030917  
AB030917.1 GI:5738921  
18S rRNA; 18S ribosomal RNA.  
Aspergillus niger var. awamori (strain:IEF2) DNA.  
Aspergillus awamori  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
1 (bases 1 to 1054)  
Shintani, T. and Matsumoto, Y.  
Aspergillus awamori gene for 18S rRNA, partial sequence  
Published Only in Database (1999)  
2 (bases 1 to 1054)  
Shintani, T. and Matsumoto, Y.  
Direct Submission  
Submitted (10-ANG-1999) Tomoyoshi Shintani, Industrial Research  
Center of Ehime Prefecture, Laboratory of Food Process, 487-2  
Kumekubota, Matsuyama, Ehime 791-1101, Japan  
E-mail:shintani@iri.pref.ehime.jp, URL:www.iri.pref.ehime.jp,  
Tel:81-89-976-7612, Fax:81-89-976-7313)  
Location/Qualifiers  
1..1054  
/organism="Aspergillus awamori"  
/strain="IEF2"  
/db\_xref="taxon:105351"  
/note="synonym:Aspergillus awamori"  
<1..>1054  
/product="18S ribosomal RNA"

BASE COUNT 288 a 215 c 274 g 277 t

ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 1054;  
Best Local Similarity 95.5%; Pred. No. 12;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTCAGCATG 23  
Db 155 CGAAGTCGAGGCTTTCAGCATG 134

RESULT 11  
AE045438/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AE045438  
Amylocarpus encephaloides small subunit rRNA gene.  
U45438  
U45438.1 GI:1736923  
Amylocarpus encephaloides.  
Amylocarpus encephaloides

**REFERENCE**  
**AUTHORS** Landvik, S., Shaller, N.F.J. and Eriksson, O.E.  
**TITLE** SSU rDNA sequences support for a close relationship between the Elaphomycetes and the Eurotiales and Onygenales  
**JOURNAL** Mycoscience 37, 237-241 (1996)  
**AUTHORS** Landvik, S., Shaller, N.F.J. and Eriksson, O.E.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (11-JAN-1996) Sara Landvik, Ecological Botany, Umea, S-90187, Sweden  
**FEATURES**  
**source** 1. 1479  
 /organism="Amylocarpus encephaloides"  
 /strain="UME 29765"  
 /db\_xref="taxon:45428"  
 1. 1479  
 /product="small subunit ribosomal RNA"  
**BASE COUNT** 382 a 300 c 399 g 398 t  
**ORIGIN**  
 Query Match 88.7%; Score 20.4; DB 8; Length 1479;  
 Best Local Similarity 95.5%; Pred. No. 12;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
**Qy** 2 CGAAGTCGAGCGTTTCAGCATG 23  
 |||||  
**Db** 108 CGAAGTCGAGCGTTTCAGCATG 87  
**RESULT 12**  
**LOCUS** SCUT2712 1648 bp DNA linear PLN 30-JUL-1997  
**DEFINITION** Siphula ceratites 18S small subunit ribosomal RNA gene, complete sequence.  
**ACCESSION** U72712  
**VERSION** 072712.1 GI:2286071  
**KEYWORDS** Siphula ceratites  
**SOURCE** Siphula ceratites  
**ORGANISM** Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes; Lecanoromycetes incertae sedis; Icmadophiliaceae; Siphula.  
**REFERENCE** 1 (bases 1 to 1648)  
**AUTHORS** Steenroos, S., Lohlander, K. and Tehler, A.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (27-SEP-1996) Botany, National Museum of Natural History, Smithsonian Institution, NHB-166, 10th St. & Constitution Ave., Washington, DC 20560, USA  
**FEATURES**  
**source** 1. 1648  
 /organism="Siphula ceratites"  
 /db\_xref="taxon:53373"  
 1. 1648  
 /product="18S small subunit ribosomal RNA"  
**BASE COUNT** 424 a 343 c 442 g 439 t  
**ORIGIN**  
 Query Match 88.7%; Score 20.4; DB 8; Length 1648;  
 Best Local Similarity 95.5%; Pred. No. 12;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
**Qy** 2 CGAAGTCGAGCGTTTCAGCATG 23  
 |||||  
**Db** 110 CGAAGTCGAGCGTTTCAGCATG 89  
**RESULT 13**  
**LOCUS** AN18SR 1673 bp DNA linear PLN 13-MAR-1995  
**DEFINITION** A. niger (isolate CBS102.12) 18S rRNA gene.  
**ACCESSION** X78538  
**VERSION** X78538.1 GI:469079

**KEYWORDS** 18S ribosomal RNA.  
**SOURCE** Aspergillus niger.  
**ORGANISM** Aspergillus niger  
**REFERENCE** Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
**AUTHORS** 1 (bases 1 to 1673)  
 Melchers, W.J., Verweij, P.E., van den Hurk, P., van Belkum, A., De Pauw, B.E., Hoogkamp-Korstanje, J.A. and Meis, J.F.  
**TITLE** General primer-mediated PCR for detection of Aspergillus species  
**JOURNAL** J. Clin. Microbiol. 32 (7), 1710-1717 (1994)  
**MEDLINE** 95014936  
**PUBMED** 7929762  
**REFERENCE** 2 (bases 1 to 1673)  
**AUTHORS** Melchers, W.J.G.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (25-MAR-1994) W.J.G. Melchers, Department of Medical Microbiology, University of Nijmegen, P O Box 9101, 6500 HB Nijmegen, NETHERLANDS  
**FEATURES**  
**source** 1. 1673  
 /organism="Aspergillus niger"  
 /isolate="CBS102.12"  
 /db\_xref="taxon:5061"  
 <1. >1673  
 /product="18S ribosomal RNA"  
 /evidence="experimental"  
**BASE COUNT** 423 a 365 c 458 g 426 t 1 others  
**ORIGIN**  
 Query Match 88.7%; Score 20.4; DB 8; Length 1673;  
 Best Local Similarity 95.5%; Pred. No. 12;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
**Qy** 2 CGAAGTCGAGCGTTTCAGCATG 23  
 |||||  
**Db** 131 CGAAGTCGAGCGTTTCAGCATG 110  
**RESULT 14**  
**LOCUS** PVT13996 1678 bp DNA linear PLN 23-JUL-1997  
**DEFINITION** Paecilomyces variotii 18S rRNA gene.  
**ACCESSION** Y13996  
**VERSION** Y13996.1 GI:2224834  
**KEYWORDS** 18S ribosomal RNA; 18S rRNA gene.  
**SOURCE** Paecilomyces variotii.  
**ORGANISM** Paecilomyces variotii.  
**REFERENCE** 1 (bases 1 to 1678)  
**AUTHORS** Zakikhani, S., Okeke, C.N. and Kappe, R.  
**TITLE** 18S rDNA sequence of Paecilomyces variotii CBS339.51  
**JOURNAL** Unpublished  
**AUTHORS** 2 (bases 1 to 1678)  
 Kappe, R.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (24-JUN-1997) Kappe R., Hygiene Institute, University of Heidelberg, Im Neuenheimer Feld 324 D-69120 GERMANY  
**FEATURES**  
**source** 1. 1678  
 /organism="Paecilomyces variotii"  
 /strain="CBS339.51"  
 /isolate="Man. sputum"  
 /db\_xref="taxon:45996"  
 1. 1678  
 /gene="18S rRNA"  
 1. 1678  
 /gene="18S rRNA"  
 /product="18S ribosomal RNA"  
 /evidence="experimental"  
**BASE COUNT** 422 a 363 c 467 g 426 t  
**ORIGIN**

Query Match 88.7%; Score 20.4; DB 8; Length 1678;  
 Best Local Similarity 95.5%; Pred. No. 12;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 CGAGTCGAGGCTTCAGCATG 23  
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 DB 105 CGAGTCGAGGCTTCAGCATG 84

# RESULT 15

AF113713/C

LOCUS AF113713 1686 bp DNA linear PLN 06-DEC-1999  
 DEFINITION Dibaels baemyces isolate OSC53939 small subunit ribosomal RNA  
 gene, partial sequence.

ACCESSION AF113713

VERSION AF113713.1 GI:6502559

KEYWORDS Dibaels baemyces.

SOURCE ORGANISM

REFERENCE 1 (bases 1 to 1686)  
 Platt,J.L. and Spatafora,J.W.  
 Evolutionary relationships of nonsexual lichenized fungi: molecular  
 phylogenetic hypotheses for the genera Siphula and Thamnia from  
 SSU and LSU rDNA analyses

Unpublished

2 (bases 1 to 1686)

Platt,J.L. and Spatafora,J.W.

Direct Submission  
 Submitted (16-DEC-1998) Department of Botany & Plant Pathology,  
 Oregon State University, 2082 Cordley Hall, Corvallis, OR  
 97331-2902, USA

JOURNAL

REFERENCE

FEATURES  
 source Location/Qualifiers

source

1. 1686

/organism="Dibaels baemyces"

/isolate="OSC53939"

/db\_xref="taxon:83478"

rRNA

<1. .>1686

BASE COUNT

441 a 346 c 438 g 460 t 1 others

ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 1686;  
 Best Local Similarity 95.5%; Pred. No. 12;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 CGAGTCGAGGCTTCAGCATG 23  
 |||||||  
 DB 128 CGAGTCGAGGCTTCAGCATG 107

Search completed: June 12, 2003, 02:33:49

Job time : 351.269 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 22:17:41 ; Search time 117.802 Seconds

(without alignments)  
439.686 Million cell updates/sec

Title: US-09-674-195c-14

Perfect score: 23

Sequence: 1 dcaagtcgagcttcacgcatg 23

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues 4370478

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database : N.Geneseq\_101002:\*

1: /SID2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT:\*  
2: /SID2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:\*  
3: /SID2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:\*  
4: /SID2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:\*  
5: /SID2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:\*  
6: /SID2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:\*  
7: /SID2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT:\*  
8: /SID2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT:\*  
9: /SID2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT:\*  
10: /SID2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT:\*  
11: /SID2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT:\*  
12: /SID2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT:\*  
13: /SID2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT:\*  
14: /SID2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT:\*  
15: /SID2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT:\*  
16: /SID2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT:\*  
17: /SID2/gcgdata/geneseq/geneseq-emb1/NA1996.DAT:\*  
18: /SID2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT:\*  
19: /SID2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:\*  
20: /SID2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:\*  
21: /SID2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:\*  
22: /SID2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:\*  
23: /SID2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:\*  
24: /SID2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	22	95.7	22 15 AAQ73433	Histoplasma capsul
2	22	95.7	22 15 AAQ73436	Histoplasma capsul
3	22	95.7	22 15 AAQ73437	Histoplasma capsul
4	22	95.7	22 15 AAQ64436	Histoplasma capsul
5	20.4	88.7	568 21 AAF11545	Aspergillus niger
6	18.8	81.7	1733 20 AAZ00859	A. fumigatus 18S r
7	17.4	75.7	4403765 22 AA199683	Mycobacterium tube
8	17.4	75.7	4411529 22 AA199682	Mycobacterium tube
9	17.2	74.8	1745 24 ABA01152	Deuteromyces pol

c 10	16.8	73.0	454	22	ABA44550	Human breast cell
c 11	16.8	73.0	454	22	ABA54997	Human foetal liver
c 12	16.8	73.0	454	22	ABA24760	Probe #3226 for ge
c 13	16.8	73.0	454	22	AAK03266	Human brain expres
c 14	16.8	73.0	454	22	AAK28719	Human bone marrow
c 15	16.8	73.0	454	22	AAI13296	Probe #3229 for ge
c 16	16.8	73.0	454	22	AAI34650	Probe #3188 used t
c 17	16.8	73.0	454	22	AAI03197	Probe #3188 used t
c 18	16.8	73.0	454	24	ABSO3233	Human genome-deriv
c 19	16.8	73.0	492	23	AA565314	DNA encoding novel
c 20	16.4	71.3	891	19	AAV37154	DNA sequence used
c 21	16.4	71.3	891	22	AAH01747	Fibroblast succin
c 22	16.4	71.3	1097	22	ABK72888	Bacillus lichenifo
c 23	16.2	70.4	351	21	AAAC04990	Human secreted pro
c 24	16.2	70.4	1932	23	AA567693	DNA encoding novel
c 25	16.2	70.4	9228	23	ABLI1660	Drosophila melanog
c 26	16.2	70.4	7584	20	AAI19362	Rhodococcus corall
c 27	16	69.6	7600	21	AAA51878	Rhodococcus sp. OH
c 28	15.8	68.7	397	24	ABL85432	Human ovarian can
c 29	15.8	68.7	550	21	AAAC94343	Cat flea head and
c 30	15.8	68.7	654	21	AAZ53824	Neisseria gonorrhoe
c 31	15.8	68.7	695	22	AAK91828	Human cDNA 5'-end
c 32	15.8	68.7	695	22	AAK93228	Human cDNA clone r
c 33	15.8	68.7	738	14	AAQ43293	Sequence encoding
c 34	15.8	68.7	738	15	AAQ6841	CC49 VL / 217 / 4-
c 35	15.8	68.7	738	20	AAH04747	DNA encoding a pro
c 36	15.8	68.7	738	21	AAV99764	Fusion polypeptide
c 37	15.8	68.7	738	21	AAA95090	DNA encoding a sin
c 38	15.8	68.7	738	21	AAA59622	DNA encoding a sin
c 39	15.8	68.7	738	21	AAZ57095	4-4-20 Vh region a
c 40	15.8	68.7	738	21	AAZ90344	DNA (SEQ ID NO:22)
c 41	15.8	68.7	738	21	AAZ37393	Antibody CC49/anti
c 42	15.8	68.7	744	14	AAQ43288	Sequence encoding
c 43	15.8	68.7	744	20	AAQ04742	DNA encoding a pro
c 44	15.8	68.7	744	21	AAA95085	Bivalent antigen b
c 45	15.8	68.7	744	21	AAA59617	DNA encoding a het

## ALIGNMENTS

RESULT 1	AAQ73433	standard; DNA: 22 BP.
ID	AAQ73433	
XX	AAQ73433:	
AC	18-MAY-1995	(first entry)
XX		
DE	Histoplasma capsulatum-specific DNA hybridisation probe.	
XX		
KW	Probe; detection; Histoplasma capsulatum; 18S; rRNA; rDNA; hybridisation;	
KW	Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;	
KW	water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.	
XX		
OS	Synthetic.	
XX		
PN	US5352579-A.	
XX		
PD	04-OCT-1994.	
XX		
PE	28-JUN-1991; 91US-0720587.	
XX		
PR	28-JUN-1991; 91US-0720587.	
XX		
PA	(GENP-) GEN-PROBE INC.	
XX		
PI	Millman CL;	
XX		
DR	WPI: 1994-316178/39.	
XX		
PT	Hybridisation probe specific for Histoplasma capsulatum -	
PT	allowing differentiation from all other fungi for detection or	

PT quantitation in body fluids, etc.  
 XX  
 PS Claim 4; Column 11; 8pp; English.  
 XX  
 CC A probe (AA073433) or its complement (AA073436) and corresponding RNA  
 CC sequences (AA073437 and AA086436) used for the specific detection of all  
 CC strains of Histoplasma capsulatum (H.c.). The probes are manufactured  
 CC complementary to the H.c. 18S rRNA or rDNA gene. This region also  
 CC corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.  
 CC The probe is specific for H.c. and can be used to distinguish the fungus  
 CC from all others, even its nearest phylogenetic neighbour Blastomyces  
 CC dermatitidis. Nucleic acid hybridisation of the specific probe is  
 CC enhanced by the use of helper probes (AA073434-5). This method allows  
 CC the detection and/or the quantitation of H.c. from samples e.g. body  
 CC fluids, tissue samples, soil and water.  
 XX  
 SQ Sequence 22 BP; 5 A; 5 C; 7 G; 5 T; 0 other;  
 Query Match 95.7%; Score 22; DB 15; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.14;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 2 CGAAGTCGAGGCTTCAGCATG 23  
 DB 1 CGAAGTCGAGGCTTCAGCATG 22  
 RESULT 2  
 AA073436/C  
 ID AA073436 standard; DNA; 22 BP.  
 XX  
 AC AA073436;  
 XX  
 DT 18-MAY-1995 (first entry)  
 XX  
 DE Histoplasma capsulatum specific DNA probe, complementary sequence.  
 XX  
 KM Probe: detection; Histoplasma capsulatum; 18S; rRNA; rDNA; hybridisation;  
 KM Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;  
 KM water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US5352579-A.  
 XX  
 PD 04-OCT-1994.  
 XX  
 PF 28-JUN-1991; 91US-0720587.  
 XX  
 PR 28-JUN-1991; 91US-0720587.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Millman CL;  
 XX  
 DR WPI; 1994-316178/39.  
 XX  
 PT Hybridisation probe specific for Histoplasma capsulatum -  
 PT allowing differentiation from all other fungi for detection or  
 PT quantitation in body fluids, etc.  
 XX  
 PS Claim 9; Column 12; 8pp; English.  
 XX  
 CC A probe (AA073433) or its complement (AA073436) and corresponding RNA  
 CC sequences (AA073437 and AA086436) used for the specific detection of all  
 CC strains of Histoplasma capsulatum (H.c.). The probes are manufactured  
 CC complementary to the H.c. 18S rRNA or rDNA gene. This region also  
 CC corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.  
 CC The probe is specific for H.c. and can be used to distinguish the fungus  
 CC from all others, even its nearest phylogenetic neighbour Blastomyces  
 CC dermatitidis. Nucleic acid hybridisation of the specific probe is  
 CC enhanced by the use of helper probes (AA073434-5). This method allows  
 CC the detection and/or the quantitation of H.c. from samples e.g. body

CC fluids, tissue samples, soil and water.  
 XX  
 SQ Sequence 22 BP; 5 A; 7 C; 5 G; 5 T; 0 other;  
 Query Match 95.7%; Score 22; DB 15; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.14;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 2 CGAAGTCGAGGCTTCAGCATG 23  
 DB 22 CGAAGTCGAGGCTTCAGCATG 1  
 RESULT 3  
 AA073437/C  
 ID AA073437 standard; RNA; 22 BP.  
 XX  
 AC AA073437;  
 XX  
 DT 18-MAY-1995 (first entry)  
 XX  
 DE Histoplasma capsulatum-specific RNA hybridisation probe.  
 XX  
 KM Probe: detection; Histoplasma capsulatum; 18S; rRNA; rDNA; hybridisation;  
 KM Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;  
 KM water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US5352579-A.  
 XX  
 PD 04-OCT-1994.  
 XX  
 PF 28-JUN-1991; 91US-0720587.  
 XX  
 PR 28-JUN-1991; 91US-0720587.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Millman CL;  
 XX  
 DR WPI; 1994-316178/39.  
 XX  
 PT Hybridisation probe specific for Histoplasma capsulatum -  
 PT allowing differentiation from all other fungi for detection or  
 PT quantitation in body fluids, etc.  
 XX  
 PS Claim 9; Column 12-13; 8pp; English.  
 XX  
 CC A probe (AA073433) or its complement (AA073436) and corresponding RNA  
 CC sequences (AA073437 and AA086436) used for the specific detection of all  
 CC strains of Histoplasma capsulatum (H.c.). The probes are manufactured  
 CC complementary to the H.c. 18S rRNA or rDNA gene. This region also  
 CC corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.  
 CC The probe is specific for H.c. and can be used to distinguish the fungus  
 CC from all others, even its nearest phylogenetic neighbour Blastomyces  
 CC dermatitidis. Nucleic acid hybridisation of the specific probe is  
 CC enhanced by the use of helper probes (AA073434-5). This method allows  
 CC the detection and/or the quantitation of H.c. from samples e.g. body  
 CC fluids, tissue samples, soil and water.  
 XX  
 SQ Sequence 22 BP; 5 A; 7 C; 5 G; 5 T; 0 other;  
 Query Match 95.7%; Score 22; DB 15; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.14;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 2 CGAAGTCGAGGCTTCAGCATG 23  
 DB 22 CGAAGTCGAGGCTTCAGCATG 1  
 RESULT 4

```

AA086436
ID AA086436 standard; RNA: 22 BP.
AC AA086436;
XX
XX
XX 18-MAY-1995 (first entry)
XX
DE Histoplasma capsulatum-specific complementary RNA hybridisation probe.
XX
XX Probe: detection: Histoplasma capsulatum; 18S rRNA: RNA: hybridisation;
XX Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;
XX water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.
XX
XX Synthetic.
XX
XX US5352579-A.
XX
XX 04-OCT-1994.
XX
XX 28-JUN-1991; 91US-0720587.
XX
XX 28-JUN-1991; 91US-0720587.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Millman CL;
XX
XX WPI; 1994-316178/39.
XX
XX Hybridisation probe specific for Histoplasma capsulatum -
XX allowing differentiation from all other fungi for detection or
XX quantitation in body fluids, etc.
XX
XX Claim 9; Column 13; 8bp; English.
XX
XX A probe (AA073433) or its complement (AA073436) and corresponding RNA
XX sequences (AA073437 and AA086436) used for the specific detection of all
XX strains of Histoplasma capsulatum (H.c.). The probes are manufactured
XX complementary to the H.c. 18S rRNA or rDNA gene. This region also
XX corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.
XX The probe is specific for H.c. and can be used to distinguish the fungus
XX from all others, even its nearest phylogenetic neighbour Blastomyces
XX dermatitidis. Nucleic acid hybridisation of the specific probe is
XX enhanced by the use of helper probes (AA073434-5). This method allows
XX the detection and/or the quantitation of H.c. from samples e.g. body
XX fluids, tissue samples, soil and water.
XX
XX
XX Sequence 22 BP; 5 A; 5 C; 7 G; 5 U; 0 other;
SQ
Query Match 95.7%; Score 22; DB 15; Length 22;
Best Local Similarity 77.3%; Pred. No. 0.14;
Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0.
OY 2 CGAAGTCGAGGCTTCAGCATG 23
|||||:|||||:::|||||:|
DB 1 CGAAGUCGAGCUCUUCAGCAUG 22

RESULT 5
AAF11545/c
ID AAF11545 standard; cDNA; 568 BP.
XX
XX AAF11545;
XX
XX
XX 13-MAR-2001 (first entry)
XX
XX Aspergillus niger EST SEQ ID NO:4068.
XX
XX Multiple gene expression; filamentous fungal cell; EST;
XX expressed sequence tag; Fusarium venenatum; Aspergillus niger;
XX Aspergillus oryzae; Trichoderma reesei; identification; recombination;
XX culture condition; environmental stress; spore morphogenesis;
XX metabolic pathway engineering; catabolic pathway engineering; ss.

```

XX Aspergillus niger.  
XX  
XX WO200056762-A2.  
XX  
XX PD 28-SEP-2000.  
XX  
XX PF 22-MAR-2000; 2000WO-US07781.  
XX  
XX PR 22-MAR-1999; 99US-0273623.  
XX  
XX PA (NOVO ) NOVO NORDISK BIOTECH INC.  
XX PA (NOVO ) NOVO NORDISK AS.  
XX PI Berka RM, Rey MM, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;  
DR WPI: 2000-594572/56.  
XX  
PT Monitoring differential expression of genes in filamentous fungal cells  
PR uses fluorescence-labeled nucleic acids isolated from the cells and a  
PS substrate of expressed sequence tags -  
XX  
PS Claim 87; Page 1791-1792; 3161pp; English.

The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AAF07478 to AAF11247 represents ESTs from Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are all specifically claimed in the present invention.

Sequence 568 BP; 155 A; 116 C; 141 G; 150 T; 6 other;

Query Match 88.7%; Score 20.4; DB 21; Length 568;  
Best Local Similarity 95.5%; Prod. No. 1.4;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0

QY 2 CGAAGTCGAGCGCTTCCAGCATG 23  
Db 178 CGAAGTCGAGGTTCAGCATG 157  
|||||  
|||

RESULT 6  
AAZ00859/c  
ID AAZ00859 standard; DNA: 1733 BP.  
XX  
AC AAZ00859;  
XX  
DT 11-OCT-1999 (first entry)  
XX  
DE A. fumigatus 18S rRNA DNA.  
XX  
KW Detection; diagnosis; 18S rRNA; aspergillosis; oncology;  
XX  
KW Invasive infection; haematology; immune system suppression; ss.  
XX

OS Aspergillus fumigatus.  
 XX DE19806274-A1.  
 XX 19-AUG-1999.  
 XX 16-FEB-1998; 98DE-1006274.  
 XX 16-FEB-1998; 98DE-1006274.  
 XX 16-FEB-1998; 98DE-1006274.  
 XX (BUCH/) BUCHHEIDT D.  
 XX (HEHL/) HEHLMANN R.  
 XX (SKLA/) SKLADNY H.  
 XX Buchheidt D, Hehlmann R, Skladny H;  
 XX WPI; 1999-470047/40.  
 XX  
 XX Detecting Aspergillus nucleic acid in body samples by two-step  
 XX polymerase chain reaction, for diagnosing aspergillosis  
 XX  
 XX Claim 2; Fig 1; 16pp; German.  
 XX  
 XX This invention describes a novel method for detecting Aspergillus nucleic  
 XX acid (I) in a body sample which comprises the isolation of (I) followed  
 XX by a two-step polymerase chain reaction (PCR) amplification of any  
 XX nucleic acid having a sequence essentially homologous to part of the  
 XX 3'-end of the Aspergillus 18S rRNA gene using primers used in the first  
 XX step that do not overlap with those in the second step. The method is  
 XX used for early diagnosis, and monitoring, of aspergillosis, particularly  
 XX invasive infections in hematological-oncological patients with long-term  
 XX suppression of the immune system. Unlike the known method using  
 XX overlapping primers, this process provides efficient and reliable  
 XX detection of Aspergillus in clinical situations. It is specific for  
 XX Aspergillus (it detects the species terreus, niger, versicolor, clavatus,  
 XX flavus, and fumigatus, but not oryzae, nor bacteria or fungi from any  
 XX other genera). This sequence represents the DNA sequence of Aspergillus  
 XX fumigatus 18S rRNA.  
 XX  
 XX Sequence 1733 BP; 446 A; 374 C; 475 G; 438 T; 0 other;  
 XX  
 XX Query Match 81.7%; Score 18.8; DB 20; Length 1733;  
 XX Best Local Similarity 90.9%; Pred. No. 10;  
 XX Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 XX 2 CGAAGTCGAGGCTTTCACGATG 23  
 XX ||||||||| ||| |||||  
 XX DB 153 CGAAGTCGAGGCTTTCACGATG 132  
 XX  
 XX RESULT 7  
 XX AA199683  
 XX ID AA199683 standard; DNA; 4403765 BP.  
 XX AC AA199683;  
 XX AT199683;  
 XX DT 15-JAN-2002 (first entry)  
 XX DE Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 2.  
 XX KW Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome;  
 XX variation; epidemiology; patient treatment; epidemic monitoring; ds.  
 XX OS Mycobacterium tuberculosis.  
 XX PN US6294328-B1.  
 XX PD 25-SEP-2001.  
 XX PF 24-JUN-1998; 98US-0103840.  
 XX PR 24-JUN-1998; 98US-0103840.  
 XX PS Claim 3; SEQ ID NO 1; 3pp + Sequence Listing; English.

PA (GENO-) INST GENOMIC RES.  
 XX Fleischmann RD, White OR, Fraser CM, Venter JC;  
 XX WPI; 2001-647261/74.  
 XX  
 XX Evaluating strain variation of Mycobacterium tuberculosis, comprises  
 XX determining the nucleotide sequence of the strain at positions in the  
 XX genome corresponding to positions where M. tuberculosis strains CDC  
 XX 1551 and H37Rv differ  
 XX  
 XX Claim 4; SEQ ID NO 2; 3pp + Sequence Listing; English.  
 XX  
 XX The invention relates to evaluating strain variation within and between  
 XX different populations of the tuberculosis bacterial pathogen,  
 XX Mycobacterium tuberculosis or related Mycobacterium by determining the  
 XX nucleotide sequence of the first strain at positions in the complete  
 XX sequence of the genome that correspond to positions that differ in the  
 XX nucleotide sequences of M. tuberculosis strains CDC 1551 (AA199683) and  
 XX H37Rv (AA199682). The method is useful for evaluating strain variation of  
 XX M. tuberculosis and has valuable application in the fields of  
 XX tuberculosis genetics, epidemiology, patient treatment and epidemic  
 XX monitoring.  
 XX Note: The sequence data for this patent did not form part of the printed  
 XX specification, but was obtained in electronic format directly from USPTO  
 XX at seqdata.uspto.gov/sequence.html?docID=6294328B1.  
 XX  
 XX Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189 other;  
 XX  
 XX Query Match 75.7%; Score 17.4; DB 22; Length 4403765;  
 XX Best Local Similarity 82.6%; Pred. No. 11e+02;  
 XX Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 XX  
 XX 1 DCGAAGTCGAGGCTTTCACGATG 23  
 XX :|| ||||||||| |||||  
 XX DB 172049 TCGGTCGAGGCTTTCACGATG 172071  
 XX  
 XX RESULT 8  
 XX AA199682  
 XX ID AA199682 standard; DNA; 4411529 BP.  
 XX AC AA199682;  
 XX AT199682;  
 XX DT 15-JAN-2002 (first entry)  
 XX DE Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 1.  
 XX KW Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome;  
 XX variation; epidemiology; patient treatment; epidemic monitoring; ds.  
 XX OS Mycobacterium tuberculosis.  
 XX PN US6294328-B1.  
 XX PD 25-SEP-2001.  
 XX PF 24-JUN-1998; 98US-0103840.  
 XX PR 24-JUN-1998; 98US-0103840.  
 XX PS (GENO-) INST GENOMIC RES.  
 XX Fleischmann RD, White OR, Fraser CM, Venter JC;  
 XX WPI; 2001-647261/74.  
 XX  
 XX Evaluating strain variation of Mycobacterium tuberculosis, comprises  
 XX determining the nucleotide sequence of the strain at positions in the  
 XX genome corresponding to positions where M. tuberculosis strains CDC  
 XX 1551 and H37Rv differ  
 XX  
 XX Claim 3; SEQ ID NO 1; 3pp + Sequence Listing; English.

XX The invention relates to evaluating strain variation within and between  
CC different populations of the tuberculosis bacterial pathogen.  
CC Mycobacterium tuberculosis or related Mycobacterium by determining the  
CC nucleotide sequence of the first strain at positions in the complete  
CC sequence of the genome that correspond to positions that differ in the  
CC nucleotide sequences of M. tuberculosis strains CDC 1551 (A199683) and  
CC H37Rv (A199682). The method is useful for evaluating strain variation of  
CC M. tuberculosis and has valuable application in the fields of  
CC tuberculosis genetics, epidemiology, patient treatment and epidemic  
CC monitoring.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from USPRO  
CC at seqdata.uspro.gov/sequence.html?docID=6294328B1.

XX Sequence 4411529 BP; 758565 A; 1449983 C; 1444602 G; 758379 T; 0 other;  
SQ

Query Match 75.7%; Score 17.4; DB 22; Length 4411529;  
Best Local Similarity 82.6%; Pred. No. 1.1e+02;  
Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 DCGAGTCGAGCTTCAGCATG 23  
DB 171880 TCGCTGTCGAGCTTCAGCATG 171902  
: || ||||| ||||| |||||

RESULT 9  
ABA01152/c  
ID ABA01152 standard; DNA: 1745 BP.  
AC ABA01152;  
XX  
XX 24-JAN-2002 (first entry)  
DE Deuteromycetes polynucleotide SEQ ID 1.  
XX  
XX Aldonic acid; ds.  
KM  
XX Deuteromycetes sp.  
OS  
XX JP2001245657-A.  
XX  
XX 11-SEP-2001.  
PD  
XX 26-DEC-2000; 2000JP-0394766.  
PF  
XX 27-DEC-1999; 99JP-0369714.  
PR  
XX (TAKE-) TAKEHARA KAGAKU KOGYO KK.  
PA (OSAO) OSAKA CITY.  
XX  
XX WPI; 2002-002933/01.  
DR  
XX A new microbe for producing aldonic acid, comprises a new strain of  
PT Acinetobacter or Burkholderia -  
PT  
XX  
XX Disclosure; Page 17; 22pp; Japanese.  
XX  
XX The present invention relates to a new microbe of Acinetobacter or  
CC Burkholderia genus producing aldonic acid and oxidizing specifically the  
CC hemiacetal hydroxy group of a saccharide having said hydroxy group.  
CC Aldonic acid is used as a mineral reinforcing agent. The present sequence  
CC was used to illustrate the present invention.  
XX  
XX Sequence 1745 BP; 448 A; 382 C; 465 G; 450 T; 0 other;  
SQ

Query Match 74.8%; Score 17.2; DB 24; Length 1745;  
Best Local Similarity 86.4%; Pred. No. 66;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 CGAGTCGAGCTTCAGCATG 23  
DB 167 CGAGTCGAGCTTCAGCATG 146  
||||| ||||| |||||

RESULT 10  
ABA44550/c  
ID ABA44550 standard; DNA: 454 BP.  
XX  
XX ABA44550;  
AC  
XX  
XX 01-FEB-2002 (first entry)  
DT  
XX  
DE Human breast cell single exon nucleic acid probe #3245.  
XX  
XX Human; microarray; single exon probe; gene expression; breast;  
XX disease; cancer; ss.  
KW  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200157271-A2.  
PN  
XX  
XX 09-AUG-2001.  
PD  
XX  
XX 30-JAN-2001; 2001WO-US00662.  
PF  
XX  
XX 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
PI  
XX  
XX WPI; 2001-496933/54.  
DR  
XX  
XX New spatially-addressable set of single exon nucleic acid probes,  
PT useful for measuring gene expression in sample derived from human  
PT breast, comprises number of single exon nucleic acid probes -  
XX  
XX Claim 1; SEQ ID NO 3245; 327bp + sequence listing; English.

XX The invention relates to a spatially-addressable set of single exon  
CC nucleic acid probes for measuring gene expression in a sample derived  
CC from human breast and Bt 474 cells. The method involves contacting  
CC the probes with a collection of detectably labelled nucleic acids  
CC derived from mRNA of human breast, and then measuring the label  
CC bound to each probe of the microarray. The probes are useful for  
CC verifying the expression of regions of genomic DNA predicted to  
CC encode proteins. They are useful for gene discovery, and for  
CC determining predisposition and/or prognosing breast disease. Gene  
CC expression analysis is useful for assessing the toxicity of chemical  
CC agents on cells. The microarray of this invention presents a far greater  
CC diversity of probes for measuring gene expression, with far less bias  
CC than expressed sequence tag microarrays. The method is suitable for  
CC rapid production of functional information from genomic sequence. The  
CC present sequence is a single exon nucleic acid probe of the invention.  
CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;  
SQ

Query Match 73.0%; Score 16.8; DB 22; Length 454;  
Best Local Similarity 90.0%; Pred. No. 90;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 AAGTCGAGCTTCAGCATG 23  
DB 201 AAGTCGAGCTTCAGCATG 182  
||||| ||||| |||||

RESULT 11  
 ID ABA54997/c  
 AC ABA54997 standard; DNA; 454 BP.  
 XX  
 AC ABA54997;  
 XX  
 DT 01-FEB-2002 (first entry)  
 XX  
 DE Human foetal liver single exon nucleic acid probe #3302.  
 XX  
 KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157277-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US00669.  
 XX  
 PR 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI; 2001-483447/52.  
 XX  
 PT Human genome-derived single exon nucleic acid probes useful for  
 XX analyzing gene expression in human fetal liver -  
 XX  
 PS Claim 1; SEQ ID NO 3302; 639pp + sequence listing; English.  
 XX  
 CC The invention relates to a single exon nucleic acid probe for  
 CC measuring human gene expression in a sample derived from human foetal  
 CC liver. The single exon nucleic acid probes may be used for predicting,  
 CC measuring and displaying gene expression in samples derived from human  
 CC foetal liver. The present sequence is a single exon nucleic acid  
 CC probe of the invention.  
 CC Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pcl\_sequences.  
 XX  
 SQ Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;  
 XX  
 Query Match 73.0%; Score 16.8; DB 22; Length 454;  
 Best Local Similarity 90.0%; Pred. No. 90;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 OY 4 AAGTCGAGGCTTTCAGCATG 23  
 DB 201 AAGTAGAGGCTTTCGATG 182  
 ID ABA24760/c  
 AC ABA24760 standard; DNA; 454 BP.  
 XX  
 AC ABA24760;  
 XX  
 DT 23-JAN-2002 (first entry)  
 XX  
 DE Probe #3226 for gene expression analysis in human heart cell sample.  
 XX  
 KW Human; gene expression; heart; microarray; vascular system; probe;  
 KW cardiovascular disease; hypertension; cardiac arrhythmia;  
 KW congenital heart disease; ss.  
 XX

XX  
 OS Homo sapiens.  
 XX  
 AC WO200157274-A2.  
 XX  
 PN WO200157274-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US00669.  
 XX  
 PR 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI; 2001-488899/53.  
 XX  
 PT Single exon nucleic acid probes for analyzing gene expression in human  
 XX hearts -  
 XX  
 PS Claim 1; SEQ ID NO 3226; 530pp; English.  
 XX  
 CC The present invention relates to single exon nucleic acid probes for  
 CC measuring human gene expression in a sample derived from human heart. The  
 CC present sequence is one such probe. The probes may be used for  
 CC predicting, measuring and displaying gene expression in samples derived  
 CC from the human heart via microarrays. By measuring gene expression, the  
 CC probes are useful for predicting, diagnosing, grading, staging, the  
 CC monitoring and prognosing diseases of the human heart and vascular system  
 CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and  
 CC congenital heart disease.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pcl\_sequences.  
 XX  
 SQ Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;  
 XX  
 Query Match 73.0%; Score 16.8; DB 22; Length 454;  
 Best Local Similarity 90.0%; Pred. No. 90;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 OY 4 AAGTCGAGGCTTTCAGCATG 23  
 DB 201 AAGTAGAGGCTTTCGATG 182  
 ID AAK03266/c  
 AC AAK03266 standard; DNA; 454 BP.  
 XX  
 AC AAK03266;  
 XX  
 DT 05-NOV-2001 (first entry)  
 XX  
 DE Human brain expressed single exon probe SEQ ID NO: 3257.  
 XX  
 KW Human; brain expressed exon; gene expression analysis; probe;  
 KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;  
 KW epilepsy; cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157275-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US00667.  
 XX

```

XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains -
XX
XX Example 4; SEQ ID NO: 3257; 650pp + Sequence listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is one of the probes of the
XX invention.
XX
XX
XX SQ Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;
XX
XX Query Match 73.0%; Score 16.8; DB 22; Length 454;
XX Best Local Similarity 90.0%; Pred. No. 90;
XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0.
XX
OY 4 AAGTCGAGCCTTTCAGCATG 23
DB 11111111111111111111
201 AAGTCGAGCCTTTCAGCATG 182
XX
XX RESULT 14
XX AAK28719/C
XX ID AAK28719 standard; DNA; 454 BP.
XX
XX AC AAK28719;
XX
XX DT 06-NOV-2001 (first entry)
XX
XX DE Human bone marrow expressed single exon probe SEQ ID NO: 3276.
XX
XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
XX microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
XX OS Homo sapiens.
XX
XX WO200157276-A2.
XX
XX PD 09-AUG-2001.
XX
XX PF 30-JAN-2001; 2001WO-US00668.
XX
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488900/53.
XX

```

xx Human genome-derived single exon nucleic acid probes useful for  
pt analyzing gene expression in human bone marrow -  
xx  
ps Example 4: SEQ ID NO: 3276; 658bp + Sequence Listing; English.  
xx  
cc The present invention provides a number of single exon nucleic acid  
cc probes which are derived from genomic sequences expressed in the human  
cc bone marrow. They can be used to measure gene expression in bone marrow  
cc samples, which may enable the improved diagnosis and treatment of cancers  
cc such as lymphoma, leukemia and myeloma. The present sequence is one of  
cc the probes of the invention.  
xx  
sq Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;  
  
Query Match 73.0%; Score 16.8; DB 22; Length 454;  
Best Local Similarity 90.0%; Pred. No. 90;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
4 AAGTCGAGGCTTTCAGCATG 23  
|||||  
201 AAGTGAAGGCTTTCGATG 182  
  
Db  
  
RESULT 15  
AA113296/C  
ID AA113296 standard; DNA; 454 BP.  
xx  
xx AA113296;  
xx  
xx 12-OCT-2001 (first entry)  
xx  
xx  
DE Probe #3229 for gene expression analysis in human cervical cell sample.  
xx  
xx Probe; human; microarray; gene expression; cervical epithelial cell;  
xx cervical cancer; ss.  
xx  
xx Homo sapiens.  
xx  
xx WO200157278-A2.  
xx  
xx  
xx 09-AUG-2001.  
xx  
xx  
xx 30-JAN-2001; 2001WO-US00670.  
xx  
xx  
xx 04-FEB-2000; 2000US-0180312.  
xx 26-MAY-2000; 2000US-0207456.  
xx 30-JUN-2000; 2000US-0608408.  
xx 03-AUG-2000; 2000US-0632366.  
xx 21-SEP-2000; 2000US-0234687.  
xx 27-SEP-2000; 2000US-0236359.  
xx 04-OCT-2000; 2000GB-0024263.  
xx  
xx (MOLE-) MOLECULAR DYNAMICS INC.  
xx  
xx Penn SG, Hanzel DK, Chen W, Rank DR;  
xx  
xx WPI; 2001-488901/53.  
xx  
xx Human genome-derived single exon nucleic acid probes useful for  
xx analyzing gene expression in human cervical epithelial cells -  
xx  
xx Claim 25; SEQ ID NO 3229; 487bp; English.  
xx  
xx The present invention relates to human single exon nucleic acid probes  
xx (SENPs). The present sequence is one such probe. The SENPs are derived  
xx from human HeLa cells. The SENPs can be used to produce a single exon  
xx microarray, which can be used for measuring human gene expression in a  
xx sample derived from human cervical epithelial cells. By measuring gene  
xx expression, the probes are therefore useful in grading and/or staging  
xx of diseases of the cervix, notably cervical cancer.  
xx Note: The sequence data for this patent did not form part of the printed  
xx specification, but was obtained in electronic format directly from WIPO

CC at fcp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;

Query Match 73.08; Score 16.8; DB 22; Length 454;

Best Local Similarity 90.08; Pred. No. 90;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AAGTCGAGGCTTTCAGCATG 23  
 |||| |||| |||| ||||  
 Db 201 AAGTCGAGGCTTTCAGCATG 182

Search completed: June 12, 2003, 01:44:06  
 Job time : 135.802 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OW nucleic - nucleic search, using SW model

Run on: June 12, 2003, 01:18:34 ; Search time 22.066 Seconds  
(without alignments)  
319.658 Million cell updates/sec

Title: US-09-674-195c-14

Perfect score: 23

Sequence: 1 dcaagtcgagccttcagcatg 23

Scoring table: IDENTITY\_NDC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq:\*

2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq:\*

3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq:\*

4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq:\*

5: /cgn2\_6/ptodata/1/ina/PTCUTS.COMB.seq:\*

6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	95.7	22	1	US-07-720-587A-1
2	17.4	75.7	4403765	4	US-09-103-840A-2
3	17.4	75.7	4411529	4	US-09-103-840A-1
4	15.8	68.7	738	2	US-08-224-591-13
5	15.8	68.7	738	2	US-08-392-338A-22
6	15.8	68.7	738	2	US-08-926-789-13
7	15.8	68.7	738	3	US-09-166-093-22
8	15.8	68.7	738	3	US-09-172-019-22
9	15.8	68.7	738	3	US-09-166-094-22
10	15.8	68.7	738	3	US-09-166-094-22
11	15.8	68.7	738	5	US-08-392-338A-12
12	15.8	68.7	738	5	US-08-392-338A-12
13	15.8	68.7	744	3	US-09-166-750-12
14	15.8	68.7	744	3	US-09-166-093-12
15	15.8	68.7	744	3	US-09-172-019-12
16	15.8	68.7	744	3	US-09-166-094-12
17	15.8	68.7	758	4	US-09-069-821-11
18	15.8	68.7	782	4	US-09-420-592A-1
19	15.8	68.7	797	1	US-08-323-445A-3
20	15.8	68.7	797	1	US-08-515-903A-3
21	15.8	68.7	797	5	US-08-515-903A-3
22	15.8	68.7	803	1	US-08-323-445A-7
23	15.8	68.7	803	1	US-08-515-903A-7
24	15.8	68.7	803	5	US-09-420-592A-3
25	15.8	68.7	816	4	US-09-420-592A-3
26	15.8	68.7	1460	2	US-08-392-338A-18
27	15.8	68.7	1460	3	US-09-166-750-18

28	15.8	68.7	1460	3	US-09-166-093-18	Sequence 18, Appl
29	15.8	68.7	1460	3	US-09-172-019-18	Sequence 18, Appl
30	15.8	68.7	1460	3	US-09-166-094-18	Sequence 18, Appl
31	15.8	68.7	1722	1	US-08-055-945-1	Sequence 1, Appl1
32	15.6	67.8	2033	1	US-08-148-910-14	Sequence 14, Appl
33	15.6	67.8	2033	1	US-08-448-937A-14	Sequence 14, Appl
34	15.6	67.8	2293	4	US-08-645-073-1	Sequence 1, Appl1
35	15.4	67.0	870	1	US-08-411-706-1	Sequence 1, Appl1
36	15.4	67.0	9515	1	US-08-920-812-13	Sequence 13, Appl
37	15.4	67.0	9515	1	US-08-920-827-13	Sequence 13, Appl
38	15.4	67.0	9515	1	US-08-921-177-13	Sequence 13, Appl
39	15.4	67.0	9515	1	US-08-362-577C-13	Sequence 13, Appl
40	15.4	67.0	9515	2	US-08-920-828-13	Sequence 13, Appl
41	15.4	67.0	12412	1	US-08-390-878-18	Sequence 18, Appl
42	15.4	67.0	4403765	4	US-09-103-840A-2	Sequence 2, Appl1
43	15.2	66.1	522	4	US-09-221-017B-1065	Sequence 1065, Ap
44	15.2	66.1	709	4	US-08-998-416-281	Sequence 281, App
45	14.8	64.3	1029	2	US-08-899-011-1	Sequence 1, Appl1

## ALIGNMENTS

RESULT 1  
US-07-720-587A-1  
; Sequence 1, Application US/07720587A  
; Patent No. 5352579  
; GENERAL INFORMATION:  
; APPLICANT: Curt L. Millman  
; TITLE OF INVENTION: NUCLEIC ACIDS PROBES  
; TITLE OF INVENTION: TO HISTOPLASMA CAPSULATUM  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM PS/2 Model 50z or 55SX  
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
; SOFTWARE: WordPerfect (Version 5.0)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07720, 587A  
; FILING DATE: 19910628  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION DATA: including application  
; PRIOR APPLICATION DATA: described below:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 193/121  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 22  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-07-720-587A-1

Query Match 95.7%; Score 22; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTCAGCATG 23  
Db 1 CGAAGTCGAGGCTTTCAGCATG 22

## RESULT 2

US-09-103-840A-2  
; Sequence 2, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; FILE REFERENCE: 24366-20007.00  
; CURRENT APPLICATION NUMBER: US/09/103,840A  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 4403765  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; FEATURE:  
; OTHER INFORMATION: CDC 1551  
; OTHER INFORMATION: "n" bases at various positions throughout the sequence  
US-09-103-840A-2

## Query Match

Best Local Similarity 75.7%; Score 17.4; DB 4; Length 4403765;  
Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DCGAAGTCGAGGCTTTCAGCATG 23  
Db 172049 TCGCTGTGAGGCTTTCACCATG 172071

## RESULT 3

US-09-103-840A-1  
; Sequence 1, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; FILE REFERENCE: 24366-20007.00  
; CURRENT APPLICATION NUMBER: US/09/103,840A  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 4411529  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; OTHER INFORMATION: H37Rv  
US-09-103-840A-1

## Query Match

Best Local Similarity 75.7%; Score 17.4; DB 4; Length 4411529;  
Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DCGAAGTCGAGGCTTTCAGCATG 23  
Db 171880 TCGCTGTGAGGCTTTCACCATG 171902

## RESULT 4

US-08-224-591-13/c  
; Sequence 13, Application US/08224591  
; Patent No. 5856456  
; GENERAL INFORMATION:  
; APPLICANT: Whitlow, Marc  
; APPLICANT: Filippula, David  
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/224,591  
; FILING DATE: Herewith  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/002,845  
; FILING DATE: 15-JAN-1993  
; APPLICATION NUMBER: US 07/980,529  
; FILING DATE: 20-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0977.1920002/JAG  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 738 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: join(1..726)  
US-08-224-591-13

## Query Match

Best Local Similarity 68.7%; Score 15.8; DB 2; Length 738;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGGCTTTCAGCA 21  
Db 350 GAAGTCGAGGCTTTCAGCA 332

## RESULT 5

US-08-392-338A-22/c  
; Sequence 22, Application US/08392338A  
; Patent No. 5869620  
; GENERAL INFORMATION:  
; APPLICANT: Whitlow, Marc  
; APPLICANT: Wood, James F.  
; APPLICANT: Hardman, Karl  
; APPLICANT: Bird, Robert  
; APPLICANT: Filippula, David  
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, NW  
; CITY: Washington  
; STATE: D.C.

COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/392,338A  
FILING DATE: 22-FEB-1995  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/989,846  
FILING DATE: 20-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/796,936  
FILING DATE: 25-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.0030007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 738 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..726  
US-08-392-338A-22

Query Match 68.7%; Score 15.8; DB 2; Length 738;  
Best Local Similarity 89.5%; Pred. No. 44;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCAGGCTTCAGCA 21  
||||| ||| ||||| |||  
Db 350 GAAGTAGAGCCTTCAGCA 332

RESULT 6  
US-08-926-789-13/C  
Sequence 13, Application US/08926789  
Patent No. 5990275  
GENERAL INFORMATION:  
APPLICANT: Whitlow, Marc  
APPLICANT: Filpula, David  
TITLE OF INVENTION: Linker For Linked Fusion Polypeptides  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/926,789  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/724,591  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021

FILING DATE: 15-JAN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/980,529  
FILING DATE: 20-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.1920002/JAG  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 738 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(1..726)  
US-08-926-789-13

Query Match 68.7%; Score 15.8; DB 2; Length 738;  
Best Local Similarity 89.5%; Pred. No. 44;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCAGGCTTCAGCA 21  
||||| ||| ||||| |||  
Db 350 GAAGTAGAGCCTTCAGCA 332

RESULT 7  
US-09-166-750-22/C  
Sequence 22, Application US/09166750  
Patent No. 6025165  
GENERAL INFORMATION:  
APPLICANT: Whitlow, Marc  
APPLICANT: Wood, James F.  
APPLICANT: Hardman, Karl  
APPLICANT: Bird, Robert  
APPLICANT: Filpula, David  
TITLE OF INVENTION: Methods for Producing Multivalent Antigen-Binding  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, NW  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/166,750  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/392,338  
FILING DATE: 22-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/989,846  
FILING DATE: 20-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/796,936  
FILING DATE: 25-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021

REFERENCE/DOCKET NUMBER: 0977.003000C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 738 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..726  
US-09-166-750-22

Query Match 68.7%; Score 15.8; DB 3; Length 738;  
Best Local Similarity 89.5%; Pred. No. 44;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGCCTTCAGCA 21  
DB 350 GAAGTAGAGCCTTCAGCA 332

RESULT 8  
US-09-166-093-22/c  
Sequence 22, Application US/09166093  
Patent No. 6027725  
GENERAL INFORMATION:  
APPLICANT: Whitlow, Marc  
APPLICANT: Wood, James F.  
APPLICANT: Hardman, Karl  
APPLICANT: Bird, Robert  
APPLICANT: Filpula, David  
APPLICANT: Rolence, Michelle  
TITLE OF INVENTION: Multivalent Antigen-Binding Proteins  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, NW  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/166,093  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/392,338  
FILING DATE: 22-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/989,846  
FILING DATE: 20-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/796,936  
FILING DATE: 25-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.003000B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 738 base pairs  
TYPE: nucleic acid

STRANDEDNESS: both  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..726  
US-09-166-093-22

Query Match 68.7%; Score 15.8; DB 3; Length 738;  
Best Local Similarity 89.5%; Pred. No. 44;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGCCTTCAGCA 21  
DB 350 GAAGTAGAGCCTTCAGCA 332

RESULT 9  
US-09-172-019-22/c  
Sequence 22, Application US/09172019  
Patent No. 6103889  
GENERAL INFORMATION:

APPLICANT: Whitlow, Marc  
APPLICANT: Hardman, Karl  
APPLICANT: Bird, Robert  
APPLICANT: Filpula, David  
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Single-Chain  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, NW  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/172,019  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/392,338  
FILING DATE: 22-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/989,846  
FILING DATE: 20-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/796,936  
FILING DATE: 25-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.003000D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:  
LENGTH: 738 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..726  
US-09-172-019-22

Query Match 68.7%; Score 15.8; DB 3; Length 738;  
Best Local Similarity 89.5%; Pred. No. 44;

Matches 17: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGCCTTCAGCA 21  
||||| ||| |||||  
Db 350 GAAGTAGAGCCTTCAGCA 332

RESULT 10  
US-09-166-094-22/c  
; Sequence 22, Application US/09166094  
; Patent No. 6121424  
; GENERAL INFORMATION:  
; APPLICANT: Whitlow, Marc  
; APPLICANT: Wood, James F.  
; APPLICANT: Hardman, Karl  
; APPLICANT: Bird, Robert  
; APPLICANT: Filpula, David  
; APPLICANT: Rollence, Michelle  
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, NW  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/166,094  
; FILING DATE: Herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/392,338  
; FILING DATE: 22-FEB-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/989,846  
; FILING DATE: 20-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/796,936  
; FILING DATE: 25-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0977.003000A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 738 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..726  
; US-09-166-094-22

Query Match 68.7%; Score 15.8; DB 3; Length 738;  
Best Local Similarity 89.5%; Pred. No. 44;  
Matches 17: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGCCTTCAGCA 21  
||||| ||| |||||  
Db 350 GAAGTAGAGCCTTCAGCA 332

RESULT 11

PCT-US93-11138-13/c  
; Sequence 13, Application PC/RUS9311138  
; GENERAL INFORMATION:  
; APPLICANT: Enzon, Inc.  
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/11138  
; FILING DATE: Herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/980,529  
; FILING DATE: 20-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/002,845  
; FILING DATE: 15-JAN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0977.2006604/JAG  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 738 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..738  
; PCT-US93-11138-13

Query Match 68.7%; Score 15.8; DB 5; Length 738;  
Best Local Similarity 89.5%; Pred. No. 44;  
Matches 17: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGCCTTCAGCA 21  
||||| ||| |||||  
Db 350 GAAGTAGAGCCTTCAGCA 332

RESULT 12  
US-08-392-338A-12/c  
; Sequence 12, Application US/08392338A  
; Patent No. 5869620  
; GENERAL INFORMATION:  
; APPLICANT: Whitlow, Marc  
; APPLICANT: Wood, James F.  
; APPLICANT: Hardman, Karl  
; APPLICANT: Bird, Robert  
; APPLICANT: Filpula, David  
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, NW  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.

ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/392,338A  
FILING DATE: 22-FEB-1995  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/989,846  
FILING DATE: 20-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/796,936  
FILING DATE: 25-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.0030007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 744 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..732  
US-08-392-338A-12

Query Match 68.7%; Score 15.8; DB 2; Length 744;  
Best Local Similarity 89.5%; Pred. No. 44;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 350 GAAGTCAGCGCTTTCAGCA 332

RESULT 13  
US-09-166-750-12/C  
Sequence 12, Application US/09166750  
Patent No. 6025165  
GENERAL INFORMATION:  
APPLICANT: Whitlow, Marc  
APPLICANT: Wood, James F.  
APPLICANT: Hardman, Karl  
APPLICANT: Bird, Robert  
APPLICANT: Filpula, David  
APPLICANT: Rollence, Michelle  
TITLE OF INVENTION: Methods for Producing Multivalent Antigen-Binding  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, NW  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/166,750  
FILING DATE: Herewith  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/392,338  
FILING DATE: 22-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/989,846  
FILING DATE: 20-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/796,936  
FILING DATE: 25-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.003000C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 744 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..732  
US-09-166-750-12

Query Match 68.7%; Score 15.8; DB 3; Length 744;  
Best Local Similarity 89.5%; Pred. No. 44;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 350 GAAGTCAGCGCTTTCAGCA 332

RESULT 14  
US-09-166-093-12/C  
Sequence 12, Application US/09166093  
Patent No. 6027725  
GENERAL INFORMATION:  
APPLICANT: Whitlow, Marc  
APPLICANT: Wood, James F.  
APPLICANT: Hardman, Karl  
APPLICANT: Bird, Robert  
APPLICANT: Filpula, David  
APPLICANT: Rollence, Michelle  
TITLE OF INVENTION: Multivalent Antigen-Binding Proteins  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, NW  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/166,093  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/392,338  
FILING DATE: 22-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/989,846  
FILING DATE: 20-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/796,936

FILING DATE: 25-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Goldstein, Jorge A.  
 REGISTRATION NUMBER: 29,021  
 REFERENCE/DOCKET NUMBER: 0977.003000B  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 371-2600  
 TELEFAX: (202) 371-2540  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 744 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: both  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..732  
 US-09-166-093-12

Query Match 68.7%; Score 15.8; DB 3; Length 744;  
 Best Local Similarity 89.5%; Pred. No. 44;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGCCTTCAGCA 21  
 ||||| ||| |||||  
 Db 350 GAAGTAGAGCCTTCAGCA 332

RESULT 15  
 US-09-172-019-12/c  
 ; Sequence 12, Application US/09172019  
 ; Patent No. 6103889  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Whitlow, Marc  
 ; APPLICANT: Hartman, Karl  
 ; APPLICANT: Bird, Robert  
 ; APPLICANT: Filpula, David  
 ; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Single-Chain  
 ; TITLE OF INVENTION: Antigen-Binding Proteins (As Amended)  
 ; NUMBER OF SEQUENCES: 23  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
 ; STREET: 1100 New York Avenue, NW  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: U.S.A.  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/172,019  
 ; FILING DATE: Herewith  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/392,338  
 ; FILING DATE: 22-FEB-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/989,846  
 ; FILING DATE: 20-NOV-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/796,936  
 ; FILING DATE: 25-NOV-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Goldstein, Jorge A.  
 ; REGISTRATION NUMBER: 29,021  
 ; REFERENCE/DOCKET NUMBER: 0977.003000D  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202) 371-2600  
 ; TELEFAX: (202) 371-2540  
 ; INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 744 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: both  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..732  
 US-09-172-019-12

Query Match 68.7%; Score 15.8; DB 3; Length 744;  
 Best Local Similarity 89.5%; Pred. No. 44;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGCCTTCAGCA 21  
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 Db 350 GAAGTAGAGCCTTCAGCA 332

Search completed: June 12, 2003, 04:38:51  
 Job time : 55.066 secs

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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 01:27:04 ; Search time 134.381 Seconds  
(without alignments)  
239.539 Million cell updates/sec

Title: US-09-674-195c-14

Perfect score: 23  
Sequence: 1 dcaagtcgagcgttcacgcatg 23

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PC1\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/PC1US\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.							
1	17.2	74.8	1691139	9	US-10-067-514-1		Sequence 1, Appl
2	16.8	73.0	454	10	US-09-864-761-3226		Sequence 3226, Ap
3	16.4	71.3	891	9	US-09-989-643-155		Sequence 155, App
4	16.4	71.3	1097	10	US-09-974-300-179		Sequence 179, App
5	15.8	68.7	310	10	US-09-878-574-665		Sequence 665, App
6	15.8	68.7	375	10	US-09-878-574-3603		Sequence 3603, Ap
7	15.8	68.7	397	10	US-09-867-701-8410		Sequence 8410, Ap
8	15.8	68.7	550	9	US-09-991-936-838		Sequence 838, App
9	15.8	68.7	723	10	US-09-791-578-5		Sequence 5, Appl
10	15.8	68.7	723	10	US-09-791-540-5		Sequence 5, Appl
11	15.8	68.7	758	9	US-09-956-086-1		Sequence 1, Appl
12	15.8	68.7	758	9	US-09-956-087-1		Sequence 1, Appl
13	15.8	68.7	782	9	US-09-985-442-1		Sequence 1, Appl
14	15.8	68.7	782	10	US-09-791-578-3		Sequence 3, Appl
15	15.8	68.7	782	10	US-09-791-540-3		Sequence 3, Appl
16	15.8	68.7	782	10	US-09-983-580-1		Sequence 3, Appl
17	15.8	68.7	818	9	US-09-985-442-3		Sequence 3, Appl
18	15.8	68.7	818	10	US-09-983-580-3		Sequence 3, Appl
19	15.8	68.7	933	9	US-09-938-842A-536		Sequence 536, App

C	20	15.8	68.7	981	10	US-09-770-445-271	Sequence 271, App
	21	15.8	68.7	1279	9	US-10-165-603-19	Sequence 19, Appl
	22	15.8	68.7	177556	10	US-09-952-213D-6	Sequence 6, Appl
C	23	15.6	67.8	2036	10	US-09-954-456-552	Sequence 552, App
C	24	15.6	67.8	2036	10	US-09-880-107-1612	Sequence 1612, Ap
C	25	15.6	67.8	2036	10	US-09-880-107-1945	Sequence 3945, Ap
C	26	15.4	67.0	1413	9	US-09-894-844-25	Sequence 25, Appl
C	27	15.4	67.0	1579	10	US-09-822-849A-139	Sequence 139, App
C	28	15.4	67.0	3119	10	US-09-867-701-10873	Sequence 10873, A
C	29	15.4	67.0	34094	9	US-10-199-550-1	Sequence 1, Appl
	30	15.4	67.0	1503841	9	US-09-946-867-1	Sequence 1, Appl
	31	15.4	67.0	1503841	10	US-09-785-668-1	Sequence 1, Appl
	32	15.4	67.0	1503841	10	US-09-795-686-1	Sequence 1, Appl
	33	15.2	66.1	365	10	US-09-783-590-10265	Sequence 10265, A
	34	15.2	66.1	768	10	US-09-910-943-408	Sequence 408, App
C	35	15.2	66.1	843	9	US-10-164-433-1	Sequence 1, Appl
C	36	15.2	66.1	1014	10	US-09-815-242-7828	Sequence 7828, Ap
C	37	15.2	66.1	1186	9	US-09-925-299-98	Sequence 98, Appl
C	38	15.2	66.1	1186	10	US-09-925-299-98	Sequence 98, Appl
C	39	15.2	66.1	7090	9	US-09-832-292-28	Sequence 28, Appl
C	40	15.2	66.1	8268	9	US-10-074-095-868	Sequence 868, App
C	41	15.2	66.1	8268	10	US-09-764-860-868	Sequence 868, App
C	42	15.2	66.1	8272	9	US-10-074-095-867	Sequence 867, App
C	43	15.2	66.1	8272	10	US-09-764-860-867	Sequence 867, App
C	44	15.2	66.1	24768	9	US-10-073-961-602	Sequence 602, App
C	45	15.2	66.1	24768	10	US-09-764-887-602	Sequence 602, App

## ALIGNMENTS

RESULT 1  
US-10-067-514-1  
Sequence 1, Application US/10067514  
Publication No. US20030054531A1  
GENERAL INFORMATION:  
APPLICANT: Gietarsdottr, Solveig  
APPLICANT: Jonsdottr, Sif  
APPLICANT: Regnsdottr, Sigrdur Th.  
TITLE OF INVENTION: HUMAN STROKE GENE  
FILE REFERENCE: 2345.2010-003  
CURRENT APPLICATION NUMBER: US/10/067,514  
CURRENT FILING DATE: 2002-02-04  
PRIORITY FILING DATE: 2001-03-19  
PRIORITY FILING DATE: 2001-03-19  
NUMBER OF SEQ ID NOS: 84  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 1691139  
TYPE: DNA  
ORGANISM: Human  
US-10-067-514-1

Query Match 74.8% Score 17.2; DB 9; Length 1691139;  
Best Local Similarity 86.4%; Pred. No. 37;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGCCTTCAGCATG 23  
Db 758783 CGAAGTCGAGCCTTCAGCATG 758804

RESULT 2  
US-09-864-761-3226/c  
Sequence 3226, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chan, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO  
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

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FILE REFERENCE: Aecm1ca-x-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 3226
LENGTH: 454
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL050331.11
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.39
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.98
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
US-09-864-761-3226

Query Match          73.0%; Score 16.8; DB 10; Length 454;
Best Local Similarity 90.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AAGTCGAGGCTTCACGATG 23
    ||| ||||| |||||
DB 201 AAGTAGAGGCTTCTGCATG 182
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RESULT 3
US-09-989-643-155/c
Sequence 155, Application US/09989643
Publication No. US20030049636A1
GENERAL INFORMATION:
```

```
APPLICANT: Bergeron, Michel G.
APPLICANT: Picard, Francois J.
APPLICANT: Ouellette, Marc
APPLICANT: Roy, Paul H.
TITLE OF INVENTION: Species-Specific, Genus-Specific and Universal DNA
TITLE OF INVENTION: Probes and Amplification Primers to Rapidly Detect and
TITLE OF INVENTION: Identify Common Bacterial and Fungal Pathogens and
TITLE OF INVENTION: Associated Antibiotic Resistance Genes from
FILE REFERENCE: 12287.29
CURRENT APPLICATION NUMBER: US/09/989,643
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/297,539
PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/743,637
PRIOR FILING DATE: EARLIER FILING DATE: 1996-11-04
NUMBER OF SEQ ID NOS: 174
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 155
LENGTH: 891
TYPE: DNA
ORGANISM: Fibrobacter succinogenes
US-09-989-643-155
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Query Match          71.3%; Score 16.4; DB 9; Length 891;
Best Local Similarity 81.8%; Pred. No. 57;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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```
QY 1 DCGAAGTCGAGGCTTCACGAT 22
    ||| ||||| |||||
DB 179 ACGAGTCGAGAAATTCACGAT 158
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RESULT 4
US-09-974-300-179
Sequence 179, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 179
LENGTH: 1097
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-179
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Query Match          71.3%; Score 16.4; DB 10; Length 1097;
Best Local Similarity 81.8%; Pred. No. 58;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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```
QY 1 DCGAAGTCGAGGCTTCACGAT 22
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DB 314 TCGAGTCGCGGCTTCACGAT 335
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RESULT 5
US-09-878-574-665
Sequence 665, Application US/09878574
Patent No. US20020110548A1
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
```

```
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 665
; LENGTH: 310
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-047-Q1-B1-H11
US-09-878-574-665

Query Match      68.7%; Score 15.8; DB 10; Length 310;
Best Local Similarity 78.3%; Pred. No. 1.1e+02;
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY      1 DCGAGTCGAGGCTTCAGCATG 23
DB      263 TCCAGTCAGAGCTTTAAGCATG 285

RESULT 6
US-09-878-574-3603/c
; Sequence 3603, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 3603
; LENGTH: 375
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-008-Q1-B1-D10
US-09-878-574-3603

Query Match      68.7%; Score 15.8; DB 10; Length 375;
Best Local Similarity 78.3%; Pred. No. 1.1e+02;
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY      1 DCGAGTCGAGGCTTCAGCATG 23
DB      180 TCGAGTCGAGGCTTTCAGATTC 158

RESULT 7
US-09-867-701-8410
; Sequence 8410, Application US/09867701
; Patent No. US2002013237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8410
; LENGTH: 397
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; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-8410

Query Match      68.7%; Score 15.8; DB 10; Length 397;
Best Local Similarity 78.3%; Pred. No. 1.1e+02;
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY      1 DCGAGTCGAGGCTTCAGCATG 23
DB      282 TCAAGTCAGGCTTTCAGATG 304

RESULT 8
US-09-991-936-838
; Sequence 838, Application US/09991936
; Publication No. US20030073827A1
; GENERAL INFORMATION:
; APPLICANT: Brandt, Kevin S.
; APPLICANT: Gaines, Patrick J.
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: FLUA HEAD, NERVE CORD, HINDGUT AND MALPIGHIAN TUBULE
; FILE OF INVENTION: NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
; FILE REFERENCE: FC-6-C1
; CURRENT APPLICATION NUMBER: US/09/991,936
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US/09/543,668
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/128,704
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1959
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 838
; LENGTH: 550
; TYPE: DNA
; ORGANISM: Ctenocephalides felis
US-09-991-936-838

Query Match      68.7%; Score 15.8; DB 9; Length 550;
Best Local Similarity 89.5%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      3 GAAGTCGAGGCTTCAGCA 21
DB      156 GAAGTCGAGGCTTTCAGCA 174

RESULT 9
US-09-791-578-5/c
; Sequence 5, Application US/09791578
; Patent No. US20020061307A1
; GENERAL INFORMATION:
; APPLICANT: WHITLOW, MARC
; APPLICANT: SHORR, ROBERT G.L.
; APPLICANT: FILPULA, DAVID R.
; APPLICANT: LEE, LISHYNG S.
; TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN
; FILE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNER, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/09/791,578  
FILING DATE: 26-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/069,842  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 60/050,472  
FILING DATE: 23-JUN-1997  
APPLICATION NUMBER: US 60/063,074  
FILING DATE: 27-OCT-1997  
APPLICATION NUMBER: US 60/067,341  
FILING DATE: 02-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: JORGE A. GOLDSTEIN  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.1840002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 723 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..723  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-791-578-5

Query Match  
Best Local Similarity 68.7%; Score 15.8; DB 10; Length 723;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAAGTCGAGGCTTCAGCA 21  
Db 350 GAAGTAGAGCCTTCAGCA 332

RESULT 10  
US-09-791-540-5/c  
Sequence 5, Application US/09791540  
Patent No. US20020098192A1  
GENERAL INFORMATION:  
APPLICANT: WHITLOW, MARC  
SHORR, ROBERT G.L.  
FILPULA, DAVID R.  
LEE, LHSYNG S.  
TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVENUE, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/791,540  
FILING DATE: 26-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/069,842  
FILING DATE: 1998-04-30  
APPLICATION NUMBER: US 60/050,472  
FILING DATE: 23-JUN-1997

APPLICATION NUMBER: US 60/063,074  
FILING DATE: 27-OCT-1997  
APPLICATION NUMBER: US 60/067,341  
FILING DATE: 02-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: JORGE A. GOLDSTEIN  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.1840002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 723 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..723  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-791-540-5

Query Match  
Best Local Similarity 68.7%; Score 15.8; DB 10; Length 723;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAAGTCGAGGCTTCAGCA 21  
Db 350 GAAGTAGAGCCTTCAGCA 332

RESULT 11  
US-09-956-086-1/c  
Sequence 1, Application US/09956086  
Patent No. US20020158498A1  
GENERAL INFORMATION:  
APPLICANT: FILPULA, DAVID  
WANG, MAOLIAN  
SHORR, ROBERT  
WHITLOW, MARC  
LEE, LHSYNG S.  
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS  
CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVE., NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/956,086  
FILING DATE: 20-Sep-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/069,821  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 60/063,074  
FILING DATE: 27-OCT-1997  
APPLICATION NUMBER: US 60/050,472  
FILING DATE: 23-JUN-1997  
APPLICATION NUMBER: US 60/044,449  
FILING DATE: 30-APR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: KIM, JUDITH D.  
REGISTRATION NUMBER: 40,679

REFERENCE/DOCKET NUMBER: 0977.2280003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)371-2600  
TELEFAX: (202)371-2540  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 758 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..747  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-956-086-1

Query Match  
Best Local Similarity 68.7%; Score 15.8; DB 9; Length 758;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 3 GAAGTCGAGCCTTCAGCA 21  
350 GAAGTAGAGCCTTCAGCA 332

RESULT 12  
US-09-956-087-1/C  
Sequence 1, Application US/09956087  
Patent No. US20020161201A1  
GENERAL INFORMATION:  
APPLICANT: FILIPULA, DAVID  
WANG, MAOLIANG  
SHORR, ROBERT  
WHITLOW, MARC  
LEE, LIHSYNG S.  
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS  
CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVE., NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/09/956,087  
FILING DATE: 20-SEP-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/069,821  
FILING DATE: 1998-04-30  
APPLICATION NUMBER: US 60/063,074  
FILING DATE: 27-OCT-1997  
APPLICATION NUMBER: US 60/050,472  
FILING DATE: 23-JUN-1997  
APPLICATION NUMBER: US 60/044,449  
FILING DATE: 30-APR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: KIM, JUDITH U.  
REGISTRATION NUMBER: 40,679  
REFERENCE/DOCKET NUMBER: 0977.2280003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)371-2600  
TELEFAX: (202)371-2540  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:

LENGTH: 758 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..747  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-956-087-1

Query Match  
Best Local Similarity 68.7%; Score 15.8; DB 9; Length 758;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 3 GAAGTCGAGCCTTCAGCA 21  
350 GAAGTAGAGCCTTCAGCA 332

RESULT 13  
US-09-985-442-1/C  
Sequence 1, Application US/09985442  
Patent No. US20020156248A1  
GENERAL INFORMATION:  
APPLICANT: FILIPULA, David R.  
APPLICANT: Wang, Maoliang  
APPLICANT: Whitlow, Marc D.  
TITLE OF INVENTION: NO. US20020156248A1a1 Method for Targeted Delivery of Nucleic  
FILE REFERENCE: 0977.2300003  
CURRENT APPLICATION NUMBER: US/09/985,442  
CURRENT FILING DATE: 2001-11-02  
PRIOR APPLICATION NUMBER: 09/420,592  
PRIOR FILING DATE: 1999-10-19  
PRIOR APPLICATION NUMBER: 60/104,949  
PRIOR FILING DATE: 1998-10-20  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 782  
TYPE: DNA  
ORGANISM: Artificial Sequence.  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: CC49/218 srf  
NAME/KEY: CDS  
LOCATION: (1)..(771)  
US-09-985-442-1

Query Match  
Best Local Similarity 68.7%; Score 15.8; DB 9; Length 782;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 3 GAAGTCGAGCCTTCAGCA 21  
350 GAAGTAGAGCCTTCAGCA 332

RESULT 14  
US-09-791-578-3/C  
Sequence 3, Application US/09791578  
Patent No. US20020061307A1  
GENERAL INFORMATION:  
APPLICANT: WHITLOW, MARC  
SHORR, ROBERT G. L.  
FILIPULA, DAVID R.  
LEE, LIHSYNG S.  
TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN  
POLYPEPTIDES  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVENUE, SUITE 600  
CITY: WASHINGTON



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 00:35:54 ; Search time 844.228 seconds  
(without alignments)  
441.227 Million cell updates/sec

Title: US-09-674-195c-14

Perfect score: 23

Sequence: 1 dcaagtcgaggtcttcagcatg 23

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_estl:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_est3:\*  
12: gb\_est4:\*  
13: gb\_est5:\*  
14: gb\_est6:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_hiv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vtl:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	18.8	81.7	123	12	BF251708 EST418892
C 2	18.8	81.7	351	12	BF251693 EST418877
C 3	18.8	81.7	362	12	BF251811 EST419073
C 4	18.8	81.7	377	12	BF251964 EST419226
C 5	18.8	81.7	378	12	BF251967 EST419229
C 6	18.8	81.7	391	12	BF251561 EST418910

C 7	18.8	81.7	486	10	AM792005
C 8	18.8	81.7	488	12	BF251704
C 9	18.8	81.7	502	12	BF252581
C 10	18.8	81.7	515	10	AM792430
C 11	18.8	81.7	518	12	BF251715
C 12	18.8	81.7	541	12	BF252371
C 13	18.8	81.7	546	12	BF253171
C 14	18.8	81.7	567	12	BF252094
C 15	18.8	81.7	568	12	BF252878
C 16	18.8	81.7	572	12	BF252095
C 17	18.8	81.7	605	12	BF252135
C 18	18.8	81.7	679	12	BF251385
C 19	18.8	81.7	687	12	BF251001
C 20	18.8	81.7	701	12	BF251666
C 21	18.8	81.7	836	12	BF250962
C 22	18	78.3	578	14	W36400
C 23	17.8	77.4	222	10	AM791051
C 24	17.8	77.4	905	17	CNS077PT
C 25	17.8	77.4	914	17	CNS079TL
C 26	17.8	77.4	944	17	CNS07827
C 27	17.8	77.4	957	17	CNS0797C
C 28	17.8	77.4	992	17	CNS0784M
C 29	17.8	77.4	997	17	CNS07819
C 30	17.8	77.4	1008	17	CNS076RF
C 31	17.8	77.4	1012	17	CNS079X1
C 32	17.8	77.4	1020	17	CNS077XC
C 33	17.8	77.4	1031	17	CNS076VJ
C 34	17.8	77.4	1060	17	CNS078EU
C 35	17.4	75.7	572	17	A2361913
C 36	17.4	75.7	661	17	BH738995
C 37	17.4	75.7	735	17	BH532538
C 38	17.4	75.7	861	12	BG283071
C 39	17.2	74.8	85	17	AQ025794
C 40	17.2	74.8	176	9	A1213893
C 41	17.2	74.8	244	9	A1212196
C 42	17.2	74.8	250	9	AA784878
C 43	17.2	74.8	252	9	A1211979
C 44	17.2	74.8	260	9	A1329914
C 45	17.2	74.8	269	9	AA966666

#### ALIGNMENTS

RESULT 1  
LOCUS BF251708 123 bp mRNA linear EST 15-NOV-2001  
DEFINITION BF251708 Coccidioides immitis spherule cDNA library Coccidioides  
limitis CDNA clone C1AK37 5' sequence, mRNA sequence.

ACCESSION BF251708  
VERSION BF251708.1 GI:16931774  
KEYWORDS EST.  
SOURCE Coccidioides immitis.  
ORGANISM Coccidioides immitis.

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; mitosporic Onygenales; Coccidioides.

AUTHORS 1 (bases 1 to 123)  
TITLE Gardner M.J. and Kirkland T.  
JOURNAL Generation of ESTs from Coccidioides immitis spherule cDNA library  
COMMENT Unpublished (2000)  
Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardneretjg.org

FEATURES  
source Location/Qualifiers

1..123  
/organism="Coccidioides immitis"  
/db\_xref="taxon:5501"  
/clone="C1AK37"  
/clone\_lib="Coccidioides immitis spherule cDNA library"

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/dev_stage="spherule"
/lab_host="SOLR"
/notes="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT      37 a      23 c      27 g      36 t
ORIGIN

Query Match      81.7%; Score 18.8; DB 12; Length 123;
Best Local Similarity 90.9%; Pred. NO. 50;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CGAGTCGAGCGCTTTCAGCATG 23
      |||||
      80 CGAGTCGAGCGCTTTCAGCATG 59

RESULT 2
BF251693/c
LOCUS      BF251693      351 bp      mRNA      linear      EST 15-NOV-2001
DEFINITION      Coccioidioides immitis spherule cDNA library Coccioidioides
immitis cDNA clone CIAAK21 5' sequence, mRNA sequence.
ACCESSION      BF251693
VERSION
KEYWORDS
SOURCE
ORGANISM
COMMENT      Contact: Malcolm J. Gardner
      Department of Eukaryotic Genomics
      The Institute for Genomic Research
      9712 Medical Center Drive, Rockville, MD 20850, USA
      Tel: 301 838 3519
      Fax: 301 838 0208
      Email: gardner@tigr.org.
      Location/Qualifiers
      1..351
      /organism="Coccioidioides immitis"
      /db_xref="taxon:5501"
      /clone="CIAAK21"
      /clone_lib="Coccioidioides immitis spherule cDNA library"
      /dev_stage="spherule"
      /lab_host="SOLR"
      /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
      XhoI"

BASE COUNT      97 a      69 c      81 g      104 t
ORIGIN

Query Match      81.7%; Score 18.8; DB 12; Length 351;
Best Local Similarity 90.9%; Pred. NO. 94;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CGAGTCGAGCGCTTTCAGCATG 23
      |||||
      176 CGAGTCGAGCGCTTTCAGCATG 155

RESULT 3
BF251811/c
LOCUS      BF251811      362 bp      mRNA      linear      EST 15-NOV-2001
DEFINITION      Coccioidioides immitis spherule cDNA library Coccioidioides
immitis cDNA clone CIAAM73 5' sequence, mRNA sequence.
ACCESSION      BF251811
VERSION      GI:16931954
KEYWORDS
SOURCE
ORGANISM
COMMENT      Coccioidioides immitis.
      Coccioidioides immitis
      Eukaryote; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
      Omygenales; mitosporic Omygenales; Coccioidioides.

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REFERENCE
AUTHORS      1 (bases 1 to 362)
TITLE        Gardner,M.J. and Kirkland,T.
JOURNAL      Generation of ESTs from Coccidioides immitis spherule cDNA library
COMMENT      Unpublished (2000)
              Contact: Malcolm J. Gardner
              Department of Eukaryotic Genomics
              The Institute for Genomic Research
              9712 Medical Center Drive, Rockville, MD 20850, USA
              Tel: 301 838 3519
              Fax: 301 838 0208
              Email: gardner@tigr.org.

FEATURES
    source
    1..362
    /organism="Coccidioides immitis"
    /db_xref="taxon:5501"
    /clone="CIAAP15"
    /clone_1lb="Coccidioides immitis spherule cDNA library"
    /dev_stage="spherule"
    /lab_host="SOLR"
    /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
    XhoI"

BASE COUNT
ORIGIN      98 a      69 c      84 g      111 t

Query Match
Best Local Similarity  81.7%; Score 18.8; DB 12; Length 362;
Matches                20; Conservative  0; Mismatches  2; Indels  0; Gaps  0;

QY      2 CGAAGTCGAGCCTTCACATG 23
        |||||||  ||| |||||
Db      171 CGAAGTCGAGCTTTAGCATG 150

RESULT 4
BF251964/c 377 bp. mRNA linear EST 15-NOV-2001
LOCUS      BF251964.1 GI:16932107
DEFINITION BF251964 Coccidioides immitis spherule cDNA library Coccidioides
            immitis cDNA clone CIAAP15 5' sequence, mRNA sequence.
ACCESSION  BF251964
VERSION     BF251964.1 GI:16932107
KEYWORDS   EST.
SOURCE      Coccidioides immitis.
ORGANISM   Coccidioides immitis.
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Onygenales; mitosporic Onygenales; Coccidioides.
REFERENCE  1 (bases 1 to 377)
AUTHORS   Gardner,M.J. and Kirkland,T.
TITLE     Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL   Unpublished (2000)
COMMENT   Contact: Malcolm J. Gardner
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301 838 3519
            Fax: 301 838 0208
            Email: gardner@tigr.org.

FEATURES
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    1..377
    /organism="Coccidioides immitis"
    /db_xref="taxon:5501"
    /clone="CIAAP15"
    /clone_1lb="Coccidioides immitis spherule cDNA library"
    /dev_stage="spherule"
    /lab_host="SOLR"
    /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
    XhoI"

BASE COUNT
ORIGIN      103 a      85 c      94 g      95 t

Query Match
Best Local Similarity  81.7%; Score 18.8; DB 12; Length 377;
Matches                20; Conservative  0; Mismatches  2; Indels  0; Gaps  0;

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OY 2 CGAAGTCGAGGCTTTCAGCATG 23  
|||||  
Db 75 CGAAGTCGAGGCTTTCAGCATG 54

RESULT 5  
BF251967/c 378 bp mRNA linear EST 15-NOV-2001  
LOCUS EST191229 Coccidioides immitis spherule cDNA library Coccidioides  
DEFINITION immitis cDNA clone CIAAP18 5' sequence, mRNA sequence.  
ACCESSION BF251967  
VERSION BF251967.1 GI:16932110  
KEYWORDS EST  
SOURCE Coccidioides immitis.  
ORGANISM Coccidioides immitis  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; mitosporic Onygenales; Coccidioides.  
REFERENCE 1 (bases 1 to 378)  
AUTHORS Gardner, M.J. and Kirkland, T.  
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library  
JOURNAL Unpublished (2000)  
COMMENT Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org

FEATURES  
source  
1. 378  
Location/Qualifiers  
/organism="Coccidioides immitis"  
/db\_xref="taxon:5501"  
/clone\_lib="Coccidioides immitis spherule cDNA library"  
/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI"

BASE COUNT 104 a 75 c 94 g 105 t

ORIGIN  
Query Match 81.7%; Score 18.8; DB 12; Length 378;  
Best Local Similarity 90.9%; Pred. No. 98;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CGAAGTCGAGGCTTTCAGCATG 23  
|||||  
Db 169 CGAAGTCGAGGCTTTCAGCATG 148

RESULT 6  
BF251561/c 391 bp mRNA linear EST 15-NOV-2001  
LOCUS EST418910 Coccidioides immitis spherule cDNA library Coccidioides  
DEFINITION immitis cDNA clone CIAK57 5' sequence, mRNA sequence.  
ACCESSION BF251561  
VERSION BF251561.1 GI:16931792  
KEYWORDS EST  
SOURCE Coccidioides immitis.  
ORGANISM Coccidioides immitis  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; mitosporic Onygenales; Coccidioides.  
REFERENCE 1 (bases 1 to 391)  
AUTHORS Gardner, M.J. and Kirkland, T.  
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library  
JOURNAL Unpublished (2000)  
COMMENT Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org

FEATURES  
source  
Location/Qualifiers  
1. 391  
/organism="Coccidioides immitis"  
/db\_xref="taxon:5501"  
/clone\_lib="Coccidioides immitis spherule cDNA library"  
/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI"

BASE COUNT 107 a 76 c 96 g 112 t

ORIGIN  
Query Match 81.7%; Score 18.8; DB 12; Length 391;  
Best Local Similarity 90.9%; Pred. No. 1e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CGAAGTCGAGGCTTTCAGCATG 23  
|||||  
Db 176 CGAAGTCGAGGCTTTCAGCATG 155

RESULT 7  
AW792005/c 486 bp mRNA linear EST 01-MAY-2001  
LOCUS D00948-R Lambda Zap, Stratagene Blumeria graminis f. sp. hordei  
DEFINITION cDNA clone D00948 similar to non-functional folate binding protein,  
mRNA sequence.  
ACCESSION AW792005  
VERSION AW792005.1 GI:13903602  
KEYWORDS EST  
SOURCE Blumeria graminis f. sp. hordei.  
ORGANISM Blumeria graminis f. sp. hordei  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;  
Erysiphales; Erysiphaceae; Blumeria.  
REFERENCE 1 (bases 1 to 486)  
AUTHORS Thomas, S.W., Rasmussen, S.W., Glaring, M.A., Rousier, J.A. and Oliver  
R.P.  
TITLE Gene identification in the fungal pathogen Blumeria graminis by  
JOURNAL expressed sequence tag analysis  
COMMENT Unpublished (2000)  
Contact: Rasmussen, S.W.  
Department of Yeast Genetics  
Carlsberg Laboratory  
10 GL Carlsbergvej, DK-2500, Copenhagen, Denmark  
Tel: 45 3327 5230  
Fax: 45 3327 4766  
Email: swr@erc.dk  
High quality sequence stop: 486  
POLYA-No.

FEATURES  
source  
Location/Qualifiers  
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/organism="Blumeria graminis f. sp. hordei"  
/db\_xref="taxon:62688"  
/clone\_lib="D00948"  
/clone\_lib="Lambda Zap, Stratagene"  
/cell\_type="confidia"  
/lab\_host="Hordium vulgare"

BASE COUNT 138 a 101 c 115 g 132 t

ORIGIN  
Query Match 81.7%; Score 18.8; DB 10; Length 486;  
Best Local Similarity 90.9%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CGAAGTCGAGGCTTTCAGCATG 23  
|||||  
Db 176 CGAAGTCGAGGCTTTCAGCATG 155

RESULT 8  
BF251704/c 488 bp mRNA linear EST 15-NOV-2001  
LOCUS BF251704

DEFINITION EST418888 Coccidioides immitis spherule CDNA library Coccidioides immitis CDNA clone CIAK33 5' sequence, mRNA sequence.

ACCESSION BF251704

VERSION BF251704.1 GI:16931770

KEYWORDS EST

SOURCE Coccidioides immitis.

ORGANISM Coccidioides immitis.

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; mitosporic Onygenales; Coccidioides.

AUTHORS 1 (bases 1 to 488)

TITLE Gardner, M.J. and Kirkland, T.

JOURNAL Generation of ESTs from Coccidioides immitis spherule CDNA library unpublished (2000)

COMMENT Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardneretlgr.org.

FEATURES  
source Location/Qualifiers  
1..488

BASE COUNT 129 a 97 c 126 g 136 t

ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 488;  
Best Local Similarity 90.9%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CGAAGTCGAGGCTTCAGCATG 23  
|||||

Db 176 CGAAGTCGAGGCTTTTACGATG 155

RESULT 9  
LOCUS BF252581 502 bp mRNA linear EST 15-NOV-2001

DEFINITION EST419843 Coccidioides immitis spherule CDNA library Coccidioides immitis CDNA clone CIAV35 5' sequence, mRNA sequence.

ACCESSION BF252581

VERSION BF252581.1 GI:16932724

KEYWORDS EST.

SOURCE Coccidioides immitis.

ORGANISM Coccidioides immitis.

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; mitosporic Onygenales; Coccidioides.

AUTHORS 1 (bases 1 to 502)

TITLE Gardner, M.J. and Kirkland, T.

JOURNAL Generation of ESTs from Coccidioides immitis spherule CDNA library unpublished (2000)

COMMENT Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardneretlgr.org.

FEATURES  
source Location/Qualifiers  
1..502

BASE COUNT 142 a 101 c 126 g 133 t

ORIGIN

Query Match 81.7%; Score 18.8; DB 10; Length 515;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CGAAGTCGAGGCTTCAGCATG 23  
|||||

Db 169 CGAAGTCGAGGCTTTTACGATG 148

RESULT 11  
LOCUS BF251715 518 bp mRNA linear EST 15-NOV-2001

DEFINITION EST418899 Coccidioides immitis spherule CDNA library Coccidioides immitis CDNA clone CIAK45 5' sequence, mRNA sequence.

ACCESSION BF251715

VERSION BF251715.1 GI:16931781

KEYWORDS EST.

SOURCE Coccidioides immitis.

ORGANISM Coccidioides immitis.

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

BASE COUNT 142 a 101 c 126 g 133 t

ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 502;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CGAAGTCGAGGCTTCAGCATG 23  
|||||

Db 179 CGAAGTCGAGGCTTTTACGATG 158

RESULT 10  
LOCUS AW792430 515 bp mRNA linear EST 01-MAY-2001

DEFINITION D01189-R Lambda Zap, StrataGene Blumeria graminis f. sp. hordei CDNA clone D01189 similar to non-functional folate binding protein, mRNA sequence.

ACCESSION AW792430

VERSION AW792430.1 GI:13904027

KEYWORDS EST.

SOURCE Blumeria graminis f. sp. hordei.

ORGANISM Blumeria graminis f. sp. hordei.

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes; Erysiphales; Erysiphaceae; Blumeria.

AUTHORS 1 (bases 1 to 515)

TITLE Thomas, S.W., Rasmussen, S.W., Glarling, M.A., Rouster, J.A. and Oliver, R.P.

JOURNAL Gene identification in the fungal pathogen Blumeria graminis by expressed sequence tag analysis unpublished (2000)

COMMENT Contact: Rasmussen, S.W.  
Department of Yeast Genetics  
Carlsberg Laboratory  
10 GL, Carlsbergvej, DK-2500, Copenhagen, Denmark  
Tel: 45 3327 5230  
Fax: 45 3327 4766  
Email: svr@erc.dk

FEATURES  
source Location/Qualifiers  
1..515

BASE COUNT 150 a 104 c 119 g 142 t

ORIGIN

Query Match 81.7%; Score 18.8; DB 10; Length 515;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CGAAGTCGAGGCTTCAGCATG 23  
|||||

Db 169 CGAAGTCGAGGCTTTTACGATG 148

RESULT 11  
LOCUS BF251715 518 bp mRNA linear EST 15-NOV-2001

DEFINITION EST418899 Coccidioides immitis spherule CDNA library Coccidioides immitis CDNA clone CIAK45 5' sequence, mRNA sequence.

ACCESSION BF251715

VERSION BF251715.1 GI:16931781

KEYWORDS EST.

SOURCE Coccidioides immitis.

ORGANISM Coccidioides immitis.

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Onygenales; mitosporic Onygenales; Coccidioides.

REFERENCE  
1 (bases 1 to 518)  
AUTHORS  
Gardner, M.J. and Kirkland, T.  
TITLE  
Generation of ESTs from Coccidioides immitis spherule cDNA library  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org

FEATURES  
source  
1..518  
/organism="Coccidioides immitis"  
/db\_xref="taxon:5501"  
/clone="C1AAK45"  
/clone\_1lb="Coccidioides immitis spherule cDNA library"  
/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT  
141 a 104 c 133 g 140 t

ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 518;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CGAAGTCGAGGCTTCAGCATG 23  
|||||  
Db 176 CGAAGTCGAGGCTTCAGCATG 155

RESULT 12  
BF252371/c 541 bp mRNA linear EST 15-NOV-2001  
LOCUS  
EST41933 Coccidioides immitis spherule cDNA library Coccidioides  
DEFINITION  
Immitis cDNA clone C1AAV41 5' sequence, mRNA sequence.  
ACCESSION  
BF252371  
VERSION  
BF252371.1 GI:16932514  
KEYWORDS  
EST.  
SOURCE  
Coccidioides immitis.  
ORGANISM  
Coccidioides immitis  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; mitosporic Onygenales; Coccidioides.  
REFERENCE  
1 (bases 1 to 541)  
AUTHORS  
Gardner, M.J. and Kirkland, T.  
TITLE  
Generation of ESTs from Coccidioides immitis spherule cDNA library  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org

FEATURES  
source  
1..541  
/organism="Coccidioides immitis"  
/db\_xref="taxon:5501"  
/clone="C1AAV41"  
/clone\_1lb="Coccidioides immitis spherule cDNA library"  
/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT  
157 a 109 c 133 g 142 t

ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 541;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CGAAGTCGAGGCTTCAGCATG 23  
|||||  
Db 175 CGAAGTCGAGGCTTCAGCATG 154

RESULT 13  
BF253171/c 546 bp mRNA linear EST 15-NOV-2001  
LOCUS  
EST445666 Coccidioides immitis spherule cDNA library Coccidioides  
DEFINITION  
Immitis cDNA clone C1GAB68 5' sequence, mRNA sequence.  
ACCESSION  
BF253171  
VERSION  
BF253171.1 GI:16933314  
KEYWORDS  
EST.  
SOURCE  
Coccidioides immitis.  
ORGANISM  
Coccidioides immitis  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; mitosporic Onygenales; Coccidioides.  
REFERENCE  
1 (bases 1 to 546)  
AUTHORS  
Gardner, M.J. and Kirkland, T.  
TITLE  
Generation of ESTs from Coccidioides immitis spherule cDNA library  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org

FEATURES  
source  
1..546  
/organism="Coccidioides immitis"  
/db\_xref="taxon:5501"  
/clone="C1GAB68"  
/clone\_1lb="Coccidioides immitis spherule cDNA library"  
/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT  
157 a 109 c 135 g 145 t

ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 546;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CGAAGTCGAGGCTTCAGCATG 23  
|||||  
Db 179 CGAAGTCGAGGCTTCAGCATG 158

RESULT 14  
BF252094/c 567 bp mRNA linear EST 15-NOV-2001  
LOCUS  
EST419356 Coccidioides immitis spherule cDNA library Coccidioides  
DEFINITION  
Immitis cDNA clone C1AAQ80 5' sequence, mRNA sequence.  
ACCESSION  
BF252094  
VERSION  
BF252094.1 GI:16932237  
KEYWORDS  
EST.  
SOURCE  
Coccidioides immitis.  
ORGANISM  
Coccidioides immitis  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; mitosporic Onygenales; Coccidioides.  
REFERENCE  
1 (bases 1 to 567)  
AUTHORS  
Gardner, M.J. and Kirkland, T.  
TITLE  
Generation of ESTs from Coccidioides immitis spherule cDNA library  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519

Fax: 301 838 0208  
Email: gardner@tigr.org

FEATURES  
Source Location/Qualifiers

1..567  
/organism="Coccidioides immitis"  
/db\_xref="taxon:5501"  
/clone="CINA080"  
/clone\_lib="Coccidioides immitis spherule cDNA library"  
/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT 161 a 118 c 142 g 146 t  
ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 567;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CGAAGTCGAGGCTTTCAGCATG 23  
|||||  
Db 182 CGAAGTCGAGGCTTTCAGCATG 161

RESULT 15  
BF252878/c 568 bp mRNA linear EST 15-NOV-2001  
LOCUS BF252878 Coccidioides immitis spherule cDNA library Coccidioides  
DEFINITION  
BF252878  
ACCESSION BF252878  
VERSION BF252878.1 GI:16933021  
KEYWORDS EST.  
SOURCE Coccidioides immitis.  
ORGANISM Coccidioides immitis.  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Oxygenales; Mitosporic Oxygenales; Coccidioides.

REFERENCE  
AUTHORS Gardner M.J. and Kirkland T.  
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library  
JOURNAL Unpublished (2000)  
COMMENT Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org

FEATURES  
Source Location/Qualifiers

1..568  
/organism="Coccidioides immitis"  
/db\_xref="taxon:5501"  
/clone="CIAB92"  
/clone\_lib="Coccidioides immitis spherule cDNA library"  
/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT 162 a 117 c 143 g 146 t  
ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 568;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CGAAGTCGAGGCTTTCAGCATG 23  
|||||  
Db 182 CGAAGTCGAGGCTTTCAGCATG 161

Search completed: June 12, 2003, 04:34:58  
Job time: 853.943 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 22:21:06 ; Search time 620.827 Seconds

(without alignments)  
1921.975 Million cell updates/sec

Title: US-09-674-195c-15

Perfect score: 41  
Sequence: 1 dtatagcctagattacc.....cggatcccaagtagaag 41Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:\*

1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pln:\*  
35: em\_htg\_rnd:\*  
36: em\_htg\_mam:\*  
37: em\_htg\_vrt:\*  
38: em\_sy:\*  
39: em\_htgo\_hum:\*  
40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	40.2	98.0	1686	8	AB015768	AB015768 Spiromast
C 2	40.2	98.0	1699	8	CP029390	U29390 Chrysospori
C 3	40.2	98.0	1704	8	HCC18SRN	Z75306 H.capsulatu
C 4	40.2	98.0	1704	8	HCC18SRN	Z75307 H.capsulatu
C 5	40.2	98.0	1713	8	BDRNA	X59420 B.dermatidi
C 6	40.2	98.0	1713	8	HCI18SR	X58572 H.capsulatu
C 7	40.2	98.0	1713	8	MBORGED	L28066 Malbranchea
C 8	40.2	98.0	1721	8	AF242259	AF242259 Acrosporm
C 9	40.2	98.0	1726	8	AF241655	AF241655 Paracocci
C 10	40.2	98.0	1726	8	AF320009	AF320009 Ajellomyc
C 11	40.2	98.0	1726	8	AF320010	AF320010 Ajellomyc
C 12	40.2	98.0	1759	8	AF227151	AF227151 Paracocci
C 13	40.2	98.0	1771	8	AF238302	AF238302 Paracocci
C 14	40.2	98.0	1799	8	BLODA	M55624 Blastomyces
C 15	40.2	98.0	1800	8	BLO18SRNA	M63096 Blastomyces
C 16	39.4	96.1	803	8	AF289656	AF289656 Hobsonia
C 17	39.2	95.6	1177	8	AF356695	AF356695 Rhytisma
C 18	38.6	94.1	1894	8	AY100023	AY100023 Muscodor
C 19	38.6	94.1	144	8	AB046947	AB046947 Endophyte
C 20	38.6	94.1	145	8	AB046949	AB046949 Endophyte
C 21	38.6	94.1	145	8	GS025153	U25153 Glomus sp.
C 22	38.6	94.1	191	8	AF062657	AF062657 Ascomycet
C 23	38.6	94.1	192	8	AF062658	AF062658 Endophyte
C 24	38.6	94.1	192	8	AF062659	AF062659 Endophyte
C 25	38.6	94.1	192	8	AF062661	AF062661 Endophyte
C 26	38.6	94.1	192	8	AF062662	AF062662 Endophyte
C 27	38.6	94.1	192	8	AF062664	AF062664 Endophyte
C 28	38.6	94.1	192	8	AF062673	AF062673 Endophyte
C 29	38.6	94.1	192	8	AF062674	AF062674 Endophyte
C 30	38.6	94.1	192	8	AF062675	AF062675 Endophyte
C 31	38.6	94.1	192	8	AF062677	AF062677 Endophyte
C 32	38.6	94.1	192	8	AF062679	AF062679 Endophyte
C 33	38.6	94.1	192	8	AF062680	AF062680 Endophyte
C 34	38.6	94.1	192	8	AF062682	AF062682 Endophyte
C 35	38.6	94.1	192	8	AF062683	AF062683 Endophyte
C 36	38.6	94.1	192	8	AF062698	AF062698 Endophyte
C 37	38.6	94.1	193	8	AF062663	AF062663 Ascomycet
C 38	38.6	94.1	193	8	AF062668	AF062668 Endophyte
C 39	38.6	94.1	193	8	AF062685	AF062685 Ascomycet
C 40	38.6	94.1	194	8	AF062684	AF062684 Endophyte
C 41	38.6	94.1	359	8	UF0311479	AJ311479 Unculture
C 42	38.6	94.1	373	8	UF0311476	AJ311476 Unculture
C 43	38.6	94.1	420	8	294123	294123 Fusarium cu
C 44	38.6	94.1	421	8	294124	294124 Fusarium cu
C 45	38.6	94.1	421	8	294125	294125 Fusarium cu

## ALIGNMENTS

RESULT 1

AB015768/c 1686 bp DNA linear PLN 17-NOV-1999

LOCUS Spiromastix warcupii 18S rRNA gene, isolate CBS 576.63, partial sequence.

ACCESSION AB015768

VERSION AB015768.1 GI:6440558

KEYWORDS Spiromastix warcupii (isolate: CBS 576.63) DNA.

ORGANISM Spiromastix warcupii

REFERENCE Sugiyama, M., Ohara, A. and Mikawa, T.

AUTHORS Molecular phylogeny of onygenalean fungi based on small subunit

TITLE

JOURNAL Ribosomal DNA (SSU rDNA) sequences  
 REFERENCE Mycoscience 40, 251-258 (1999)  
 AUTHORS Sugiyama, M.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-JUN-1998) Masato Sugiyama, Mitsubishi Chemical Co.  
 Yokohama Research Center, Biochemicals Laboratory, 1000,  
 Kamoshida-cho, Aoba-ku, Yokohama, Kanagawa 227-8502, Japan  
 (E-mail: 4200779@cc.m.kagaku.co.jp, Tel: +81-45-963-3474,  
 Fax: +81-45-963-3992)  
 FEATURES Location/Qualifiers  
 source 1. 1686  
 /organism="Spiroplasma wacupii"  
 /isolate="CBS 576.63"  
 /db\_xref="taxon:37235"  
 <1..>1686  
 /product="18S ribosomal RNA"  
 /note="small subunit rRNA"  
 BASE COUNT 434 a 364 c 462 g 426 t  
 ORIGIN

Query Match 98.0%; Score 40.2; DB 8; Length 1686;  
 Best Local Similarity 97.6%; Pred. No. 2.7e-06;  
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTATTAGCTCTAGATTACACAGGGTATCCAGTAGTAAGG 41  
 :|||||  
 DB 88 GTATTAGCTCTAGATTACACAGGGTATCCAGTAGTAAGG 48

RESULT 2  
 LOCUS CPU29390 1699 bp DNA linear PLN 25-FEB-1997  
 DEFINITION Chrysosporium parvum 18S ribosomal RNA gene, partial sequence.  
 ACCESSION U29390  
 VERSION U29390.1 GI:1046282  
 KEYWORDS Chrysosporium parvum.  
 SOURCE Chrysosporium parvum.  
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 Onygenales; Mitoportic Onygenales; Chrysosporium.  
 REFERENCE 1 (bases 1 to 1699)  
 AUTHORS Bowman, B.H., White, T.J. and Taylor, J.W.  
 TITLE Human pathogenic fungi and their close nonpathogenic relatives  
 JOURNAL Mol. Phylogenet. Evol. 6 (1), 89-96 (1996)  
 MEDLINE 96426663  
 PUBMED 8612309  
 REFERENCE 2 (bases 1 to 1699)  
 AUTHORS Bowman, B.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-JUN-1995) Roche Molecular Systems, Infectious  
 Diseases, 1145 Atlantic Avenue, Alameda, CA 94501, USA  
 FEATURES Location/Qualifiers  
 source 1. 1699  
 /organism="Chrysosporium parvum"  
 /strain="UAMH1067"  
 /db\_xref="taxon:41283"  
 /note="Sequenced in both directions directly from PCR  
 product"  
 <1..>1699  
 /product="18S ribosomal RNA"  
 /note="Missing an estimated 50 bases from the 5' and 49  
 from the 3' end of the rRNA gene"  
 BASE COUNT 431 a 366 c 468 g 434 t  
 ORIGIN

Query Match 98.0%; Score 40.2; DB 8; Length 1699;  
 Best Local Similarity 97.6%; Pred. No. 2.7e-06;  
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTATTAGCTCTAGATTACACAGGGTATCCAGTAGTAAGG 41  
 :|||||  
 DB 118 GTATTAGCTCTAGATTACACAGGGTATCCAGTAGTAAGG 78

RESULT 3  
 LOCUS HCC18SRN/C 1704 bp DNA linear PLN 10-DEC-1999  
 DEFINITION H. capsulatum ssp. duboisii 18S rRNA gene.  
 ACCESSION 275306  
 VERSION 275306.1 GI:1419549  
 KEYWORDS 18S ribosomal RNA; 18S rRNA gene; small subunit ribosomal RNA.  
 SOURCE Ajellomyces capsulatus.  
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 Onygenales; Onygenaceae; Ajellomyces.  
 REFERENCE 1 (bases 1 to 1704)  
 AUTHORS Okeke, C.N., Kappe, R., Zakikhani, S., Nolte, O. and Sonntag, H.G.  
 TITLE Ribosomal genes of Histoplasma capsulatum var. duboisii and var.  
 farciminosum  
 JOURNAL Mycoses 41 (9-10), 355-362 (1998)  
 MEDLINE 9914487  
 PUBMED 9916456  
 REFERENCE 2 (bases 1 to 1704)  
 AUTHORS Kappe, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-JUL-1996) Reinhard Kappe, Hygiene & Med.  
 Microbiology, University of Heidelberg, Hygiene Institute, Im  
 Neuenheimer Feld 324, Heidelberg, D-69120, Germany  
 FEATURES Location/Qualifiers  
 source 1. 1704  
 /organism="Ajellomyces capsulatus"  
 /strain="CBS175.57"  
 /sub\_species="duboisii"  
 /db\_xref="taxon:5037"  
 1..1704  
 /gene="18S rRNA"  
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 /gene="18S rRNA"  
 /product="18S ribosomal RNA"  
 BASE COUNT 432 a 365 c 470 g 437 t  
 ORIGIN

Query Match 98.0%; Score 40.2; DB 8; Length 1704;  
 Best Local Similarity 97.6%; Pred. No. 2.7e-06;  
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTATTAGCTCTAGATTACACAGGGTATCCAGTAGTAAGG 41  
 :|||||  
 DB 112 GTATTAGCTCTAGATTACACAGGGTATCCAGTAGTAAGG 72

RESULT 4  
 LOCUS HCF18SRN 1704 bp DNA linear PLN 10-DEC-1999  
 DEFINITION H. capsulatum ssp. farciminosum 18S rRNA gene.  
 ACCESSION 275307  
 VERSION 275307.1 GI:1419550  
 KEYWORDS 18S ribosomal RNA; 18S rRNA gene; small subunit ribosomal RNA.  
 SOURCE Ajellomyces capsulatus.  
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 Onygenales; Onygenaceae; Ajellomyces.  
 REFERENCE 1 (bases 1 to 1704)  
 AUTHORS Okeke, C.N., Kappe, R., Zakikhani, S., Nolte, O. and Sonntag, H.G.  
 TITLE Ribosomal genes of Histoplasma capsulatum var. duboisii and var.  
 farciminosum  
 JOURNAL Mycoses 41 (9-10), 355-362 (1998)  
 MEDLINE 9914487  
 PUBMED 9916456  
 REFERENCE 2 (bases 1 to 1704)  
 AUTHORS Kappe, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-JUL-1996) Reinhard Kappe, Hygiene & Med.  
 Microbiology, University of Heidelberg, Hygiene Institute, Im  
 Neuenheimer Feld 324, Heidelberg, D-69120, Germany

FEATURES  
SOURCE  
Location/Qualifiers  
1. .1704  
/organism="Ajellomyces capsulatus"  
/strain="CBS205.35, CBS478.64"  
/sub\_species="farciminosum"  
/db\_xref="taxon:5037"  
gene  
1. .1704  
/gene="18S rRNA"  
1. .1704  
/gene="18S rRNA"  
/product="18S ribosomal RNA"  
BASE COUNT 432 a 364 c 471 g 437 t  
ORIGIN

Query Match 98.0%; Score 40.2; DB 8; Length 1704;  
Best Local Similarity 97.6%; Pred. No. 2.7e-06;  
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTATTAGCTCTAGATTACACGGGTATCCAGTAGTAGG 41  
:|||||  
112 GTATTAGCTCTAGATTACACGGGTATCCAGTAGTAGG 72

RESULT 5  
BDRRNA/c  
LOCUS BDRRNA 1713 bp DNA linear PLN 17-JAN-1993  
DEFINITION B.dermatitidis, gene for 18S rRNA.  
ACCESSION X59420  
VERSION X59420.1 GI:58322  
KEYWORDS 18S ribosomal RNA; rRNA.  
SOURCE Ajellomyces dermatitidis.  
ORGANISM Ajellomyces dermatitidis  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; Onygenaceae; Ajellomyces.  
REFERENCE 1 (bases 1 to 1713)  
AUTHORS Bowman, B.  
TITLE Direct Submission  
JOURNAL Submitted (08-MAY-1991) B. Bowman, Roche Molecular Systems, 1145  
Atlantic Avenue, Alameda CA 94501, USA  
REFERENCE 2 (bases 1 to 1713)  
AUTHORS Bowman, B.H., Taylor, J.W. and White, T.J.  
TITLE Molecular evolution of the fungi: human pathogens  
JOURNAL Mol. Biol. Evol. 9 (5), 893-904 (1992)  
MEDLINE 92408455  
PUBMED 1528111

FEATURES  
source  
Location/Qualifiers  
1. .1713  
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/strain="ATCC 21693"  
/db\_xref="taxon:5039"  
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1. .>1713  
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/note="missing estimated 38 bases from 5' and 49 bases  
from 3' end of rRNA coding region. Directly sequenced  
from full-length PCR product."  
BASE COUNT 437 a 367 c 470 g 439 t  
ORIGIN

Query Match 98.0%; Score 40.2; DB 8; Length 1713;  
Best Local Similarity 97.6%; Pred. No. 2.7e-06;  
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTATTAGCTCTAGATTACACGGGTATCCAGTAGTAGG 41  
:|||||  
132 GTATTAGCTCTAGATTACACGGGTATCCAGTAGTAGG 92

RESULT 6  
HC18SR/c  
LOCUS HC18SR 1713 bp DNA linear PLN 30-JUN-1993  
DEFINITION H.capsulatum DNA for 18S ribosomal RNA, partial.  
ACCESSION X58572.545469  
VERSION X58572.1 GI:2759

KEYWORDS  
SOURCE 18S ribosomal RNA.  
ORGANISM Ajellomyces capsulatus.  
Ajellomyces capsulatus  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; Onygenaceae; Ajellomyces.  
REFERENCE 1 (bases 1 to 1713)  
AUTHORS Bowman, B.H.  
TITLE Direct Submission  
JOURNAL Submitted (19-MAR-1991) B.H. Bowman, Roche Molecular Systems, 1145  
Atlantic Avenue, Alameda CA 94501, USA  
REFERENCE 2 (bases 1 to 1713)  
AUTHORS Bowman, B.H., Taylor, J.W. and White, T.J.  
TITLE Molecular evolution of the fungi: human pathogens  
JOURNAL Mol. Biol. Evol. 9 (5), 893-904 (1992)  
MEDLINE 92408455  
PUBMED 1528111

REFERENCE 3 (bases 1 to 1713)  
AUTHORS Berbee, M.L. and Taylor, J.W.  
TITLE Convergence in ascospore discharge mechanism among pyrenomycete  
fungi based on 18S ribosomal RNA gene sequence  
JOURNAL Mol. Phylogenet. Evol. 1 (1), 59-71 (1992)  
MEDLINE 94115689  
PUBMED 1342925

REMARK  
Annotation

FEATURES  
source  
Location/Qualifiers  
1. .1713  
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/strain="ATCC 11408"  
/db\_xref="taxon:5037"  
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1. .>1713  
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end of coding region"  
BASE COUNT 434 a 368 c 473 g 438 t  
ORIGIN

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Best Local Similarity 97.6%; Pred. No. 2.7e-06;  
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DTATTAGCTCTAGATTACACGGGTATCCAGTAGTAGG 41  
:|||||  
132 GTATTAGCTCTAGATTACACGGGTATCCAGTAGTAGG 92

RESULT 7  
MBRCED/c  
LOCUS MBRCED 1713 bp DNA linear PLN 10-SEP-2001  
DEFINITION Malbranchea gypsea 18S ribosomal RNA gene, complete sequence.  
ACCESSION L28066  
VERSION L28066.1 GI:452094  
KEYWORDS Malbranchea gypsea.  
SOURCE Malbranchea gypsea  
ORGANISM Malbranchea gypsea  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; Onygenaceae; Malbranchea.  
REFERENCE 1 (bases 1 to 1713)  
AUTHORS Pan, S., Sigler, L. and Cole, G.T.  
TITLE Evidence for a phylogenetic connection between Coccidioides immitis  
and Uncinocarpus reesei (Onygenaceae)  
JOURNAL Microbiology 140 (Pt 6), 1461-1494 (1994)  
MEDLINE 94362911  
PUBMED 7915941

FEATURES  
source  
Location/Qualifiers  
1. .1713  
/organism="Malbranchea gypsea"  
/isolate="UMH 1841"  
/db\_xref="taxon:33182"  
/cell\_type="hyphae"  
/dev\_stage="mycelial"  
/germline  
1. .1713  
/product="18S ribosomal RNA"

BASE COUNT	440 a	362 c	467 g	444 t	/note="putative"
ORIGIN					
Query Match		98.0%;	Score 40.2;	DB 8;	Length 1713;
Best Local Similarity		97.6%;	Pred. No. 2.7e-06;		
Matches	40;	Conservative	1;	Mismatches	0;
				Indels	0;
				Gaps	0;
Oy	1	DTATTAGCTCTAGATTACACGGGATATCCAAAGTAGTAGG	41		
	:				
Db	120	GTATTAGCTCTAGATTACACGGGATATCCAAAGTAGTAGG	92		
RESULT 8					
AF242259/c		1721 bp	DNA	linear	PLN 19-SEP-2000
LOCUS					
DEFINITION		AcrospERMum gramineum specimen-voucher UME 31190 18S ribosomal RNA			
ACCESSION		AF242259			
VERSION		AF242259.1	GI:15592874		
KEYWORDS					
SOURCE					
ORGANISM		AcrospERMum gramineum.			
REFERENCE		Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes et			
AUTHORS		Chetochytrionycetes Incertae sedis; AcrospERMaceae; AcrospERMum.			
TITLE		1 (bases 1 to 1721)			
FEATURES		Phylogenetic relationships within the Ascomycota based on 18S rDNA			
SOURCE		Sequences			
JOURNAL		Thesis (2000) Umea University, Sweden			
REFERENCE		2 (bases 1 to 1721)			
AUTHORS		Winka,K. and Eriksson,O.E.			
TITLE		Direct Submission			
JOURNAL		Submitted (06-MAR-2000) Ecology and Environmental Science, Umea			
UNIVERSITY		University, Umea 90187, Sweden			
LOCATION/Qualifiers					
1..1721					
/organism="AcrospERMum gramineum"					
/specimen_voucher="UME 31190"					
/db_xref="taxon:152640"					
<1..>1721					
/product="18S ribosomal RNA"					
441 a	372 c	471 g	437 t		
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ORIGIN					
Query Match		98.0%;	Score 40.2;	DB 8;	Length 1721;
Best Local Similarity		97.6%;	Pred. No. 2.7e-06;		
Matches	40;	Conservative	1;	Mismatches	0;
				Indels	0;
				Gaps	0;
Oy	1	DTATTAGCTCTAGATTACACGGGATATCCAAAGTAGTAGG	41		
	:				
Db	120	GTATTAGCTCTAGATTACACGGGATATCCAAAGTAGTAGG	80		
RESULT 9					
AF241655/c		1726 bp	DNA	linear	PLN 12-JUN-2000
LOCUS					
DEFINITION		Paracoccidioides brasiliensis 18S ribosomal RNA gene, partial			
ACCESSION		AF241655			
VERSION		AF241655.3	GI:8469174		
KEYWORDS					
SOURCE					
ORGANISM		Paracoccidioides brasiliensis.			
REFERENCE		Paracoccidioides brasiliensis			
AUTHORS		Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;			
TITLE		Omygenales; mitosporic Omygenales; Paracoccidioides.			
JOURNAL		1 (bases 1 to 1726)			
REFERENCE		Kasuga,T., Taylor,J.W., White,T.J., Pires de Camargo,Z. and			
AUTHORS		Bagagali,E.			
TITLE		Evolution of Histoplasma capsulatum			
JOURNAL		Unpublished			
REFERENCE		2 (bases 1 to 1726)			
AUTHORS		Kasuga,T., Taylor,J.W., White,T.J., Pires de Camargo,Z. and			

```

JOURNAL      TITLE Direct Submission
REFERENCE    Submitted (03-MAR-2000) Roche Molecular Systems, 1145 Atlantic
AUTHORS     Ave., Alameda, CA 94501, USA
            3 (bases 1 to 1726)
TITLE       Kasuga,T., Taylor,J.W., White,T.J., Pires de Camargo,Z. and
            Bagagli,E.
JOURNAL     Direct Submission
REFERENCE   Submitted (23-MAY-2000) Roche Molecular Systems, 1145 Atlantic
AUTHORS     Ave., Alameda, CA 94501, USA
            4 (bases 1 to 1726)
TITLE       Kasuga,T., Taylor,J.W., White,T.J., Pires de Camargo,Z. and
            Bagagli,E.
REMARK      Direct Submission
COMMENT     Submitted (12-JUN-2000) Roche Molecular Systems, 1145 Atlantic
FEATURES    Sequence update by submitter
            On Jun 12, 2000 this sequence version replaced gi|8050239.
SOURCE      Location/Qualifiers
            1..1726
             /organism="Paracoccidioides brasiliensis"
             /isolate="pb1g"
             /db_xref="taxon:121759"
             /country="Brazil"
             <1..>1726
              /product="18S ribosomal RNA"
BASE COUNT  446 a          371 c          472 g          437 t
ORIGIN
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Best Local Similarity 97.6%; Pred.No.2.7e-06;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY           1 DTATTAGCTGATGATTACACAGGGGTATCCAAAGTGTAGG 41
Db           132 GTATTAGCTGATGATTACCAAGGGGTATCCAAAGTAGTAGG 92
RESULT 10 AF320009          1726 bp DNA linear PLN 13-FEB-2001
LOCUS      Afjellomyces capsulatus ATCC26032 18S ribosomal RNA gene, partial
DEFINITION Afjellomyces capsulatus ATCC26032 18S ribosomal RNA gene, partial
ACCESSION  AF320009
VERSION    AF320009
KEYWORDS   AF320009.1 GI:12751371
SOURCE     Afjellomyces capsulatus.
ORGANISM   Afjellomyces capsulatus.
REFERENCE  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
AUTHORS    Ouyenales; Ouyenaceae; Afjellomyces.
TITLE      1 (bases 1 to 1726)
JOURNAL    The Molecular Clock in Fungi in the Class Plectomycetes
AUTHORS    Kasuga,T., White,T.J. and Taylor,J.W.
TITLE      2 (bases 1 to 1726)
JOURNAL    Unpublished
AUTHORS    Kasuga,T., White,T.J. and Taylor,J.W.
TITLE      Direct Submission
JOURNAL    Submitted (07-NOV-2000) Roche Molecular Systems, 1145 Atlantic
AUTHORS    Ave., Alameda, CA 94501, USA
FEATURES    Location/Qualifiers
            1..1726
             /organism="Afjellomyces capsulatus"
             /strain="ATCC26032: G217B"
             /db_xref="ATCC:26032"
             /db_xref="taxon:5037"
             /note="class 2 North American population"
             <1..>1726
              /product="18S ribosomal RNA"
BASE COUNT  440 a          371 c          475 g          440 t
ORIGIN
Query Match 98.0%; Score 40.2; DB 8; Length 1726;
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Best Local Similarity 97.6%; Pred. No. 2.7e-06;  
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTATTAGCTCTAGATTACACGGGTATCCAGTAGTAAG 41  
:|||||  
132 GTATTAGCTCTAGATTACACGGGTATCCAGTAGTAAG 92

Db

RESULT 11  
AF320010/c 1726 bp DNA linear PLN 13-FEB-2001  
DEFINITION Ajellomyces dermatitidis ATCC60915 18S ribosomal RNA gene, partial  
sequence.  
ACCESSION AF320010  
VERSION AF320010.1 GI:12751372  
KEYWORDS  
SOURCE Ajellomyces dermatitidis.  
ORGANISM  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; Onygenaceae; Ajellomyces.

REFERENCE  
AUTHORS Kasuga,T., White,T.J. and Taylor,J.W.  
TITLE The Molecular Clock in Fungi in the Class Plecomycetes  
JOURNAL Unpublished  
2 (bases 1 to 1726)  
REFERENCE Kasuga,T., White,T.J. and Taylor,J.W.  
AUTHORS Direct Submission  
TITLE Submitted (07-NOV-2000) Roche Molecular Systems, 1145 Atlantic  
JOURNAL Ave., Alameda, CA 94501, USA

FEATURES  
Source  
1. .1726  
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/strain="ATCC60915"  
/db\_xref="ATCC:60915"  
/db\_xref="taxon:5039"  
<1..>1726  
/product="18S ribosomal RNA"

BASE COUNT 443 a 370 c 471 g 442 t

ORIGIN

Query Match 98.0%; Score 40.2; DB 8; Length 1726;  
Best Local Similarity 97.6%; Pred. No. 2.7e-06;  
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTATTAGCTCTAGATTACACGGGTATCCAGTAGTAAG 41  
:|||||  
132 GTATTAGCTCTAGATTACACGGGTATCCAGTAGTAAG 92

Db

RESULT 12  
AF227151/c 1759 bp DNA linear PLN 12-SEP-2000  
DEFINITION Paracoccidioides brasiliensis small subunit ribosomal RNA gene,  
complete sequence.  
ACCESSION AF227151  
VERSION AF227151.1 GI:9367108  
KEYWORDS  
SOURCE Paracoccidioides brasiliensis.  
ORGANISM  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; mitosporic Onygenales; Paracoccidioides.

REFERENCE  
AUTHORS Blahk,R., Ibrilevic,A., Fothergill,A. and Begerow,D.  
TITLE Small subunit ribosomal DNA sequence shows Paracoccidioides  
brasiliensis closely related to Blastomyces dermatitidis  
JOURNAL J. Clin. Microbiol. 38 (9), 3190-3193 (2000)

MEDLINE 20440627  
PUBMED 10970355  
REFERENCE 2 (bases 1 to 1759)  
AUTHORS Begerow,D.  
TITLE Direct Submission  
JOURNAL Submitted (20-JAN-2000) Spezielle Botanik/Mykologie, Universitaet  
Tuebingen, Auf der Morgenstelle 1, Tuebingen 72076, Germany

FEATURES  
Source  
1. .1759  
/organism="Paracoccidioides brasiliensis"  
/strain="R-2878"  
/db\_xref="taxon:121759"  
1. .1759  
/product="small subunit ribosomal RNA"

BASE COUNT 451 a 379 c 483 g 446 t

ORIGIN

Query Match 98.0%; Score 40.2; DB 8; Length 1759;  
Best Local Similarity 97.6%; Pred. No. 2.7e-06;  
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTATTAGCTCTAGATTACACGGGTATCCAGTAGTAAG 41  
:|||||  
140 GTATTAGCTCTAGATTACACGGGTATCCAGTAGTAAG 100

Db

RESULT 13  
AF238302/c 1771 bp DNA linear PLN 24-JAN-2001  
DEFINITION Paracoccidioides brasiliensis 18S small subunit ribosomal RNA gene,  
partial sequence.  
ACCESSION AF238302  
VERSION AF238302.1 GI:8164018  
KEYWORDS  
SOURCE Paracoccidioides brasiliensis.  
ORGANISM  
Paracoccidioides brasiliensis.  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; mitosporic Onygenales; Paracoccidioides.

REFERENCE  
AUTHORS Herr,R.A., Tarcha,E.J., Taborda,P.R., Taylor,J.W., Ajello,L. and  
Mendoza,L.  
TITLE Phylogenetic analysis of Lacazia loboi places this previously  
uncharacterized pathogen within the dimorphic Onygenales  
JOURNAL J. Clin. Microbiol. 39 (1), 309-314 (2001)

MEDLINE 20579048  
PUBMED 11136789  
REFERENCE 2 (bases 1 to 1771)  
AUTHORS Herr,R.A., Tarcha,E.J., de Elias-Costa,M.R.I., Carnevale,S.I. and  
Mendoza,L.  
TITLE Paracoccidioides brasiliensis 18S SSU rDNA  
JOURNAL Unpublished  
3 (bases 1 to 1771)  
REFERENCE Herr,R.A., Taborda,P.R., Tarcha,E.J., Taylor,J.W., Ajello,L. and  
Mendoza,L.  
TITLE Direct Submission  
JOURNAL Submitted (24-FEB-2000) Medical Technology Program, Michigan State  
University, 322 North Kedzie Lab, East Lansing, MI 48824-1031, USA

FEATURES  
Source  
1. .1771  
/organism="Paracoccidioides brasiliensis"  
/isolate="63265"  
/db\_xref="taxon:121759"  
/note="Argentinian isolate cultured from a clinical sample  
recovered from a patient with paracoccidioidomycosis"  
<1..>1771  
/product="18S small subunit ribosomal RNA"

BASE COUNT 454 a 380 c 485 g 452 t

ORIGIN

Query Match 98.0%; Score 40.2; DB 8; Length 1771;  
Best Local Similarity 97.6%; Pred. No. 2.7e-06;  
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DTATTAGCTCTAGATTACACGGGTATCCAGTAGTAAG 41  
:|||||  
151 GTATTAGCTCTAGATTACACGGGTATCCAGTAGTAAG 111

Db

RESULT 14  
BL0DA/c

Search completed: June 12, 2003, 02:33:51  
 Job time : 622.827 secs

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LOCUS      BLODA                      1799 bp    DNA     linear    PLN 12-APR-1994
DEFINITION Blastomyces dermatitidis small subunit ribosomal RNA gene sequence.
ACCESSION  M55624
VERSION    M55624.1 GI:166961
KEYWORDS   16S-like ribosomal RNA; ribosomal RNA small subunit.
SOURCE     B. dermatitidis DNA and RNA.
ORGANISM   B. dermatitidis dermatitidis
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Onygenales; Onygenaceae; Ajellomyces.
REFERENCE  1 (bases 1 to 1799)
            Soglin, M.L., Bibeau, C., Elwood, H., Stickel, S., Welsburg, W.G.,
            Barnes, S.R. and Lane, D.L.
            Phylogenetic relationships between major classes of fungi
            Unpublished (1990)
FEATURES             Location/Qualifiers
     source          1..1799
                     /organism="Ajellomyces dermatitidis"
                     /db_xref="taxon:5039"
BASE COUNT    460 a      384 c      491 g      462 t      2 others
ORIGIN
Query Match      98.0%; Score 40.2; DB 8; Length 1799;
Best Local Similarity 97.6%; Pred. No. 2.7e-06;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 DTATTAGCTAGAAATTACACACGGGTATCCAGTAGTAAGG 41
       :|||||
Db      170 GTATTAGCTAGAAATTACACACGGGTATCCAGTAGTAAGG 130

RESULT 15
BLO18SRRNA/c
LOCUS      BLO18SRRNA                  1800 bp    RNA     linear    PLN 27-APR-1993
DEFINITION Blastomyces dermatitidis 18S ribosomal RNA.
ACCESSION  M63096
VERSION    M63096.1 GI:173895
KEYWORDS   18S ribosomal RNA.
SOURCE     Blastomyces dermatitidis (Library: ATCC 26199) yeast RNA.
ORGANISM   Ajellomyces dermatitidis
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Onygenales; Onygenaceae; Ajellomyces.
REFERENCE  1 (bases 1 to 1800)
            Geber, A., Higgins, D.E., Waters, A.P., Bennett, J.E. and
            McCutchan, T.P.
            Small subunit ribosomal RNA of Blastomyces dermatitidis: sequence
            and phylogenetic analysis
            J. Gen. Microbiol. 138 (Pt 2), 395-399 (1992)
JOURNAL    MEDLINE 92226701
PUBMED     1564447
FEATURES             Location/Qualifiers
     source          1..1800
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                     /dev_stage="yeast"
     gene            1..1800
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     rRNA            1..1800
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                     /product="18S ribosomal RNA"
                     /note="G or C polymorphism"
     misc_feature    1352
                     /gene="18S rRNA"
BASE COUNT    459 a      384 c      490 g      466 t      1 others
ORIGIN
Query Match      98.0%; Score 40.2; DB 8; Length 1800;
Best Local Similarity 97.6%; Pred. No. 2.7e-06;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 DTATTAGCTAGAAATTACACACGGGTATCCAGTAGTAAGG 41
       :|||||
Db      170 GTATTAGCTAGAAATTACACACGGGTATCCAGTAGTAAGG 130
  
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PT quantitation in body fluids, etc.  
XX  
PS Claim 6; Column 9; 8pp; English.

CC A probe (AA073433) or its complement (AA073436) and corresponding RNA  
CC sequences (AA073437 and AA086436) used for the specific detection of all  
CC strains of Histoplasma capsulatum (H.c.). The probes are manufactured  
CC complementary to the H.c. 18S rRNA or rDNA gene. This region also  
CC corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.  
CC The probe is specific for H.c. and can be used to distinguish the fungus  
CC from all others, even its nearest phylogenetic neighbour Blastomyces  
CC dermatitidis. Nucleic acid hybridisation of the specific probe is  
CC enhanced by the use of helper probes (AA073434-5). This method allows  
CC the detection and/or the quantitation of H.c. from samples e.g. body  
CC fluids, tissue samples, soil and water.

XX Sequence 40 BP; 13 A; 7 C; 9 G; 11 T; 0 other;

Query Match 97.6%; Score 40; DB 15; Length 40;  
Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TATTAGCTCTAGAAATTACACGGGTATCCAGTAGTAAGG 41  
DB 1 TATTAGCTCTAGAAATTACACGGGTATCCAGTAGTAAGG 40

# RESULT 2

ID AA071867/c  
AA071867 standard; DNA; 447 BP.

AC AA071867;

DT 23-MAR-1995 (first entry)

DE G. vesiculiferum small ribosomal subunit RNA.

KW Nuclear 18S ribosomal gene; SSU; probe; primer;

KW arbuscular endomycorrhizal fungi; plant; root; ds.

OS Glomus vesiculiferum.

PN CA2086136-A.

PD 24-JUN-1994.

PF 23-DEC-1992; 92CA-2086136.

PR 23-DEC-1992; 92CA-2086136.

PA (SIMO/) SIMON L.

PI Lalonde M, Simon L;

DR WPI; 1994-264577/33.

PT New oligonucleotide probes - used for the detection of arbuscular  
PT endomycorrhizal fungi in plant root samples

PS Disclosure; Page 18; 40pp; English.

CC The gene sequence of the small ribosomal subunit RNA of arbuscular  
CC endomycorrhizal fungi obtained from Glomus vesiculiferum, Glomus  
CC intraradices and Gigaspora margarita were compared with that of a  
CC non-arbuscular endomycorrhizal fungus, Endogone pisiformis,  
CC in order to design taxon specific primers/probes.

XX Sequence 447 BP; 135 A; 86 C; 107 G; 118 T; 1 other;

Query Match 94.1%; Score 38.6; DB 15; Length 447;  
Best Local Similarity 95.1%; Pred. No. 9.4e-07;  
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DTATTAGCTCTAGAAATTACACGGGTATCCAGTAGTAAGG 41  
DB :|||||  
61 GTATTAGCTCTAGAAATTACACGGGTATCCAGTAGTAAGG 21

# RESULT 3

ID AA071868/c  
AA071868 standard; DNA; 447 BP.

AC AA071868;

DT 23-MAR-1995 (first entry)

DE G. intraradices small ribosomal subunit RNA.

KW Nuclear 18S ribosomal gene; SSU; probe; primer;

KW arbuscular endomycorrhizal fungi; plant; root; ds.

OS Glomus intraradices.

PN CA2086136-A.

PD 24-JUN-1994.

PF 23-DEC-1992; 92CA-2086136.

PR 23-DEC-1992; 92CA-2086136.

PA (SIMO/) SIMON L.

PI Lalonde M, Simon L;

DR WPI; 1994-264577/33.

PT New oligonucleotide probes - used for the detection of arbuscular  
PT endomycorrhizal fungi in plant root samples

PS Disclosure; Page 19; 40pp; English.

CC The gene sequence of the small ribosomal subunit RNA of arbuscular  
CC endomycorrhizal fungi obtained from Glomus vesiculiferum, Glomus  
CC intraradices and Gigaspora margarita were compared with that of a  
CC non-arbuscular endomycorrhizal fungus, Endogone pisiformis,  
CC in order to design taxon specific primers/probes.

XX Sequence 447 BP; 137 A; 86 C; 107 G; 117 T; 0 other;

Query Match 94.1%; Score 38.6; DB 15; Length 447;  
Best Local Similarity 95.1%; Pred. No. 9.4e-07;  
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DTATTAGCTCTAGAAATTACACGGGTATCCAGTAGTAAGG 41  
DB :|||||  
61 GTATTAGCTCTAGAAATTACACGGGTATCCAGTAGTAAGG 21

# RESULT 4

ID AAF08498  
AAF08498 standard; cDNA; 570 BP.

AC AAF08498;

DT 13-MAR-2001 (first entry)

DE Fusarium venenatum EST SEQ ID NO:1021.

XX Multiple gene expression: filamentous fungal cell; EST;  
XX expressed sequence tag; Fusarium venenatum; Aspergillus niger;  
XX Aspergillus oryzae; Trichoderma reesei; identification; recombination;  
XX culture condition; environmental stress; spore morphogenesis;  
XX metabolic pathway engineering; catabolic pathway engineering; ss.  
OS Fusarium venenatum.

```

XX PN WO200056762-A2.
XX PD 28-SEP-2000.
XX PF 22-MAR-2000; 2000WO-US07781.
XX PR 22-MAR-1999; 99US-0273623.
XX PA (NOVO ) NOVO NORDISK BIOTECH INC.
XX PA (NOVO ) NOVO NORDISK AS.
XX PI Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;
XX WPI: 2000-594572/56.
XX DR
XX PT Monitoring differential expression of genes in filamentous fungal cells
XX PT uses fluorescence-labeled nucleic acids isolated from the cells and a
XX PT substrate of expressed sequence tags -
XX PS Claim 86; Page 772; 3161pp; English.
XX PS
CC The present invention describes a method for monitoring differential
CC expression of genes in a first filamentous fungal (FF) cell relative to
CC expression of the same genes in one or more second filamentous fungal
CC cells. The method uses fluorescence-labeled nucleic acids isolated from
CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs
CC are used in the methods for monitoring differential expression of genes
CC in a first filamentous fungal (FF) cell relative to expression of the
CC same genes in one or more second filamentous fungal cells. Monitoring
CC the global expression of genes from FF cells allows the production
CC potential of the microorganisms to be improved. New genes may be
CC discovered, possible functions of unknown open reading frames can be
CC identified and gene copy number variation and stability can be
CC monitored. The expression of genes can be used to study how FF cells
CC adapt to changes in culture conditions, environmental stress, spore
CC morphogenesis, recombination, metabolic or catabolic pathway
CC engineering. Using ESTs provides several advantages over genomic or
CC random cDNA clones including elimination of redundancy as one spot on an
CC array equals one gene or open reading frame, and organisation of the
CC array equals one gene or open reading frame, and organisation of the
CC microarrays based on function of the gene products to facilitate
CC analysis of the results. AAF07478 to AAF11247 represents ESTs from
CC Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus
CC niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and
CC AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are
CC all specifically claimed in the present invention.
XX XX
SQ Sequence 570 BP; 153 A; 136 C; 113 G; 166 T; 2 other;
Query Match 94.1%; Score 38.6; DB 21; Length 570;
Best Local Similarity 95.1%; Pred. No. 9.7e-07;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 DTAATGCTCTAGAAATTACACCGGTTATCCAGTAGTAAGG 41
Db 393 GTATTAGCTCTAGAAATTACACCGGTTATCCAGTAGTAAGG 433

```

RESULT 5  
AAFI0913/C  
ID AAF10913 standard; cDNA: 617 BP.

XX AAF10913;

XX 13-MAR-2001 (first entry)

XX Fusarium venenatum EST SEQ ID NO:3436.

XX Multiple gene expression; filamentous fungal cell; EST;  
XX expressed sequence tag; Fusarium venenatum; Aspergillus niger;  
XX Aspergillus oryzae; Trichoderma reesei; identification; recombination;  
XX culture condition; environmental stress; spore morphogenesis;  
XX metabolic pathway engineering; catabolic pathway engineering; ss.

```

XX OS Fusarium venenatum.
XX XX
XX PN WO200056762-A2.
XX PD 28-SEP-2000.
XX PF 22-MAR-2000; 2000WO-US07781.
XX PR 22-MAR-1999; 99US-0273623.
XX PA (NOVO ) NOVO NORDISK BIOTECH INC.
XX PA (NOVO ) NOVO NORDISK AS.
XX PI Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;
XX WPI: 2000-594572/56.
XX DR
XX PT Monitoring differential expression of genes in filamentous fungal cells
XX PT uses fluorescence-labeled nucleic acids isolated from the cells and a
XX PT substrate of expressed sequence tags -
XX PS Claim 86; Page 1589; 3161pp; English.
XX PS
CC The present invention describes a method for monitoring differential
CC expression of genes in a first filamentous fungal (FF) cell relative to
CC expression of the same genes in one or more second filamentous fungal
CC cells. The method uses fluorescence-labeled nucleic acids isolated from
CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs
CC are used in the methods for monitoring differential expression of genes
CC in a first filamentous fungal (FF) cell relative to expression of the
CC same genes in one or more second filamentous fungal cells. Monitoring
CC the global expression of genes from FF cells allows the production
CC potential of the microorganisms to be improved. New genes may be
CC discovered, possible functions of unknown open reading frames can be
CC identified and gene copy number variation and stability can be
CC monitored. The expression of genes can be used to study how FF cells
CC adapt to changes in culture conditions, environmental stress, spore
CC morphogenesis, recombination, metabolic or catabolic pathway
CC engineering. Using ESTs provides several advantages over genomic or
CC random cDNA clones including elimination of redundancy as one spot on an
CC array equals one gene or open reading frame, and organisation of the
CC array equals one gene or open reading frame, and organisation of the
CC microarrays based on function of the gene products to facilitate
CC analysis of the results. AAF07478 to AAF11247 represents ESTs from
CC Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus
CC niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and
CC AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are
CC all specifically claimed in the present invention.
XX XX
SQ Sequence 617 BP; 155 A; 139 C; 140 G; 171 T; 12 other;
Query Match 94.1%; Score 38.6; DB 21; Length 617;
Best Local Similarity 95.1%; Pred. No. 9.8e-07;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 DTAATGCTCTAGAAATTACACCGGTTATCCAGTAGTAAGG 41
Db 154 GTATTAGCTCTAGAAATTACACCGGTTATCCAGTAGTAAGG 114

```

RESULT 6  
AAI68286/C  
ID AAI68286 standard; DNA: 1731 BP.

XX AAI68286;

XX 19-DEC-2001 (first entry)

XX Bulgarica linguans M-3 18S rDNA.

XX Bulgarica linguans M-3; 18S rDNA; Indole; M-3-A; antifungal;  
XX rice leaf spot; ds.

OS Bulgaria Inquilans.  
 XX JP2001247566-A.  
 XX  
 PD 11-SEP-2001.  
 XX  
 PF 03-MAR-2000; 2000JP-0059685.  
 XX  
 PR 03-MAR-2000; 2000JP-0059685.  
 XX  
 PA (KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.  
 XX  
 DR WPI: 2001-621605/72.  
 XX  
 PT New indole derivative M-3-A, prepared by culture of Ascomycetes sp.  
 PT M-3, has antifungal activity -  
 XX  
 PS Claim 3; Page 6; 9pp; Japanese.  
 XX  
 CC The invention relates to a fungal derived indole derivative M-3-A with  
 CC antifungal activity useful in the treatment of leaf spot of rice with  
 CC M-3-A. The present sequence is that of the Bulgaria Inquilans M-3 18S  
 CC rDNA sequence.  
 XX  
 SQ Sequence 1731 BP; 459 A; 351 C; 447 G; 474 T; 0 other;

Query Match 94.1%; Score 38.6; DB 22; Length 1731;  
 Best Local Similarity 95.1%; Pred. No. 1.1e-06;  
 Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DTATTAGCTCTAGATTACACGCGGTATCCAGTAGTAGG 41  
 :|||||  
 DB 133 GTATTAGCTCTAGATTACACGCGGTATCCAGTAGTAGG 93

RESULT 7  
 ABA01154/C  
 ID ABA01154 standard; DNA; 1731 BP.  
 XX  
 AC ABA01154;  
 XX  
 DT 24-JAN-2002 (first entry)  
 XX  
 DE Deuteromycetes polynucleotide SEQ ID 3.  
 XX  
 KW Aldonic acid; ds.  
 XX  
 OS Deuteromycetes sp.  
 XX  
 PN JP2001245657-A.  
 XX  
 PD 11-SEP-2001.  
 XX  
 PF 26-DEC-2000; 2000JP-0394766.  
 XX  
 PR 27-DEC-1999; 99JP-0369714.  
 XX  
 PA (TAKE-) TAKEHARA KAGAKU KOGYO KK.  
 PA (OSAO) OSAKA CITY.  
 XX  
 DR WPI: 2002-002933/01.  
 XX  
 PT A new microbe for producing aldonic acid, comprises a new strain of  
 PT Acinetobacter or Burkholderis -  
 XX  
 PS Disclosure; Page 18-19; 22pp; Japanese.  
 XX  
 CC The present invention relates to a new microbe of Acinetobacter or  
 CC Burkholderis genus producing aldonic acid and oxidizing specifically the  
 CC hemiacetal hydroxy group of a saccharide having said hydroxy group.  
 CC Aldonic acid is used as a mineral reinforcing agent. The present sequence  
 CC was used to illustrate the present invention.  
 XX

SQ Sequence 1731 BP; 447 A; 366 C; 459 G; 459 T; 0 other;

Query Match 94.1%; Score 38.6; DB 24; Length 1731;  
 Best Local Similarity 95.1%; Pred. No. 1.1e-06;  
 Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DTATTAGCTCTAGATTACACGCGGTATCCAGTAGTAGG 41  
 :|||||  
 DB 131 GTATTAGCTCTAGATTACACGCGGTATCCAGTAGTAGG 91

RESULT 8  
 AAV61668/C  
 ID AAV61668 standard; DNA; 1771 BP.  
 XX  
 AC AAV61668;  
 XX  
 DT 03-DEC-1998 (first entry)  
 XX  
 DE Fusarium oxysporum f.sp. fragaria 18S rRNA DNA fragment.  
 DE  
 KW 18S rRNA; detection; identification; fungus; ss.  
 XX  
 OS Fusarium oxysporum.  
 XX  
 PN JP10234380-A.  
 XX  
 PD 08-SEP-1998.  
 XX  
 PF 28-FEB-1997; 97JP-0062104.  
 XX  
 PR 28-FEB-1997; 97JP-0062104.  
 XX  
 PA (SHIN-) SHINKINRUI KINO KAIHATSU KENKYUSHO KK.  
 XX  
 DR WPI: 1998-535034/46.  
 XX  
 PT Use of oligo:nucleotide for detecting and identification of fungus  
 PT of Fusarium genus - as primer or probe to detect of identify  
 PT microbes rapidly and exactly  
 XX  
 PS Example 1; Page 7-8; 20pp; Japanese.  
 XX  
 CC This DNA sequence encodes a fragment of a Fusarium oxysporum f.sp.  
 CC fragaria 18S rRNA gene which is used in a method for the detection  
 CC and identification of a fungus of Fusarium genus. The process can be  
 CC used to detect or identify microbes rapidly and exactly.  
 XX  
 SQ Sequence 1771 BP; 438 A; 377 C; 477 G; 461 T; 18 other;

Query Match 94.1%; Score 38.6; DB 19; Length 1771;  
 Best Local Similarity 95.1%; Pred. No. 1.1e-06;  
 Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DTATTAGCTCTAGATTACACGCGGTATCCAGTAGTAGG 41  
 :|||||  
 DB 166 GTATTAGCTCTAGATTACACGCGGTATCCAGTAGTAGG 126

RESULT 9  
 AAS16211/C  
 ID AAS16211 standard; DNA; 2293 BP.  
 XX  
 AC AAS16211;  
 XX  
 DT 29-JAN-2002 (first entry)  
 XX  
 DE Fungus genomic DNA spanning 18S, 5.8S and 28S rRNA and ITS sequences.  
 DE  
 KW Gibberellin; 18S rRNA; internal transcribed spacer region; ITS1;  
 KW ITS2; 5.8S rRNA; LTR-1027; species differentiation; GA<sub>4</sub>; GA<sub>3</sub>; GA<sub>7</sub>;  
 KW flowering; fruit cell elongation; apple; pear; grape; fruit;  
 KW russet control; fungus; ds.

OS	Gibberella fujikuroi.
XX	
XX	
FT	Key
FT	Location/Qualifiers
FT	misc_feature
FT	1..1774
FT	/tag= a
FT	/note= "18S rRNA gene"
FT	1775..1921
FT	/tag= b
FT	/note= "ITS1 region"
FT	1922..2078
FT	/tag= c
FT	/note= "5.8S rRNA gene"
FT	2079..2243
FT	/tag= d
FT	/note= "ITS2 region"
FT	2244..2293
FT	/tag= e
FT	/note= "28S rRNA gene"
XX	
PN	US6287800-B1.
XX	
PD	11-SEP-2001.
XX	
PE	23-AUG-2000; 2000US-0645073.
XX	
PR	31-AUG-1999; 99US-151770P.
XX	
PA	(GALL/) GALLAZZO J L.
XX	(LEEM/) LEE M D.
PI	Gallazzo JL, Lee MD;
DR	WPI: 2001-662197/76.
XX	
PT	A new method for producing a mixture of gibberellins from Gibberella
PT	fujikuroi results in high titers of GA4 and GA7 useful to promote
PT	flowering and fruit growth in the fruit growing industry
XX	
PS	Example 4; Column 9-12; 7pp; English.
XX	
CC	This sequence represents a genomic DNA sequence containing the 18S rRNA
CC	gene, internal transcribed spacer regions 1 and 2 (ITS1, ITS2) and 5.8S
CC	rRNA sequences from a mutant strain of Gibberella fujikuroi (L78-1027)
CC	of the invention. This region of DNA is highly variable and can be used
CC	for species and strain differentiation. The L78-1027 mutant produces a
CC	mixture of gibberellins which is at least 70 % GA4 and GA7.
CC	Gibberellins GA4 and GA7 promote flowering and fruit cell elongation,
CC	and are used by growers of apples, pears and grapes to produce larger
CC	fruits and earlier harvests. The mixture of GA3, GA4 and GA7 achieved
CC	using the method of this invention should be particularly useful in the
CC	apple industry where GA4 has been found more effective in russet
CC	control and in promoting fruit set. This method produces GA4 and GA7
CC	in much higher titers than prior art methods.
SQ	Sequence 2293 BP; 596 A; 527 C; 592 G; 578 T; 0 other;
XX	
Query Match	94.1%; Score 38.6; DB 23; Length 2293;
Best Local Similarity	95.1%; Pred. No. 1.2e-06;
Matches	39; Conservative 1; Mismatches 1; Indels 0; Gaps 0
OY	1 DTATTAGCTTAGAATTCACAGGGTATCCAGTAGTAGG 41
DB	146 GTATTAGCTTAGAATTCACAGGGTATCCAGTAGTAGG 106
RESULT 10	
ID	AAQ71870/c
AC	AAQ71870 standard; DNA; 447 BP.
DT	23-MAR-1995 (first entry)

XX	E. pisliformis small ribosomal subunit RNA.
DE	
XX	Nuclear 18S ribosomal gene; SSU; probe; primer;
KW	arbuscular endomycorrhizal fungi; plant; root; ds.
XX	
OS	Endogone pisliformis.
XX	
FH	Key Location/Qualifiers
FT	misc_difference 116..115
FT	/*tag= a
FT	/note= "bases not determined"
XX	
PN	CA2086136-A.
XX	
PD	24-JUN-1994.
XX	
PE	23-DEC-1992; 92CA-2086136.
XX	
PR	23-DEC-1992; 92CA-2086136.
PA	(SIMO/) SIMON L.
PI	Lalonde M, Simon L;
XX	
DR	WPI; 1994-264577/73.
XX	
PT	New oligonucleotide probes - used for the detection of arbuscular
PT	endomycorrhizal fungi in plant root samples
XX	
PS	Disclosure; Page 20; 40pp; English.
XX	
CC	The gene sequence of the small ribosomal subunit RNA of arbuscular
CC	endomycorrhizal fungi obtained from Glomus vesiculiferum, Glomus
CC	intraradices and Glasporea margarita were compared with that of a
CC	non-arbuscular endomycorrhizal fungus, Endogone pisliformis,
CC	in order to design taxon specific primers/probes.
XX	
SQ	Sequence 447 BP; 133 A; 77 C; 100 G; 117 T; 20 other;
XX	
Query Match	90.2%; Score 37; DB 15; Length 447;
Best Local Similarity	92.7%; Pred. No. 4.5e-06;
Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	
QY	1 DTATTAGCTCTAGATTACACAGGGTATCCAAAGTAGTAGG 41
DB	62 GTATTAGCTCTAGAAATTACACAGGGTATCCAAAGTAGTAAG 22
XX	
RESULT 11	
AAF11545/C	
ID	AAF11545 standard; cDNA; 568 BP.
XX	
AC	AAF11545;
XX	
DT	13-MAR-2001 (first entry)
XX	
DE	Aspergillus niger EST SEQ ID NO:4068.
XX	
KM	Multiple gene expression; filamentous fungal cell; EST;
KM	expressed sequence tag; Fusarium venenatum; Aspergillus niger;
KM	Aspergillus oryzae; Trichoderma reesei; identification; recombination;
KM	culture condition; environmental stress; spore morphogenesis;
XX	metabolic pathway engineering; catabolic pathway engineering; ss.
OS	Aspergillus niger.
XX	
PN	WO200056762-A2.
XX	
PD	28-SEP-2000.
XX	
PF	22-MAR-2000; 2000WO-US07781.
XX	

PR 22-MAR-1999; 990S-0273623.  
XX  
XX (NOVO ) NOVO NORDISK BIOTECH INC.  
PA (NOVO ) NOVO NORDISK AS.  
XX  
XX Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;  
PI WPI; 2000-594572/56.  
XX  
XX Monitoring differential expression of genes in filamentous fungal cells  
PT uses fluorescence-labeled nucleic acids isolated from the cells and a  
PT substrate of expressed sequence tags -  
XX  
XX Claim 87; Page 1791-1792; 3161pp; English.  
XX  
XX The present invention describes a method for monitoring differential  
CC expression of genes in a first filamentous fungal (FF) cell relative to  
CC expression of the same genes in one or more second filamentous fungal  
CC cells. The method uses fluorescence-labeled nucleic acids isolated from  
CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs  
CC are used in the methods for monitoring differential expression of the  
CC same genes in one or more second filamentous fungal cells. Monitoring  
CC the global expression of genes from FF cells allows the production  
CC potential of the microorganisms to be improved. New genes may be  
CC discovered, possible functions of unknown open reading frames can be  
CC identified, and gene copy number variation and stability can be  
CC monitored. The expression of genes can be used to study how FF cells  
CC adapt to changes in culture conditions, environmental stress, spore  
CC morphogenesis, recombination, metabolic or catabolic pathway  
CC engineering. Using ESTs provides several advantages over genomic or  
CC random cDNA clones including elimination of redundancy as one spot on an  
CC array equals one gene or open reading frame, and organization of the  
CC microarrays based on function of the gene products to facilitate  
CC analysis of the results. AAF07478 to AAF11247 represents ESTs from  
CC *Fusarium venenatum*; AAF11248 to AAF11853 represents ESTs from  
CC *Niger*; AAF11854 to AAF14878 represents ESTs from *Aspergillus*  
CC *niger*; AAF15337 represents ESTs from *Trichoderma reesei*, which are  
CC all specifically claimed in the present invention.  
XX  
XX Sequence 568 BP; 155 A; 116 C; 141 G; 150 T; 6 other;  
SQ  
XX  
XX Query Match 90.28; Score 37; DB 21; Length 568;  
XX Best Local Similarity 92.78; Pred. No. 4.0e-06;  
XX Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 DTATTAGCTAGATACACGGGTATCCAGTAGTAGG 41  
DB 157 GTATTAGCTAGATACACAGGTATCCATGATAGTAGG 117  
XX  
XX RESULT 12  
XX AAZ00859/c  
ID AAZ00859 standard; DNA; 1733 BP.  
XX  
XX AAZ00859;  
AC  
XX  
XX 11-OCT-1999 (first entry)  
DT  
XX  
XX A. fumigatus 18S rRNA DNA.  
DE  
XX  
XX Detection; diagnosis; 18S rRNA; aspergillosis; oncology;  
KM Invasive infection; haematology; immune system suppression; ss.  
XX  
XX *Aspergillus fumigatus*.  
OS  
XX  
XX DE19806274-A1.  
PN  
XX  
XX 19-AUG-1999.  
PD  
XX  
XX 16-FEB-1998; 98DE-1006274.  
PF  
XX  
XX 16-FEB-1998; 98DE-1006274.  
PR

XX  
XX (BUCH/) BUCHHEIDT D.  
PA (HEHL/) HEHLMANN R.  
PA (SKLA/) SKLADNY H.  
XX  
XX Buchheidt D, Hehlmann R, Skladny H;  
PI WPI; 1999-470047/40.  
XX  
XX  
XX Detecting *Aspergillus* nucleic acid in body samples by two-step  
PT polymerase chain reaction, for diagnosing aspergillosis  
PT  
XX  
XX Claim 2; Fig 1; 16pp; German.  
PS  
XX  
XX This invention describes a novel method for detecting *Aspergillus* nucleic  
CC acid (1) in a body sample which comprises the isolation of (1) followed  
CC by a two-step polymerase chain reaction (PCR) amplification of any  
CC nucleic acid having a sequence essentially homologous to part of the  
CC 3'-end of the *Aspergillus* 18S rRNA gene using primers used in the first  
CC step that do not overlap with those in the second step. The method is  
CC used for early diagnosis, and monitoring, of aspergillosis, particularly  
CC invasive infections in hematological-oncological patients with long-term  
CC suppression of the immune system. Unlike the known method using  
CC overlapping primers, this process provides efficient and reliable  
CC detection of *Aspergillus* in clinical situations. It is specific for  
CC *Aspergillus* (it detects the species *terreus*, *niger*, *versicolor*, *clavatus*,  
CC other genera). This sequence represents the DNA sequence of *Aspergillus*  
CC *fumigatus* 18S rRNA.  
XX  
XX Sequence 1733 BP; 446 A; 374 C; 475 G; 438 T; 0 other;  
SQ  
XX  
XX Query Match 90.28; Score 37; DB 20; Length 1733;  
XX Best Local Similarity 92.78; Pred. No. 5.4e-06;  
XX Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 DTATTAGCTAGATACACGGGTATCCAGTAGTAGG 41  
DB 132 GTATTAGCTAGATACACAGGTATCCATGATAGTAGG 92  
XX  
XX RESULT 13  
XX ABA01152/c  
ID ABA01152 standard; DNA; 1745 BP.  
XX  
XX ABA01152;  
AC  
XX  
XX 24-JAN-2002 (first entry)  
DT  
XX  
XX *Deuteromycetes polynucleotide seq ID 1*.  
DE  
XX  
XX Aldonic acid; ds.  
XX  
XX *Deuteromycetes* sp.  
OS  
XX  
XX JP2001245657-A.  
PN  
XX  
XX 11-SEP-2001.  
PD  
XX  
XX 26-DEC-2000; 2000UP-0394766.  
PF  
XX  
XX 27-DEC-1999; 99JP-0369714.  
PR  
XX  
XX (TAKE-) TAKEHARA KAGAKU KOGYO KK.  
PA (OSAKA ) OSAKA CITY.  
XX  
XX WPI; 2002-002933/01.  
DR  
XX  
XX A new microbe for producing aldonic acid, comprises a new strain of  
PT *Acinetobacter* or *Burkholderis* -  
PT  
XX  
XX Disclosure; Page 17; 22pp; Japanese.  
PS  
XX

CC The present invention relates to a new microbe of *Actinobacter* or  
 CC *Burkholderia* genus producing aldonic acid and oxidising specifically the  
 CC hemiacetal hydroxy group of a saccharide having said hydroxy group.  
 CC Aldonic acid is used as a mineral reinforcing agent. The present sequence  
 CC was used to illustrate the present invention.

SO Sequence 1745 BP; 448 A; 382 C; 465 G; 450 T; 0 other;

Query Match 90.2%; Score 37; DB 24; Length 1745;  
 Best Local Similarity 92.7%; Pred. No. 5.4e-06;

Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DTAATAGCTCTAGATTAACCGGGTATCCAGTAGTAGG 41  
 :|||||  
 DB 146 GTATTAGCTCTAGATTAACCGGGTATCCAGTAGTAGG 106

RESULT 14  
 AAV54087/c  
 ID AAV54087 standard; DNA; 1821 BP.

XX AAV54087;

XX 04-DEC-1998 (first entry)

DE Nucleotide sequence of *Pythium spinosum* OPA-1.

KM KPMS; probe: hybridisation; fungus; ss.

OS *Pythium spinosum*.

PN JP10234399-A.

PD 08-SEP-1998.

PF 28-FEB-1997; 97JP-0062114.

PR 28-FEB-1997; 97JP-0062114.

PA (SHIN-) SHINKINRUI KINO KAIHATSU KENKYUSHO KK.

DR WPI; 1998-535049/46.

PT New oligo-nucleotide probe - for rapid and precise detection and  
 PT identification of *Pythium* genus fungus

PS Disclosure; Page 9; 22pp; Japanese.

CC This is the nucleotide sequence of the *Pythium spinosum* OPA-1 used  
 CC in the method of the invention where novel probes are used for the  
 CC detection and identification of a fungus of *Pythium* genus.

SO Sequence 1821 BP; 460 A; 329 C; 466 G; 518 T; 48 other;

Query Match 90.2%; Score 37; DB 19; Length 1821;  
 Best Local Similarity 92.7%; Pred. No. 5.4e-06;

Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DTAATAGCTCTAGATTAACCGGGTATCCAGTAGTAGG 41  
 :|||||  
 DB 168 GTATTAGCTCTAGATTAACCGGGTATCCAGTAGTAGG 128

RESULT 15  
 AAV54086/c

ID AAV54086 standard; DNA; 1840 BP.

XX AAV54086;

XX 04-DEC-1998 (first entry)

DE Nucleotide sequence of *Pythium myrtillyum* KPMS.

KM KPMS; probe: hybridisation; fungus; ss.

OS *Pythium myrtillyum*.

PN JP10234399-A.

PD 08-SEP-1998.

PF 28-FEB-1997; 97JP-0062114.

PR 28-FEB-1997; 97JP-0062114.

PA (SHIN-) SHINKINRUI KINO KAIHATSU KENKYUSHO KK.

DR WPI; 1998-535049/46.

PT New oligo-nucleotide probe - for rapid and precise detection and  
 PT identification of *Pythium* genus fungus

PS Disclosure; Page 8; 22pp; Japanese.

CC This is the nucleotide sequence of the *Pythium myrtillyum* KPMS used  
 CC in the method of the invention where novel probes are used for the  
 CC detection and identification of a fungus of *Pythium* genus.

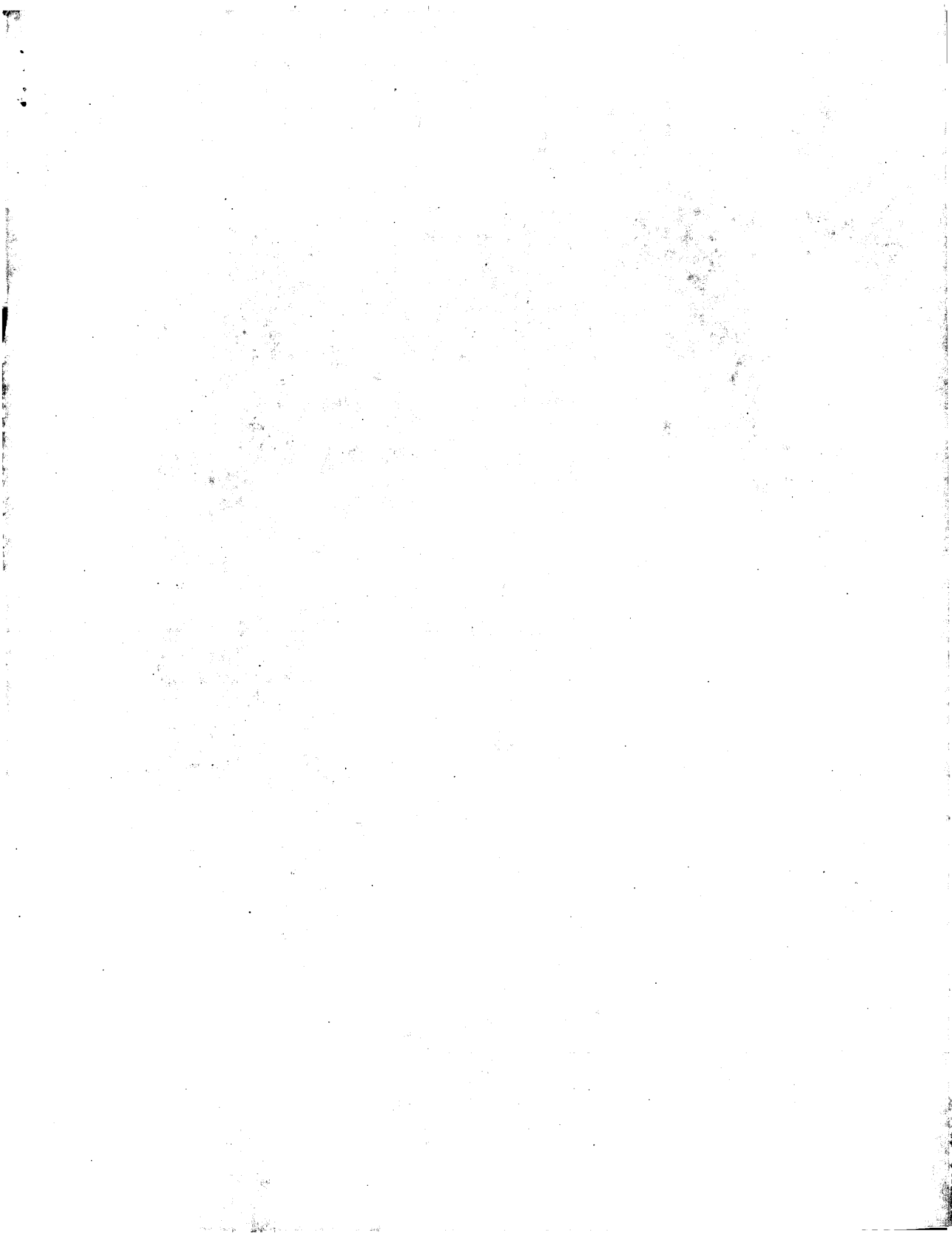
SO Sequence 1840 BP; 481 A; 350 C; 472 G; 525 T; 12 other;

Query Match 90.2%; Score 37; DB 19; Length 1840;  
 Best Local Similarity 92.7%; Pred. No. 5.4e-06;

Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DTAATAGCTCTAGATTAACCGGGTATCCAGTAGTAGG 41  
 :|||||  
 DB 169 GTATTAGCTCTAGATTAACCGGGTATCCAGTAGTAGG 129

Search completed: June 12, 2003, 01:44:08  
 Job time : 211.995 secs



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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 01:18:34 ; Search time 39.335 Seconds

(without alignments)  
319.658 Million cell updates/sec

Title: US-09-674-195c-15

Perfect score: 41  
Sequence: 1 dtatagctctagaattacc.....cggatccaagtagaag 41

Scoring table: IDENTITY\_NT  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Issued\_Patents\_NA:\*  
1: /cgn2\_6/prodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/prodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/prodata/1/ina/5A\_COMB.seq:\*  
4: /cgn2\_6/prodata/1/ina/5B\_COMB.seq:\*  
5: /cgn2\_6/prodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/prodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	97.6	40	1	US-07-720-587A-2
2	38.6	94.1	446	1	US-08-093-144-4
3	38.6	94.1	1788	2	US-08-867-820A-1
4	38.6	94.1	2293	4	US-09-645-073-1
5	37	90.2	444	1	US-08-093-144-6
6	36.6	89.3	444	1	US-08-093-144-5
7	33.8	82.4	703	4	US-08-998-416-178
8	33.8	82.4	706	4	US-08-998-416-814
9	33.8	82.4	712	4	US-08-998-416-910
10	33.8	82.4	717	4	US-08-998-416-602
11	33.8	82.4	723	4	US-08-998-416-952
12	32.2	78.5	1747	1	US-08-327-516-1
13	32.2	78.5	1747	1	US-08-281-766-1
14	31	75.6	1750	3	US-08-949-770-1
15	28.4	69.3	709	4	US-08-998-416-281
16	27.6	67.3	1608	2	US-08-899-371-2
17	27.4	66.8	1744	1	US-07-879-647A-25
18	27.4	66.8	1744	1	US-07-879-584A-25
19	27.4	66.8	1744	1	US-07-879-470A-25
20	27.4	66.8	1744	1	US-07-879-644A-25
21	27.4	66.8	1744	1	US-07-879-640A-25
22	27.4	66.8	1744	1	US-07-879-594A-25
23	27.4	66.8	1744	1	US-07-879-469A-25
24	27.4	66.8	1744	1	US-07-879-647A-29
25	27.4	66.8	1747	1	US-07-879-584A-29
26	27.4	66.8	1747	1	US-07-879-470A-29
27	27.4	66.8	1747	1	US-07-879-644A-29

C 28	27.4	66.8	1747	1	US-07-879-640A-29	Sequence 29, Appl
C 29	27.4	66.8	1747	1	US-07-879-594A-29	Sequence 29, Appl
C 30	27.4	66.8	1747	1	US-07-879-469A-29	Sequence 29, Appl
C 31	27.4	66.8	1749	1	US-07-879-647A-27	Sequence 27, Appl
C 32	27.4	66.8	1749	1	US-07-879-584A-27	Sequence 27, Appl
C 33	27.4	66.8	1749	1	US-07-879-470A-27	Sequence 27, Appl
C 34	27.4	66.8	1749	1	US-07-879-644A-27	Sequence 27, Appl
C 35	27.4	66.8	1749	1	US-07-879-640A-27	Sequence 27, Appl
C 36	27.4	66.8	1749	1	US-07-879-594A-27	Sequence 27, Appl
C 37	27.4	66.8	1749	1	US-07-879-469A-27	Sequence 27, Appl
C 38	27.4	66.8	1750	1	US-07-879-647A-26	Sequence 26, Appl
C 39	27.4	66.8	1750	1	US-07-879-584A-26	Sequence 26, Appl
C 40	27.4	66.8	1750	1	US-07-879-470A-26	Sequence 26, Appl
C 41	27.4	66.8	1750	1	US-07-879-644A-26	Sequence 26, Appl
C 42	27.4	66.8	1750	1	US-07-879-640A-26	Sequence 26, Appl
C 43	27.4	66.8	1750	1	US-07-879-594A-26	Sequence 26, Appl
C 44	27.4	66.8	1750	1	US-07-879-469A-26	Sequence 26, Appl
C 45	26.4	64.4	1756	1	US-07-879-647A-28	Sequence 28, Appl

#### ALIGNMENTS

RESULT 1  
US-07-720-587A-2  
Sequence 2, Application US/07720587A  
Patent No. 5352579

#### GENERAL INFORMATION:

APPLICANT: Curt L. Millman  
TITLE OF INVENTION: NUCLEIC ACIDS PROBES  
TITLE OF INVENTION: TO HISTOPLASMA CAPSULATUM  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017

#### COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM PS/2 Model 502 or 555X  
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
SOFTWARE: WordPerfect (Version 5.0)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07720,587A  
FILING DATE: 19910628

#### CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER:  
FILING DATE:

#### ATTORNEY/AGENT INFORMATION:

NAME: Waidburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 193/121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

#### INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
LENGTH: 40  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-07-720-587A-2

Query Match 97.6%; Score 40; DB 1; Length 40;  
Best local similarity 100.0%; Pred. No. 33e-08;  
Matches 40; Conservative 0; Mismatches 0; indels 0;

OY 2 TATTAGCTCTAGAAATTACACGGGTATCCAGTAGTAGG 41  
DB 1 TATTAGCTCTAGAAATTACACGGGTATCCAGTAGTAGG 40

## RESULT 2

US-08-093-144-4/c  
Sequence 4, Application US/08093144  
Patent No. 5434048  
GENERAL INFORMATION:  
APPLICANT: SIMON, LUC  
APPLICANT: LATONDE, MAURICE  
TITLE OF INVENTION: DNA PROBES FOR THE DETECTION OF  
TITLE OF INVENTION: ARBUSCULAR ENDOMYCORRHIZAL FUNGI  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN  
STREET: Eleventh Floor, 1615 L. Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20036-5601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Tape  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/093,144  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,192  
FILING DATE: 15-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Hymo, Lawrence A.  
REGISTRATION NUMBER: 19,057  
REFERENCE/DOCKET NUMBER: LAH/3122/92223/MTM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
TELEX: 6714627 CUSH  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 446 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

US-08-093-144-4

Query Match 94.1%; Score 38.6; DB 1; Length 446;  
Best Local Similarity 95.1%; Pred. No. 1.8e-07;  
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DTATTAGCTCTAGAAATTACACGGGTATCCAGTAGTAGG 41  
DB 61 GTATTAGCTCTAGAAATTACACGGGTATCCAGTAGTAGG 21

## RESULT 3

US-08-867-820A-1/c  
Sequence 1, Application US/08867820A  
Patent No. 5891685  
GENERAL INFORMATION:  
APPLICANT: YAMAGISHI Masahiro  
APPLICANT: TAKAI Yukie  
APPLICANT: MIRAWA Takashi  
APPLICANT: HARA Mari  
APPLICANT: UEDA Makoto  
APPLICANT: OHARA Akiko  
TITLE OF INVENTION: METHOD FOR PRODUCING ESTER OF (S) - HALOGENATED - HYDROXYBUTY  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:

ADDRESSEE: WENDEROTH, LIND & PONACK, L.L.P.  
STREET: 2033 K Street, N.W., Suite 800  
CITY: Washington, D.C.  
COUNTRY: USA  
ZIP: 20006

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/867,820A  
FILING DATE: June 3, 1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee Cheng  
REGISTRATION NUMBER: 40,949  
REFERENCE/DOCKET NUMBER: 1416/OP574US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1788 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
ORIGINAL SOURCE:  
ORGANISM: Candida albicans  
STRAIN: MCL29800

US-08-867-820A-1

Query Match 94.1%; Score 38.6; DB 2; Length 1788;  
Best Local Similarity 95.1%; Pred. No. 2.2e-07;  
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DTATTAGCTCTAGAAATTACACGGGTATCCAGTAGTAGG 41  
DB 170 GTATTAGCTCTAGAAATTACACGGGTATCCAGTAGTAGG 130

RESULT 4  
US-09-645-073-1/c  
Sequence 1, Application US/09645073  
Patent No. 6287800

GENERAL INFORMATION:

APPLICANT: Lee, May

TITLE OF INVENTION: Production of High Titters of Glibberellins GA4 and GA7

FILE REFERENCE: L02-01NP

CURRENT APPLICATION NUMBER: US/09/645,073

PRIOR FILING DATE: 2000-08-25

PRIOR APPLICATION NUMBER: US 60/151,770

NUMBER OF SEQ ID NOS: 1

SOFTWARE: Patentin version 3.0

SEQ ID NO 1

LENGTH: 2293

TYPE: DNA

ORGANISM: Glibberella fujikuroi

US-09-645-073-1

Query Match 94.1%; Score 38.6; DB 4; Length 2293;  
Best Local Similarity 95.1%; Pred. No. 2.3e-07;  
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DTATTAGCTCTAGAAATTACACGGGTATCCAGTAGTAGG 41  
DB 146 GTATTAGCTCTAGAAATTACACGGGTATCCAGTAGTAGG 106

## RESULT 5

US-08-093-144-6/c  
Sequence 6, Application US/08093144  
Patent No. 5434018  
GENERAL INFORMATION:  
APPLICANT: SIMON, IUC  
APPLICANT: LALONDE, MAURICE  
TITLE OF INVENTION: DNA PROBES FOR THE DETECTION OF  
TITLE OF INVENTION: ARBUSCULAR ENDOMYCORRHIZAL FUNGI  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN  
STREET: Eleventh Floor, 1615 L. Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20036-5601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Tape  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/093,144  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,192  
FILING DATE: 15-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: HYMO, Lawrence A.  
REGISTRATION NUMBER: 19,057  
REFERENCE/DOCKET NUMBER: LAH/3122/92223/MJW  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
TELEX: 6714627 CUSH  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-093-144-6  
Query Match 90.2%; Score 37; DB 1; Length 444;  
Best Local Similarity 92.7%; Pred. No. 8.5e-07;  
Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 DTATTAGCTCTAGAAATTCACGCGGTATCCAGTAGTAGG 41  
DB 62 GTATTAGCTCTAGAAATTCACGCGGTATCCAGTAGTAGG 22  
RESULT 6  
US-08-093-144-5/c  
Sequence 5, Application US/08093144  
Patent No. 5434018  
GENERAL INFORMATION:  
APPLICANT: SIMON, IUC  
APPLICANT: LALONDE, MAURICE  
TITLE OF INVENTION: DNA PROBES FOR THE DETECTION OF  
TITLE OF INVENTION: ARBUSCULAR ENDOMYCORRHIZAL FUNGI  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN  
STREET: Eleventh Floor, 1615 L. Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20036-5601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Tape  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/093,144  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,192  
FILING DATE: 15-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: HYMO, Lawrence A.  
REGISTRATION NUMBER: 19,057  
REFERENCE/DOCKET NUMBER: LAH/3122/92223/MJW  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
TELEX: 6714627 CUSH  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-093-144-5  
Query Match 89.3%; Score 36.6; DB 1; Length 444;  
Best Local Similarity 94.9%; Pred. No. 1.3e-06;  
Matches 37; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 DTATTAGCTCTAGAAATTCACGCGGTATCCAGTAGTAGG 39  
DB 62 GTATTAGCTCTAGAAATTCACGCGGTATCCAGTAGTAGG 24  
RESULT 7  
US-08-998-416-178  
Sequence 178, Application US/08998416  
Patent No. 6239264  
GENERAL INFORMATION:  
APPLICANT: Philippson, Peter  
APPLICANT: Pohlmann, Rainer  
APPLICANT: Steiner, Sabine  
APPLICANT: Mohr, Christine  
APPLICANT: Wendland, Jurgen  
APPLICANT: Knechtel, Philipp  
APPLICANT: Reibschung, Corinne  
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPPII  
TITLE OF INVENTION: AND USES THEREOF  
NUMBER OF SEQUENCES: 1152  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6239264artis Corporation  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: No. 6239264th Carolina  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/998,416  
FILING DATE: 24-DEC-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: CH 0016/97  
FILING DATE: 31-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976  
TELECOMMUNICATION INFORMATION:

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/093,144  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,192  
FILING DATE: 15-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: HYMO, Lawrence A.  
REGISTRATION NUMBER: 19,057  
REFERENCE/DOCKET NUMBER: LAH/3122/92223/MJW  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
TELEX: 6714627 CUSH  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-093-144-5  
Query Match 89.3%; Score 36.6; DB 1; Length 444;  
Best Local Similarity 94.9%; Pred. No. 1.3e-06;  
Matches 37; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 DTATTAGCTCTAGAAATTCACGCGGTATCCAGTAGTAGG 39  
DB 62 GTATTAGCTCTAGAAATTCACGCGGTATCCAGTAGTAGG 24  
RESULT 7  
US-08-998-416-178  
Sequence 178, Application US/08998416  
Patent No. 6239264  
GENERAL INFORMATION:  
APPLICANT: Philippson, Peter  
APPLICANT: Pohlmann, Rainer  
APPLICANT: Steiner, Sabine  
APPLICANT: Mohr, Christine  
APPLICANT: Wendland, Jurgen  
APPLICANT: Knechtel, Philipp  
APPLICANT: Reibschung, Corinne  
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPPII  
TITLE OF INVENTION: AND USES THEREOF  
NUMBER OF SEQUENCES: 1152  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6239264artis Corporation  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: No. 6239264th Carolina  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/998,416  
FILING DATE: 24-DEC-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: CH 0016/97  
FILING DATE: 31-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-541-8687  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 178:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 703 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: PAG1070RP  
US-08-998-416-178

Query Match 82.4%; Score 33.8; DB 4; Length 703;  
Best Local Similarity 87.8%; Pred. No. 2e-05;  
Matches 36; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

1 DTATTAGCTCTAGATTACACGGGTATCCAGTAGTAGG 41  
510 GTATTAGCTCTAGATTACACGATATTCATGTAAG 550

RESULT 8  
US-08-998-416-814/c

Sequence 814, Application US/08998416  
Patent No. 6239264

## GENERAL INFORMATION:

APPLICANT: Philippsen, Peter  
APPLICANT: Pohlmann, Rainer  
APPLICANT: Steiner, Sabine  
APPLICANT: Mohr, Christine  
APPLICANT: Wendland, Jürgen  
APPLICANT: Knechtle, Philipp  
APPLICANT: Redischung, Corinne  
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPYII  
TITLE OF INVENTION: AND USES THEREOF  
NUMBER OF SEQUENCES: 1152  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6239264artis Corporation  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: No. 6239264th Carolina  
COUNTRY: USA  
ZIP: 27709

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/998,416  
FILING DATE: 24-DEC-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: CH 0016/97  
FILING DATE: 31-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Meligs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8587  
TELEFAX: 919-541-8689

## INFORMATION FOR SEQ ID NO: 814:

SEQUENCE CHARACTERISTICS:  
LENGTH: 706 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: PAG1518UP  
US-08-998-416-814

Query Match 82.4%; Score 33.8; DB 4; Length 706;  
Best Local Similarity 87.8%; Pred. No. 2e-05;  
Matches 36; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

1 DTATTAGCTCTAGATTACACGGGTATCCAGTAGTAGG 41  
675 GTATTAGCTCTAGATTACACGATATTCATGTAAG 635

RESULT 9  
US-08-998-416-910/c

Sequence 910, Application US/08998416  
Patent No. 6239264

## GENERAL INFORMATION:

APPLICANT: Philippsen, Peter  
APPLICANT: Pohlmann, Rainer  
APPLICANT: Steiner, Sabine  
APPLICANT: Mohr, Christine  
APPLICANT: Wendland, Jürgen  
APPLICANT: Knechtle, Philipp  
APPLICANT: Redischung, Corinne  
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPYII  
TITLE OF INVENTION: AND USES THEREOF  
NUMBER OF SEQUENCES: 1152  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6239264artis Corporation  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: No. 6239264th Carolina  
COUNTRY: USA  
ZIP: 27709

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/998,416  
FILING DATE: 24-DEC-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: CH 0016/97  
FILING DATE: 31-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Meligs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8587  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 910:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 712 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: PAG1567UP  
US-08-998-416-910

Query Match 82.4%; Score 33.8; DB 4; Length 712;  
Best Local Similarity 87.8%; Pred. No. 2e-05;  
Matches 36; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

1 DTATTAGCTCTAGATTACACGGGTATCCAGTAGTAGG 41  
674 GTATTAGCTCTAGATTACACGATATTCATGTAAG 634

RESULT 10  
US-08-998-416-602/c

Sequence 602, Application US/08998416  
Patent No. 6239264  
GENERAL INFORMATION:  
APPLICANT: Philippsen, Peter  
APPLICANT: Pohlmann, Rainer  
APPLICANT: Steiner, Sabine  
APPLICANT: Mohr, Christine  
APPLICANT: Wendland, Jürgen  
APPLICANT: Knechtle, Philipp  
APPLICANT: Reibschung, Corline  
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSTYPII  
TITLE OF INVENTION: AND USES THEREOF  
NUMBER OF SEQUENCES: 1152  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6239264artis Corporation  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: No. 6239264th Carolina  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/998,416  
FILING DATE: 24-DEC-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: CH 0016/97  
FILING DATE: 31-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8587  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 602:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 717 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: PAG1411UP  
US-08-998-416-602  
Query Match 82.4%; Score 33.8; DB 4; Length 717;  
Best Local Similarity 87.8%; Pred. No. 2e-05;  
Matches 36; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DTATTAGCTCTAGATTACACGGGTATCCAGTAGTAAG 41  
:|||||  
Db 674 GTATTAGCTCTAGATTACACAGATATCCATGATGTAAG 634

RESULT 11  
US-08-998-416-952  
Sequence 952, Application US/08998416  
Patent No. 6239264  
GENERAL INFORMATION:  
APPLICANT: Philippsen, Peter  
APPLICANT: Pohlmann, Rainer  
APPLICANT: Steiner, Sabine  
APPLICANT: Mohr, Christine  
APPLICANT: Wendland, Jürgen  
APPLICANT: Knechtle, Philipp  
APPLICANT: Reibschung, Corline  
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSTYPII  
TITLE OF INVENTION: AND USES THEREOF

NUMBER OF SEQUENCES: 1152  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6239264artis Corporation  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: No. 6239264th Carolina  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/998,416  
FILING DATE: 24-DEC-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: CH 0016/97  
FILING DATE: 31-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8587  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 952:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 723 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: PAG1588UP  
US-08-998-416-952  
Query Match 82.4%; Score 33.8; DB 4; Length 723;  
Best Local Similarity 87.8%; Pred. No. 2e-05;  
Matches 36; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DTATTAGCTCTAGATTACACGGGTATCCAGTAGTAAG 41  
:|||||  
Db 510 GTATTAGCTCTAGATTACACAGATATCCATGATGTAAG 550

RESULT 12  
US-08-327-516-1/c  
Sequence 1, Application US/08327516  
Patent No. 5707617  
GENERAL INFORMATION:  
APPLICANT: CONRAD, Patricia A.  
APPLICANT: BARR, Bradd C.  
APPLICANT: ANDERSON, Mark L.  
APPLICANT: SVERLOW, Karen W.  
TITLE OF INVENTION: Bovine Neospora Isolates and Their Uses  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourile and Crew  
STREET: Steuart Street Tower, One Market Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94105-1493  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/327,516  
FILING DATE: 20-OCT-1994

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,858  
FILING DATE: 21-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Baslian, Kevin L.  
REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 2307E-539-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1747 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-327-516-1

Query Match 78.5%; Score 32.2; DB 1; Length 1747;  
Best Local Similarity 85.4%; Pred. No. 0.00011;  
Matches 35; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 DTATTAGCTAGATTACACGGGTATCCAGTAGTAGG 41  
DB 147 GTATTAGCATGATTACACGGGTATCCATGTAGTAGG 107

RESULT 13  
US-09-281-766-1/c  
Sequence 1, Application US/09281766  
Patent No. 6376196  
GENERAL INFORMATION:  
APPLICANT: Conrad, Patricia C.  
APPLICANT: Louie, Kitland  
TITLE OR INVENTION: The Regents of the University of California  
FILE REFERENCE: 023070-082510US  
CURRENT APPLICATION NUMBER: US/09/281,766  
PRIOR FILING DATE: 1999-03-30  
PRIOR APPLICATION NUMBER: US 08/645,951  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 1  
LENGTH: 1747  
TYPE: DNA  
ORGANISM: Neospora sp.  
FEATURE:  
OTHER INFORMATION: nuclear small subunit (nss)-rRNA gene  
US-09-281-766-1

Query Match 78.5%; Score 32.2; DB 4; Length 1747;  
Best Local Similarity 85.4%; Pred. No. 0.00011;  
Matches 35; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 DTATTAGCTAGATTACACGGGTATCCAGTAGTAGG 41  
DB 147 GTATTAGCATGATTACACGGGTATCCATGTAGTAGG 107

RESULT 14  
US-08-949-770-1/c  
Sequence 1, Application US/08949770  
Patent No. 6063604  
GENERAL INFORMATION:  
APPLICANT: Wick, James F.  
APPLICANT: Mueller, Reinhold  
APPLICANT: Blasasak, Michele  
APPLICANT: Wilkows, Richard K.  
TITLE OF INVENTION: Target Nucleic Acid Sequence Amplification  
Patent No. 6063604

NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/949,770  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/617,045  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Pochoplen, Donald J.  
REGISTRATION NUMBER: 32,167  
REFERENCE/DOCKET NUMBER: 28003/33045  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1750 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: misc.feature  
OTHER INFORMATION: /- "18s rRNA gene of Cryptosporidium"  
OTHER INFORMATION: parvum"  
US-08-949-770-1

Query Match 75.6%; Score 31; DB 3; Length 1750;  
Best Local Similarity 91.4%; Pred. No. 0.00034;  
Matches 32; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DTATTAGCTAGATTACACGGGTATCCAGTA 35  
DB 170 GTATTAGCTAGATTACACGGGTATCCATGTA 136

RESULT 15  
US-08-998-416-281  
Sequence 281, Application US/08998416  
Patent No. 6239264  
GENERAL INFORMATION:  
APPLICANT: Phillipsen, Peter  
APPLICANT: Pohlmann, Rainer  
APPLICANT: Stehner, Sabine  
APPLICANT: Mohr, Christine  
APPLICANT: Wendland, Jurgen  
APPLICANT: Knechtel, Philipp  
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPTII  
TITLE OF INVENTION: AND USES THEREOF  
NUMBER OF SEQUENCES: 1152  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6239264artis Corporation  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: No. 6239264th Carolina  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Melus, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 281:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 709 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1237UP
; US-08-998-416-281

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Query Match          69.3%; Score 28.4; DB 4; Length 709;
Best Local Similarity 88.2%; Pred.No.0.0037;
Matches 30; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 DATTAGCTCTAGCAATTACACGCGGTATCCAGT 34
       :|||||
Db      510 GTATTAGCTCTAGCAATTACACGAGATATCCATGT 543

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Search completed: June 12, 2003, 04:38:54  
 Job time : 42.335 secs

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Publication No. US20030040617A9
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 402
LENGTH: 265
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (23)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (213)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (218)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (233)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (255)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (264)
OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-402

Query Match
Best Local Similarity 79.0%; Score 32.4; DB 9; Length 265;
Matches 34; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DTATTAGCTCTAGATTACACGGGTATCCAGTAGTA 38
DB 162 GTATTAGCTCTAGATTACACAGTATATCCAGTAGGA 125

RESULT 3
US-09-925-299-402/c
Sequence 402, Application US/09925299
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 402
LENGTH: 265
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (23)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (213)
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (218)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (233)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (235)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (264)
OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-402

Query Match
Best Local Similarity 79.0%; Score 32.4; DB 10; Length 265;
Matches 34; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DTATTAGCTCTAGATTACACGGGTATCCAGTAGTA 38
DB 162 GTATTAGCTCTAGATTACACAGTATATCCAGTAGGA 125

RESULT 4
US-10-079-623-137/c
Sequence 137, Application US/10079623
Patent No. US20020169302A1
GENERAL INFORMATION:
APPLICANT: Havukala, Ilka J.
APPLICANT: Glenn, Matthew
APPLICANT: Grigor, Murray R.
APPLICANT: Molesnar, Adrian J.
TITLE OF INVENTION: Compositions isolated from bovine
FILE REFERENCE: 11000.1044c3
CURRENT APPLICATION NUMBER: US/10/079,623
CURRENT FILING DATE: 2002-02-19
NUMBER OF SEQ ID NOS: 370
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 137
LENGTH: 374
TYPE: DNA
ORGANISM: Bovine
US-10-079-623-137

Query Match
Best Local Similarity 79.0%; Score 32.4; DB 9; Length 374;
Matches 34; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DTATTAGCTCTAGATTACACGGGTATCCAGTAGTA 38
DB 138 GTATTAGCTCTAGATTACACAGTATATCCAGTAGGA 101

RESULT 5
US-09-918-995-37407/c
Sequence 37407, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 37407
LENGTH: 389
TYPE: DNA
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ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(389)  
OTHER INFORMATION: n = A,T,C or G  
US-09-918-995-37407

Query Match  
Best Local Similarity 79.0%; Score 32.4; DB 9; Length 389;  
Matches 34; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DTATTAGCTCTAGATTACACGGGTATCCCAAGTAGTA 38  
DB 161 GTATTAGCTCTAGATTACACAGTATTCACCAAGTAGGA 124

RESULT 6  
US-09-960-352-986/C  
Sequence 986, Application US/09960352  
Patent No. US20020137139A1  
GENERAL INFORMATION:  
APPLICANT: Warren, Wesley C.  
APPLICANT: Tao, Nengbing  
APPLICANT: Byatt, John C.  
APPLICANT: Mathialagan, Nagappan  
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
FILE REFERENCE: 16511.006/37-21(10298)C  
CURRENT APPLICATION NUMBER: US/09/960,352  
CURRENT FILING DATE: 2001-09-24  
NUMBER OF SEQ ID NOS: 15112  
SEQ ID NO 986  
LENGTH: 395  
TYPE: DNA  
ORGANISM: Bos taurus  
OTHER INFORMATION: Clone ID: 05-LIB2809-016-Q1-E1-B1  
US-09-960-352-986

Query Match  
Best Local Similarity 79.0%; Score 32.4; DB 10; Length 395;  
Matches 34; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DTATTAGCTCTAGATTACACGGGTATCCCAAGTAGTA 38  
DB 115 GTATTAGCTCTAGATTACACAGTATTCACCAAGTAGGA 78

RESULT 7  
US-09-764-877-829  
Sequence 829, Application US/09764877  
Patent No. US20020147140A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PC005  
CURRENT APPLICATION NUMBER: US/09/764,877  
CURRENT FILING DATE: 2001-01-17  
Prior application data removed - refer to PALM or file wrapper  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 829  
LENGTH: 395  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-764-877-829

Query Match  
Best Local Similarity 79.0%; Score 32.4; DB 10; Length 395;  
Matches 34; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DTATTAGCTCTAGATTACACGGGTATCCCAAGTAGTA 38  
DB 127 GTATTAGCTCTAGATTACACAGTATTCACCAAGTAGGA 164

RESULT 8  
US-10-198-846-9359  
Sequence 9359, Application US/10198846  
Patent No. US2003009974A1  
GENERAL INFORMATION:  
APPLICANT: Lillie, James  
APPLICANT: Xu, Yongyao  
APPLICANT: Wang, Youzhen  
APPLICANT: Steilmann, Kathleen  
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS  
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
FILE REFERENCE: NRI-049  
CURRENT APPLICATION NUMBER: US/10/198,846  
CURRENT FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: 60/306,220  
PRIOR FILING DATE: 2001-07-18  
NUMBER OF SEQ ID NOS: 14084  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9359  
LENGTH: 409  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-198-846-9359

Query Match  
Best Local Similarity 79.0%; Score 32.4; DB 9; Length 409;  
Matches 34; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DTATTAGCTCTAGATTACACGGGTATCCCAAGTAGTA 38  
DB 135 GTATTAGCTCTAGATTACACAGTATTCACCAAGTAGGA 172

RESULT 9  
US-09-960-352-9712/C  
Sequence 9712, Application US/09960352  
Patent No. US20020137139A1  
GENERAL INFORMATION:  
APPLICANT: Warren, Wesley C.  
APPLICANT: Tao, Nengbing  
APPLICANT: Byatt, John C.  
APPLICANT: Mathialagan, Nagappan  
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
FILE REFERENCE: 16511.006/37-21(10298)C  
CURRENT APPLICATION NUMBER: US/09/960,352  
CURRENT FILING DATE: 2001-09-24  
NUMBER OF SEQ ID NOS: 15112  
SEQ ID NO 9712  
LENGTH: 411  
TYPE: DNA  
ORGANISM: Bos taurus  
OTHER INFORMATION: Clone ID: 42-LIB2809-010-Q1-E1-C6  
US-09-960-352-9712

Query Match  
Best Local Similarity 79.0%; Score 32.4; DB 10; Length 411;  
Matches 34; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DTATTAGCTCTAGATTACACGGGTATCCCAAGTAGTA 38  
DB 98 GTATTAGCTCTAGATTACACAGTATTCACCAAGTAGGA 61

RESULT 10  
US-09-918-995-16742/C  
Sequence 16742, Application US/09918995  
Patent No. US20030075623A1  
GENERAL INFORMATION:  
APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
 FROM VARIOUS CDNA LIBRARIES  
 FILE REFERENCE: 20411-736  
 CURRENT APPLICATION NUMBER: US/09/918,995  
 CURRENT FILING DATE: 2001-07-30  
 PRIOR APPLICATION NUMBER: US/09/235,076  
 PRIOR FILING DATE: 1999-01-20  
 NUMBER OF SEQ ID NOS: 38054  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 16742  
 LENGTH: 510  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc.feature  
 LOCATION: (1)..(510)  
 OTHER INFORMATION: n = A,T,C or G  
 US-09-918-995-16742

Query Match 79.0%; Score 32.4; DB 9; Length 510;  
 Best Local Similarity 89.5%; Pred. No. 0.00037;  
 Matches 34; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 DTATTAGCTCTAGATTACACGGGTATCCAAAGTAGTA 38  
 Db 286 GTATTAGCTCTAGATTACACAGTATATCCAAAGTAGGA 249

RESULT 11  
 US-10-198-846-6323  
 Sequence 6323, Application US/10198846  
 Publication No. US20030099974A1  
 GENERAL INFORMATION:  
 APPLICANT: Lillie, James  
 APPLICANT: Xu, Tongyao  
 APPLICANT: Wang, Youzhen  
 APPLICANT: Steinmann, Kathleen  
 TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS  
 TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
 THERAPY OF BREAST CANCER  
 FILE REFERENCE: MRI-049  
 CURRENT APPLICATION NUMBER: US/10/198,846  
 CURRENT FILING DATE: 2002-07-18  
 PRIOR APPLICATION NUMBER: 60/306,220  
 PRIOR FILING DATE: 2001-07-18  
 NUMBER OF SEQ ID NOS: 14084  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 6323  
 LENGTH: 614  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc.feature  
 LOCATION: 4, 540, 567, 594  
 OTHER INFORMATION: n = A,T,C or G  
 US-10-198-846-6323

Query Match 79.0%; Score 32.4; DB 9; Length 614;  
 Best Local Similarity 89.5%; Pred. No. 0.00038;  
 Matches 34; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 DTATTAGCTCTAGATTACACGGGTATCCAAAGTAGTA 38  
 Db 136 GTATTAGCTCTAGATTACACAGTATATCCAAAGTAGGA 173

RESULT 12  
 US-09-919-344-14/C  
 Sequence 14, Application US/09919344  
 Patent No. US20020137911A1  
 GENERAL INFORMATION:  
 APPLICANT: Pyle, Ruth A.  
 APPLICANT: Xu, Jiangchun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 AND DIAGNOSIS OF PANCREATIC CANCER  
 FILE REFERENCE: 210121.543  
 CURRENT APPLICATION NUMBER: US/09/919,344  
 CURRENT FILING DATE: 2001-07-30  
 NUMBER OF SEQ ID NOS: 32  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 14  
 LENGTH: 870  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc.feature  
 LOCATION: 56, 57, 573, 614, 714, 750, 756, 770, 771, 784, 785, 807,  
 819, 851, 859  
 OTHER INFORMATION: n = A,T,C or G  
 US-09-919-344-14

Query Match 79.0%; Score 32.4; DB 10; Length 870;  
 Best Local Similarity 89.5%; Pred. No. 0.00041;  
 Matches 34; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 DTATTAGCTCTAGATTACACGGGTATCCAAAGTAGTA 38  
 Db 141 GTATTAGCTCTAGATTACACAGTATATCCAAAGTAGGA 104

RESULT 13  
 US-09-880-107-2231/C  
 Sequence 2231, Application US/09880107  
 Patent No. US20020142981A1  
 GENERAL INFORMATION:  
 APPLICANT: Horne, Darci T.  
 APPLICANT: Vockley, Joseph G.  
 APPLICANT: Scherf, Uwe  
 APPLICANT: Gene Logic, Inc.  
 TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer  
 FILE REFERENCE: 44921-5028-WO  
 CURRENT APPLICATION NUMBER: US/09/880,107  
 CURRENT FILING DATE: 2001-06-14  
 PRIOR APPLICATION NUMBER: US 60/211,379  
 PRIOR FILING DATE: 2000-06-14  
 PRIOR APPLICATION NUMBER: US 60/237,054  
 PRIOR FILING DATE: 2000-10-02  
 NUMBER OF SEQ ID NOS: 3950  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 2231  
 LENGTH: 1969  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 OTHER INFORMATION: Genbank Accession No. US20020142981A1 M10098  
 NAME/KEY: unsure  
 LOCATION: (1)..(1969)  
 OTHER INFORMATION: n = a or c or g or t  
 US-09-880-107-2231

Query Match 79.0%; Score 32.4; DB 10; Length 1969;  
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 Matches 34; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 DTATTAGCTCTAGATTACACGGGTATCCAAAGTAGTA 38  
 Db 275 GTATTAGCTCTAGATTACACAGTATATCCAAAGTAGGA 238

RESULT 14  
 US-09-764-891-8902  
 Sequence 8902, Application US/09764891  
 Publication No. US20030077808A1  
 GENERAL INFORMATION:  
 APPLICANT: Rosen et al.  
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PC006  
CURRENT APPLICATION NUMBER: US/09/764,891  
CURRENT FILING DATE: 2001-01-17  
Prior application data removed - consult PALM or file wrapper  
NUMBER OF SEQ ID NOS: 10231  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 8902  
LENGTH: 13076  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (1259)  
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LOCATION: (5953)  
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LOCATION: (11536)  
OTHER INFORMATION: n equals a,t,g, or c  
US-09-764-891-8902

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Best Local Similarity 89.5%; Pred. No. 0.00076;  
Matches 34; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
DB 3585 GTATTAGCTCTGAAATACACAGTATCCAGTAGCA 3622  
OR 1 DTAATTAGCTCTGAAATACACAGTATCCAGTAGCA 38  
DB 3585 GTATTAGCTCTGAAATACACAGTATCCAGTAGCA 3622  
RESULT 15  
US-09-764-891-10043  
Sequence 10043, Application US/09764891  
Publication No. US20030077808A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PC006  
CURRENT APPLICATION NUMBER: US/09/764,891  
CURRENT FILING DATE: 2001-01-17  
Prior application data removed - consult PALM or file wrapper  
NUMBER OF SEQ ID NOS: 10231  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10043  
LENGTH: 13076  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (1259)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: SITE  
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: OTHER INFORMATION: n equals a,t,g, or c
US-09-764-891-10043

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Query Match 79.0%; Score 32.4; DB 9; Length 13076;
Best Local Similarity 89.5%; Pred. NO. 0.00076;
Matches 34; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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OY 1 DTATTAGCTCTAGATTACCGGGTATCCAGTAGTA 38
DB 3585 GTATTAGCTCTAGATTACCGAGTATCCAGTAGGA 3622

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Search completed: June 12, 2003, 04:58:24
Job time : 242.834 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 00:35:54 ; Search time 1504.93 seconds

(without alignments)  
441.227 Million cell updates/sec

Title: US-09-674-195C-15

Perfect score: 41  
Sequence: 1 dtatagctcagaattacc.....cggatccaaagtaag 41

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

EST:  
1: em\_estba:  
2: em\_esthum:  
3: em\_estin:  
4: em\_estnu:  
5: em\_estov:  
6: em\_estpl:  
7: em\_estro:  
8: em\_estt:  
9: gb\_est1:  
10: gb\_est2:  
11: gb\_est3:  
12: gb\_est4:  
13: gb\_est5:  
14: gb\_est6:  
15: em\_estfun:  
16: em\_estom:  
17: gb\_gss:  
18: em\_gss\_hum:  
19: em\_gss\_inv:  
20: em\_gss\_pla:  
21: em\_gss\_vit:  
22: em\_gss\_fun:  
23: em\_gss\_mam:  
24: em\_gss\_mus:  
25: em\_gss\_other:  
26: em\_gss\_pro:  
27: em\_gss\_rtd:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	38.6	94.1	222	10	AM791051
C 2	38.6	94.1	351	12	BF251693
C 3	38.6	94.1	362	12	BF251811
C 4	38.6	94.1	377	12	BF251964
C 5	38.6	94.1	391	12	BF251561
C 6	38.6	94.1	442	12	BE776737

C 7	38.6	94.1	486	10	AM792005
C 8	38.6	94.1	488	12	BE251704
C 9	38.6	94.1	500	12	BE776329
C 10	38.6	94.1	502	12	BE252581
C 11	38.6	94.1	515	10	AM792430
C 12	38.6	94.1	516	10	BE582931
C 13	38.6	94.1	518	12	BE251715
C 14	38.6	94.1	521	14	B0143465
C 15	38.6	94.1	541	12	BE252371
C 16	38.6	94.1	546	12	BE253171
C 17	38.6	94.1	558	10	BE430105
C 18	38.6	94.1	564	12	BE775624
C 19	38.6	94.1	567	12	BE252094
C 20	38.6	94.1	568	12	BE252878
C 21	38.6	94.1	572	12	BE252095
C 22	38.6	94.1	573	14	BM959171
C 23	38.6	94.1	581	9	AJ273326
C 24	38.6	94.1	587	9	AJ273809
C 25	38.6	94.1	597	14	BM959216
C 26	38.6	94.1	605	12	BE252135
C 27	38.6	94.1	625	9	AJ273227
C 28	38.6	94.1	667	13	BM027271
C 29	38.6	94.1	668	13	BT955938
C 30	38.6	94.1	679	12	BE251385
C 31	38.6	94.1	687	12	BE251001
C 32	38.6	94.1	701	12	BE251666
C 33	38.6	94.1	719	14	BQ750939
C 34	38.6	94.1	726	10	BE582613
C 35	38.6	94.1	749	13	BM439305
C 36	38.6	94.1	824	14	BQ751228
C 37	38.6	94.1	836	12	BE250962
C 38	38.6	94.1	851	17	CNS07D41
C 39	38.6	94.1	907	17	CNS07DBA
C 40	38.6	94.1	920	17	CNS07CZP
C 41	38.6	94.1	926	17	CNS07DLP
C 42	38.6	94.1	931	17	CNS07DPO
C 43	38.6	94.1	936	17	CNS07DXT
C 44	38.6	94.1	944	17	CNS07DHG
C 45	38.6	94.1	946	17	CNS07DE2

#### ALIGNMENTS

RESULT 1  
LOCUS AM791051/c 222 bp mRNA linear EST 01-MAY-2001  
DEFINITION D00369-R Lambda zap, Stragene Blumeria graminis f. sp. hordei  
CDNA clone D00369 similar to hypothetical protein 2, mRNA sequence.

ACCESSION AM791051  
VERSION AM791051.1 GI:13902648  
KEYWORDS EST.  
SOURCE Blumeria graminis f. sp. hordei.  
ORGANISM Blumeria graminis f. sp. hordei.  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;  
Erysiphales; Erysiphaceae; Blumeria.

REFERENCE 1 (bases 1 to 222)  
Thomas,S.W., Rasmussen,S.W., Glaring,M.A., Rouster,J.A. and Oliver  
R.P.  
Gene identification in the fungal pathogen Blumeria graminis by  
expressed sequence tag analysis

TITLE Unpublished (2000)  
JOURNAL Contact: Rasmussen,S.W.  
COMMENT Department of Yeast Genetics  
Carlsberg Laboratory  
10 G.L. Carlsbergvej, DK-2500, Copenhagen, Denmark  
Tel: 45 3327 5230  
Fax: 45 3327 4766  
Email: svre@cc.dk  
High quality sequence stop: 222  
POLYA-NO.  
Location/Qualifiers  
1. .222

FEATURES  
SOURCE

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/organism="Blumeria graminis f. sp. hordei"
/db_xref="taxon:62688"
/clone="D00369"
/clone_1lb="lambda zap, Stragene"
/cell_type="conidia"
/lab_host="Hordeum vulgare"
BASE COUNT      66 a 45 c 41 g 70 t
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Query Match      94.1%; Score 38.6; DB 10; Length 222;
Best Local Similarity 95.1%; Pred. No. 7.3e-05;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DTATTAGCTAGAAATACACGGGTATCCAGTAGTAAG 41
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202 GTATTAGCTAGAAATACACGGGTATCCAGTAGTAAG 162

RESULT 2
LOCUS      BF251693/c 351 bp mRNA linear EST 15-NOV-2001
DEFINITION Coccioidioides immitis spherule cDNA library Coccioidioides
immitis cDNA clone CIAAK21 5' sequence, mRNA sequence.
ACCESSION  BF251693
VERSION     BF251693.1 GI:16931759
KEYWORDS   EST.
SOURCE     Coccioidioides immitis.
ORGANISM   Coccioidioides immitis.
REFERENCE  Gardner,M.J. and Kirkland,T.
AUTHORS    Generation of ESTs from Coccioidioides immitis spherule cDNA library
TITLE       Unpublished (2000)
JOURNAL     Contact: Malcolm J. Gardner
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301 838 3519
            Fax: 301 838 0208
            Email: gardner@tigr.org.
COMMENT     Location/Qualifiers
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            /organism="Coccioidioides immitis"
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Query Match      94.1%; Score 38.6; DB 12; Length 351;
Best Local Similarity 95.1%; Pred. No. 8.9e-05;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DTATTAGCTAGAAATACACGGGTATCCAGTAGTAAG 41
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RESULT 3
LOCUS      BF251811/c 362 bp mRNA linear EST 15-NOV-2001
DEFINITION Coccioidioides immitis spherule cDNA library Coccioidioides
immitis cDNA clone CIAAM73 5' sequence, mRNA sequence.
ACCESSION  BF251811
VERSION     BF251811.1 GI:16931954
KEYWORDS   EST.
SOURCE     Coccioidioides immitis.
ORGANISM   Coccioidioides immitis.

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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Ongyinales; mitosporic Ongyinales; Coccioidioides.
1 (bases 1 to 362)
AUTHORS    Gardner,M.J. and Kirkland,T.
TITLE       Generation of ESTs from Coccioidioides immitis spherule cDNA library
JOURNAL     Unpublished (2000)
COMMENT     Contact: Malcolm J. Gardner
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301 838 3519
            Fax: 301 838 0208
            Email: gardner@tigr.org.
FEATURES
SOURCE
BASE COUNT      98 a 69 c 84 g 111 t
ORIGIN
Query Match      94.1%; Score 38.6; DB 12; Length 362;
Best Local Similarity 95.1%; Pred. No. 9e-05;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DTATTAGCTAGAAATACACGGGTATCCAGTAGTAAG 41
:|||||
150 GTATTAGCTAGAAATACACGGGTATCCAGTAGTAAG 110

RESULT 4
LOCUS      BF251964/c 377 bp mRNA linear EST 15-NOV-2001
DEFINITION Coccioidioides immitis spherule cDNA library Coccioidioides
immitis cDNA clone CIAAP15 5' sequence, mRNA sequence.
ACCESSION  BF251964
VERSION     BF251964.1 GI:16932107
KEYWORDS   EST.
SOURCE     Coccioidioides immitis.
ORGANISM   Coccioidioides immitis.
REFERENCE  Gardner,M.J. and Kirkland,T.
AUTHORS    Generation of ESTs from Coccioidioides immitis spherule cDNA library
TITLE       Unpublished (2000)
JOURNAL     Contact: Malcolm J. Gardner
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301 838 3519
            Fax: 301 838 0208
            Email: gardner@tigr.org.
FEATURES
SOURCE
BASE COUNT      103 a 85 c 94 g 95 t
ORIGIN
Query Match      94.1%; Score 38.6; DB 12; Length 377;
Best Local Similarity 95.1%; Pred. No. 9.2e-05;

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## Matches

39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DTATTACCTCTAGATTAACCGGATTCACAGTAGTAAG 41  
 DB 54 GTATTACCTCTAGATTAACCGGATTCACAGTAGTAAG 14

## RESULT 5

BF251561/c  
 LOCUS BF251561  
 DEFINITION EST148910 Coccidioides immitis spherule cDNA library Coccidioides  
 ACCESSION BF251561  
 VERSION BF251561.1 GI:16931792  
 KEYWORDS EST.  
 SOURCE Coccidioides immitis.  
 ORGANISM Coccidioides immitis.  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 Onygenales; Miltosporic Onygenales; Coccidioides.

REFERENCE  
 AUTHORS Gardner, M.J. and Kirkland, T.  
 TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Malcolm J. Gardner  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301 838 3519  
 Fax: 301 838 0208  
 Email: gardner@tigr.org.

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 XhoI"

BASE COUNT 107 a 76 c 96 g 112 t  
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Query Match  
 Best Local Similarity 94.1%; Score 38.6; DB 12; Length 391;  
 Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DTATTACCTCTAGATTAACCGGATTCACAGTAGTAAG 41  
 DB 155 GTATTACCTCTAGATTAACCGGATTCACAGTAGTAAG 115

RESULT 6  
 BE776737/c  
 LOCUS BE776737  
 DEFINITION MY-19-G-09 Pinestansky Phytophthora infestans cDNA, mRNA sequence.  
 ACCESSION BE776737  
 VERSION BE776737.1 GI:10230392  
 KEYWORDS EST.  
 SOURCE potato late blight agent.  
 ORGANISM Phytophthora infestans.  
 Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;  
 Phytophthora.

REFERENCE  
 AUTHORS Kamoun, S., Hirber, P.T., Sobral, B.W.S., Nuss, D. and Govers, F.  
 TITLE Initial assessment of gene diversity for the comycete pathogen  
 JOURNAL Phytophthora infestans based on expressed sequences  
 MEDLINE Fungal Genet. Biol. 28 (2), 94-106 (1999)  
 COMMENT 20056376  
 Contact: Govers F  
 Laboratory of Phytopathology  
 Wageningen University  
 Binnenhaven 9, P.O.Box 8025, 6700 EE, Wageningen, The Netherlands

Tel: 31 317 483 138  
 Fax: 31 317 483 412  
 Email: Francine.govers@medew.fyto.wau.nl.  
 FEATURES  
 source  
 1..442  
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 /organism="Phytophthora infestans"  
 /strain="DDR7602; A1 mating type"  
 /db\_xref="taxon:4787"  
 /clone\_1lb="Pinestansky"  
 /dev\_stage="4-week old vegetative, non-sporulating  
 mycelium in synthetic medium"  
 /lab\_host="E. coli, strain DH5-alpha"  
 /note="Vector: pSPORT1; Site.1: SalI; Site.2: NotI; Total  
 RNA was isolated from mycelium of P. infestans DDR7602  
 cultured for 4 weeks in synthetic medium. EST clones were  
 named by their position in the microtiter plate, preceded  
 by the prefix MY (for mycelial) and the successive number  
 of the microtiter plate (e.g. MY-06-A-04)."

BASE COUNT 117 a 89 c 107 g 124 t  
 ORIGIN

Query Match  
 Best Local Similarity 94.1%; Score 38.6; DB 12; Length 442;  
 Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DTATTACCTCTAGATTAACCGGATTCACAGTAGTAAG 41  
 DB 158 GTATTACCTCTAGATTAACCGGATTCACAGTAGTAAG 118

RESULT 7  
 AM792005/c  
 LOCUS AM792005  
 DEFINITION D00948-R Lambda Zap, StrataGene Blumeria graminis f. sp. hordei  
 mRNA clone D00948 similar to non-functional isolate binding protein,  
 ACCESSION AM792005  
 VERSION AM792005.1 GI:13903602  
 KEYWORDS EST.  
 SOURCE Blumeria graminis f. sp. hordei.  
 ORGANISM Blumeria graminis f. sp. hordei.  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;  
 Erysiphales; Erysiphaceae; Blumeria.

REFERENCE  
 AUTHORS Thomas, S.W., Rasmussen, S.W., Glaring, M.A., Rousier, J.A. and Oliver,  
 R.P.  
 TITLE Gene identification in the fungal pathogen Blumeria graminis by  
 JOURNAL expressed sequence tag analysis  
 COMMENT Unpublished (2000)  
 CONTACT: Rasmussen, S.W.  
 Department of Yeast Genetics  
 Carlsberg Laboratory  
 10 GL, Carlsbergvej, DK-2500, Copenhagen, Denmark  
 Tel: 45 3327 5230  
 Fax: 45 3327 4766  
 Email: sw@erc.dk

FEATURES  
 source  
 1..486  
 Location/Qualifiers  
 /organism="Blumeria graminis f. sp. hordei"  
 /db\_xref="taxon:62688"  
 /clone\_id="D00948"  
 /clone\_1lb="Lambda Zap, StrataGene"  
 /cell\_type="candida"  
 /lab\_host="Hordeum vulgare"

BASE COUNT 138 a 101 c 115 g 132 t  
 ORIGIN

Query Match  
 Best Local Similarity 94.1%; Score 38.6; DB 10; Length 486;  
 Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;



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RESULT 11
AM792430/c
LOCUS
DEFINITION
  AM792430 515 bp mRNA linear EST 01-MAY-2001
  D01189-R lambda Zap, Stragatene Blumeria graminis f. sp. hordei
  mRNA clone D01189 similar to non-functional folate binding protein,
  mRNA sequence.
ACCESSION
  AM792430
VERSION
  AM792430.1 GI:13904027
SOURCE
  EST.
  Blumeria graminis f. sp. hordei.
  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
  Erysiphales; Erysiphaceae; Blumeria.
REFERENCE
  1 (bases 1 to 515)
  Thomas, S.W., Rasmussen, S.W., Glaring, M.A., Rousster, J.A. and Oliver
  , R.P.
TITLE
  Gene identification in the fungal pathogen Blumeria graminis by
  expressed sequence tag analysis
JOURNAL
  Unpublished (2000)
COMMENT
  Contact: Rasmussen, S.W.
  Department of Yeast Genetics
  Carlsberg Laboratory
  10 Gl. Carlsbergvej, DK-2500, Copenhagen, Denmark
  Tel: 45 3327 5230
  Fax: 45 3327 4766
  Email: svre@cc.dk
  High quality sequence stop: 515
  POLYA-No.

FEATURES
  source
    location/Qualifiers
    1..515
    /organism="Blumeria graminis f. sp. hordei"
    /db_xref="taxon:62688"
    /clone="D01189"
    /clone_1lb="Lambda Zap, stragatene"
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    /lab_host="Hordeum vulgare"
    104 c 119 g 142 t

BASE COUNT
  150 a 150 c 119 g 142 t

Query Match
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  Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY
  1 DTTATAGCTGTGAAATTCACACGGGTATCCAGTAGTAAG 41
  Db
  148 GTATTAGCTGTGAAATTCACACGGGTATCCAGTAGTAAG 108

RESULT 12
BE582931/c
LOCUS
DEFINITION
  3-5F-WY Psoljaemr Phytophthora sojae mRNA linear EST 16-AUG-2000
  BE582931
ACCESSION
  BE582931
VERSION
  BE582931.1 GI:9833879
KEYWORDS
  EST.
  Phytophthora sojae.
  Phytophthora sojae.
  Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
  Phytophthora
SOURCE
  1 (bases 1 to 516)
  Outub, D., Hrader, P.T., Sobral, B.W.S. and Gijzen, M.
  Comparative analysis of expressed sequences in Phytophthora sojae
  Plant Physiol. 123 (1), 243-254 (2000)
  20267956
COMMENT
  Contact: Gijzen M
  Agriculture and Agri-Food Canada
  1391 Sandford Street, London, Ontario, Canada N5V 4T3
  Tel: 519 457 1470
  Fax: 519 457 3997
  Email: gijzen@em.agr.ca.

FEATURES
  source
    location/Qualifiers
    1..516
    /organism="Phytophthora sojae"

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/strain="race 2, strain P6497"
/db_xref="taxon:67593"
/clone_1lb="Psoljaemr"
/dev_stage="mycelium"
/lab_host="E. coli strain XLOLR"
/note="Vector: pBK-CMV. Site_1: EcoRI; Site_2: XhoI. This
  cDNA library was constructed from polyA+ enriched mRNA
  from mycelium grown in liquid medium for 3 weeks at 25 C
  in the dark in a liquid synthetic medium of 2.4 g sucrose
  and 2 mg thiamine, per liter, plus salts and minerals.
  Complementary DNA was synthesized from mRNA using an
  XhoI-poly(dT) linker-primer. EcoRI adapters were ligated
  to the blunt-ended cDNA fragments and the products were
  digested with XhoI for directional cloning into lambda Zap
  Express vector. This lambda library was amplified once
  using E. coli host strain XLI Blue MRF. Inserts were then
  subcloned by mass excision using EXASist helper phage for
  strain XLOLR. Sequenced using T3 primer: 5' ATT AAC CCT
  CAC TAA AGG GA 3'."

BASE COUNT
  152 a 98 c 123 g 142 t 1 others

ORIGIN
  152 a 98 c 123 g 142 t 1 others

Query Match
  Best Local Similarity 94.1%; Score 38.6; DB 10; Length 516;
  Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY
  1 DTTATAGCTGTGAAATTCACACGGGTATCCAGTAGTAAG 41
  Db
  153 GTATTAGCTGTGAAATTCACACGGGTATCCAGTAGTAAG 113

RESULT 13
BF251715/c
LOCUS
DEFINITION
  BF251715 518 bp mRNA linear EST 15-NOV-2001
  immitis cDNA clone CIAK45 5' sequence, mRNA sequence.
ACCESSION
  BF251715
VERSION
  BF251715.1 GI:16931781
KEYWORDS
  EST.
  Cocciidioides immitis.
  Cocciidioides immitis.
  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
  Onygenales; mitosporic Onygenales; Cocciidioides.
SOURCE
  1 (bases 1 to 518)
  Gardner M.J. and Kirkland, T.
  Generation of ESTs from Cocciidioides immitis spherule cDNA library
  Unpublished (2000)
  Contact: Malcolm J. Gardner
  Department of Eukaryotic Genomics
  The Institute for Genomic Research
  9712 Medical Center Drive, Rockville, MD 20850, USA
  Tel: 301 838 3519
  Fax: 301 838 0208
  Email: gardner@tigr.org.

FEATURES
  source
    location/Qualifiers
    1..518
    /organism="Cocciidioides immitis"
    /db_xref="taxon:5501"
    /clone="CIAK45"
    /clone_1lb="Cocciidioides immitis spherule cDNA library"
    /dev_stage="spherule"
    /lab_host="SOLR"
    /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
    XhoI"

BASE COUNT
  141 a 104 c 133 g 140 t

ORIGIN
  141 a 104 c 133 g 140 t

Query Match
  Best Local Similarity 94.1%; Score 38.6; DB 12; Length 518;
  Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Thu Jun 12 08:47:43 2003

us-09-674-195c-15.rst

QY 1 DTATTAGCTCTAGATTACACGGGTATCCAGTAGTAAG 41  
DB 155 GTATTAGCTCTAGATTACACGGGTATCCAGTAGTAAG 115

RESULT 14  
BO143465/c 521 bp mRNA linear EST 24-APR-2002

LOCUS fmlh1c.pk005.g1 Metarhizium anisopliae sf. acridum ARSEF 324  
DEFINITION Metarhizium anisopliae var. acridum cDNA, mRNA sequence.

ACCESSION BO143465  
VERSION BO143465.1 GI:20280524

KEYWORDS Metarhizium anisopliae var. acridum.  
SOURCE Metarhizium anisopliae var. acridum  
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreales; Clavicipitaceae; mitosporic Clavicipitaceae;  
Metarhizium.

REFERENCE 1 (bases 1 to 521)  
Frelmoser, F.M., Screen, S., Baga, S., Hu, G. and St. Leger, R.J.  
EST analysis of genes expressed by two different insect pathogenic  
fungi during optimized secretion of proteins

JOURNAL Unpublished (2002)  
COMMENT Contact: Frelmoser F. M.  
Department of Entomology  
University of Maryland  
4112 Plant Sciences Building, College Park, MD 20742, USA  
Tel: 301 405 16 13  
Fax: 301 314 92 90  
Email: f34@umail.umd.edu.  
Location/Qualifiers

FEATURES  
source 1..521  
/organism="Metarhizium anisopliae var. acridum"  
/strain="ARSEF 324"  
/db\_xref="taxon:32637"  
/clone\_lib="Metarhizium anisopliae sf. acridum ARSEF 324"  
/note="Vector: Unizap; Metarhizium anisopliae sf. acridum  
was grown on insect cuticle and chitin for 24 hours. A  
cDNA library was constructed in the unidirectional lambda  
vector Unizap."

BASE COUNT 152 a 110 c 125 g 133 t 1 others  
ORIGIN

Query Match 94.1%; Score 38.6; DB 14; Length 521;  
Best Local Similarity 95.1%; Pred. No. 0.00011;  
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DTATTAGCTCTAGATTACACGGGTATCCAGTAGTAAG 41  
DB 141 GTATTAGCTCTAGATTACACGGGTATCCAGTAGTAAG 101

RESULT 15  
BF252371/c 541 bp mRNA linear EST 15-NOV-2001  
LOCUS BF252371 Coccidioides immitis spherule cDNA library Coccidioides  
DEFINITION Coccidioides immitis spherule cDNA library Coccidioides  
Immitis cDNA clone C1A9A1 5' sequence, mRNA sequence.

ACCESSION BF252371  
VERSION BF252371.1 GI:16932514  
KEYWORDS Coccidioides immitis.  
SOURCE Coccidioides immitis  
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; mitosporic Onygenales; Coccidioides.

REFERENCE 1 (bases 1 to 541)  
Gardner, M.J. and Kirkland, T.  
Generation of ESTs from Coccidioides immitis spherule cDNA library  
Unpublished (2000)  
Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519

FEATURES  
source 1..541  
/organism="Coccidioides immitis"  
/db\_xref="taxon:5501"  
/clone\_lib="C1A9A1"  
/clone\_lib="Coccidioides immitis spherule cDNA library"  
/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI"

BASE COUNT 157 a 109 c 133 g 142 t  
ORIGIN

Query Match 94.1%; Score 38.6; DB 12; Length 541;  
Best Local Similarity 95.1%; Pred. No. 0.00011;  
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DTATTAGCTCTAGATTACACGGGTATCCAGTAGTAAG 41  
DB 154 GTATTAGCTCTAGATTACACGGGTATCCAGTAGTAAG 114

Search completed: June 12, 2003, 04:35:03  
Job time : 1509.64 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 22:21:06 ; Search time 620.827 Seconds

(without alignments)  
1921.975 Million cell updates/sec

Title: US-09-674-195c-16

Perfect score: 41  
Sequence: 1 dcccgaaggcattggttt.....ttatcataaacaccccc 41Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

## Database :

GenBml:\*\*  
1: gb\_da:\*\*  
2: gb\_hlg:\*\*  
3: gb\_in:\*\*  
4: gb\_om:\*\*  
5: gb\_ov:\*\*  
6: gb\_pat:\*\*  
7: gb\_ph:\*\*  
8: gb\_pl:\*\*  
9: gb\_pr:\*\*  
10: gb\_ro:\*\*  
11: gb\_stg:\*\*  
12: gb\_sy:\*\*  
13: gb\_un:\*\*  
14: gb\_vl:\*\*  
15: em\_da:\*\*  
16: em\_fun:\*\*  
17: em\_hum:\*\*  
18: em\_in:\*\*  
19: em\_mu:\*\*  
20: em\_om:\*\*  
21: em\_or:\*\*  
22: em\_ov:\*\*  
23: em\_pat:\*\*  
24: em\_ph:\*\*  
25: em\_pl:\*\*  
26: em\_ro:\*\*  
27: em\_sts:\*\*  
28: em\_un:\*\*  
29: em\_vl:\*\*  
30: em\_hlg\_hum:\*\*  
31: em\_hlg\_inv:\*\*  
32: em\_hlg\_other:\*\*  
33: em\_hlg\_mus:\*\*  
34: em\_hlg\_pin:\*\*  
35: em\_hlg\_rod:\*\*  
36: em\_hlg\_mam:\*\*  
37: em\_hlg\_vrt:\*\*  
38: em\_sy:\*\*  
39: em\_hlg\_hum:\*\*  
40: em\_hlg\_mus:\*\*  
41: em\_hlg\_other:\*\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40.2	98.0	421	8 294136	294136 Cladosporiu
2	40.2	98.0	422	8 294150	294150 uncultured
3	40.2	98.0	422	8 294151	294151 uncultured
4	40.2	98.0	494	8 AB030916	AB030916 Aspergill
5	40.2	98.0	510	8 AF0311478	AF0311478 unculture
6	40.2	98.0	519	8 EMSMRNA01	U03382 Exophiala m
7	40.2	98.0	526	8 AFU311484	AFU311484 unculture
8	40.2	98.0	544	8 AF056370	AF056370 Euscomyc
9	40.2	98.0	544	8 AF056372	AF056372 Euscomyc
10	40.2	98.0	546	8 AF053885	AF053885 Phialocyp
11	40.2	98.0	551	8 AF056371	AF056371 Euscomyc
12	40.2	98.0	657	11 PM6A1B	AL686152 Penicill
13	40.2	98.0	660	8 CNS01BM5	AL114405 Botrytis
14	40.2	98.0	762	11 PM8B3B	AL683346 Penicill
15	40.2	98.0	765	11 PM8B7B	AL682828 Penicill
16	40.2	98.0	772	8 AF088236	AF088236 Acarospor
17	40.2	98.0	785	8 AF088247	AF088247 Rimularia
18	40.2	98.0	804	8 AF088248	AF088248 Santesson
19	40.2	98.0	866	8 AF088243	AF088243 Physcia a
20	40.2	98.0	900	8 AF056375	AF056375 Leptodont
21	40.2	98.0	946	8 AF356669	AF356669 Calicium
22	40.2	98.0	949	8 AA067427	U67427 Arachnopez
23	40.2	98.0	959	8 HFU67430	U67430 Hymenoscyp
24	40.2	98.0	969	8 AF113712	AF113712 Dipels b
25	40.2	98.0	973	8 LVU67433	U67433 Lachnum vir
26	40.2	98.0	985	8 AF107347	AF107347 Baecomyces
27	40.2	98.0	989	8 AF107349	AF107349 Baecomyces
28	40.2	98.0	995	8 BD079482	U79482 Botryosphae
29	40.2	98.0	1010	8 AF356667	AF356667 Verticari
30	40.2	98.0	1016	8 AF096183	AF096183 Pseuduro
31	40.2	98.0	1020	8 CGU67428	U67428 Clastella gr
32	40.2	98.0	1025	8 AF183935	AF183935 Lobaria p
33	40.2	98.0	1030	8 AF203454	AF203454 Meloidema
34	40.2	98.0	1030	8 AF203459	AF203459 Hemiplaci
35	40.2	98.0	1031	8 AF203457	AF203457 Naemacycl
36	40.2	98.0	1031	8 AF203458	AF203458 Cycleanus
37	40.2	98.0	1031	8 AF203462	AF203462 Chloroscy
38	40.2	98.0	1032	8 AF106017	AF106017 Merlia lar
39	40.2	98.0	1032	8 AF203452	AF203452 Colpoma q
40	40.2	98.0	1032	8 AF203453	AF203453 Litula ma
41	40.2	98.0	1032	8 AF203456	AF203456 Ascocalyx
42	40.2	98.0	1032	8 AF203460	AF203460 Sarcotroc
43	40.2	98.0	1032	8 AF203461	AF203461 Chloroscy
44	40.2	98.0	1032	8 AF203463	AF203463 Chalara f
45	40.2	98.0	1032	8 AF203464	AF203464 Loramyces

## ALIGNMENTS

RESULT 1  
294136/c  
LOCUS 294136  
DEFINITION Cladosporium cladosporioides partial 18S rRNA gene, strain DR114.  
ACCESSION 294136  
VERSION 294136.1 GI:20975704  
KEYWORDS 18S ribosomal RNA; 18S rRNA.  
SOURCE Cladosporium cladosporioides.  
ORGANISM Cladosporium cladosporioides  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes et  
Chaetothyriomycetes incertae sedis; Mycosphaerellaceae; mitosporic  
Mycosphaerellaceae; Cladosporium.  
REFERENCE 1 (bases 1 to 420)  
Kowalchuk, G.A., Gerards, S. and Woldendorp, J.W.  
Detection and characterization of fungal infections of Ammophila

arenaria (marum grass) roots by denaturing gradient gel electrophoresis of specifically amplified 18S rDNA Appl. Environ. Microbiol. 63 (10), 3858-3865 (1997)

JOURNAL  
MEDLINE  
PUBMED  
97468462  
9327549

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
2 Kowalchuk, G.A.  
Direct Submission  
Submitted (16-APR-1997) Kowalchuk G.A., Netherlands Institute of Ecology, Plant-Microorganism Interactions, Boterhoeksestraat 22, PO Box 40, 6666 ZG, Heteren, the Netherlands

FEATURES  
SOURCE

1. .422  
/organism="Cladosporium cladosporioides"  
/macronuclear  
/strain="DR14"  
/specific\_host="Ammophila arenaria"  
/db\_xref="taxon:29917"  
1. .421  
/gene="18S rRNA"  
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/product="18S ribosomal RNA"

BASE COUNT  
ORIGIN  
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Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY  
Db  
1 DCCCCGAAGGCGATGTTTTCCTAATAATACACCCC 41  
184 GCCCGAAGGCGATGTTTTCCTAATAATACACCCC 144

RESULT 2  
LOCUS  
294150/c  
294150  
uncultured fungus partial 18S rRNA gene, isolate EB-8.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
18S ribosomal RNA; 18S rRNA.  
uncultured fungus.  
uncultured fungus.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
2 Kowalchuk, G.A., Gerards, S. and Woldendorp, J.W.  
Detection and characterization of fungal infections of Ammophila arenaria (marum grass) roots by denaturing gradient gel electrophoresis of specifically amplified 18S rDNA Appl. Environ. Microbiol. 63 (10), 3858-3865 (1997)

JOURNAL  
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PUBMED  
97468462  
9327549

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
2 Kowalchuk, G.A.  
Direct Submission  
Submitted (16-APR-1997) Kowalchuk G.A., Netherlands Institute of Ecology, Plant-Microorganism Interactions, Boterhoeksestraat 22, PO Box 40, 6666 ZG, Heteren, the Netherlands

FEATURES  
SOURCE

1. .422  
/organism="uncultured fungus"  
/macronuclear  
/isolate="EB-8"  
/specific\_host="Ammophila arenaria"  
/db\_xref="taxon:175245"  
1. .422  
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/gene="18S rRNA"  
/product="18S ribosomal RNA"

BASE COUNT  
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Query Match  
Best Local Similarity 98.0%; Score 40.2; DB 8; Length 422;  
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY  
Db  
1 DCCCCGAAGGCGATGTTTTCCTAATAATACACCCC 41  
185 GCCCGAAGGCGATGTTTTCCTAATAATACACCCC 145

RESULT 3  
LOCUS  
294151/c  
294151  
uncultured fungus partial 18S rRNA gene, isolate EB-9.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
18S ribosomal RNA; 18S rRNA.  
uncultured fungus.  
uncultured fungus.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
2 Kowalchuk, G.A., Gerards, S. and Woldendorp, J.W.  
Detection and characterization of fungal infections of Ammophila arenaria (marum grass) roots by denaturing gradient gel electrophoresis of specifically amplified 18S rDNA Appl. Environ. Microbiol. 63 (10), 3858-3865 (1997)

JOURNAL  
MEDLINE  
PUBMED  
97468462  
9327549

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
2 Kowalchuk, G.A.  
Direct Submission  
Submitted (16-APR-1997) Kowalchuk G.A., Netherlands Institute of Ecology, Plant-Microorganism Interactions, Boterhoeksestraat 22, PO Box 40, 6666 ZG, Heteren, the Netherlands

FEATURES  
SOURCE

1. .422  
/organism="uncultured fungus"  
/macronuclear  
/isolate="EB-9"  
/specific\_host="Ammophila arenaria"  
/db\_xref="taxon:175245"  
1. .422  
/gene="18S rRNA"  
<1. .>422  
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/product="18S ribosomal RNA"

BASE COUNT  
ORIGIN  
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Query Match  
Best Local Similarity 98.0%; Score 40.2; DB 8; Length 422;  
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY  
Db  
1 DCCCCGAAGGCGATGTTTTCCTAATAATACACCCC 41  
185 GCCCGAAGGCGATGTTTTCCTAATAATACACCCC 145

RESULT 4  
LOCUS  
AB030916/c  
AB030916  
Aspergillus niger gene for 18S rRNA, partial sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
AB030916.1 GI:5738920  
18S rRNA; 18S ribosomal RNA.  
Aspergillus niger (strain:IEF1) DNA.  
Aspergillus niger  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Eurotiales; Trichocommataceae; mitosporic Trichocommataceae; Aspergillus

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
1 (bases 1 to 494)  
Shintani, T. and Matsumoto, Y.  
Aspergillus niger gene for 18S rRNA, partial sequence.  
Published only in Database (1999)

REFERENCE 2 (bases 1 to 494)  
 AUTHORS Shintani, T. and Matsumoto, Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (10-AUG-1999) Tomoyoshi Shintani, Industrial Research Center of Ehime Prefecture, Laboratory of Food Process; 487-2 Kumebuko, Matsuyama, Ehime 791-1101, Japan  
 (E-mail:shintani@irt.pref.ehime.jp, URL:www.irt.pref.ehime.jp, Tel:81-89-976-7612, Fax:81-89-976-7313)  
 FEATURES  
 source  
 1. 494  
 /organism="Aspergillus niger"  
 /strain="IEP1"  
 /db\_xref="taxon:5061"  
 <1..>494  
 /product="18S ribosomal RNA"  
 BASE COUNT 141 a 100 c 121 g 131 t 1 others  
 ORIGIN  
 Query Match 98.0%; Score 40.2; DB 8; Length 494;  
 Best Local Similarity 97.6%; Pred. No. 0.00034;  
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 DCCCGAAGGCGATGTTTATCTAATAAATACACCCC 41  
 :|||||  
 Db 215 GCCCGAAGGCGATGTTTATCTAATAAATACACCCC 175  
 RESULT 5  
 LOCUS UF0311478/c 510 bp RNA linear PLN 06-MAR-2002  
 DEFINITION Uncultured fungus partial 18S rRNA gene.  
 ACCESSION AJ311478  
 VERSION AJ311478.1 GI:18693082  
 KEYWORDS 18S ribosomal RNA; 18S rRNA gene.  
 SOURCE uncultured fungus.  
 ORGANISM Eukaryota; Fungi; environmental samples.  
 REFERENCE 1  
 Schabereiter-Gurtner, C., Pinar, G., Lubitz, W. and Roelcke, S.  
 TITLE Analysis of fungal communities on historical church window glass by denaturing gradient gel electrophoresis and phylogenetic 18S rDNA sequence analysis  
 JOURNAL J. Microbiol. Methods 47, 347-356 (2001)  
 REFERENCE 2 (bases 1 to 510)  
 AUTHORS Schabereiter-Gurtner, C.  
 TITLE Direct Submission  
 JOURNAL Submitted (14-FEB-2001) Schabereiter-Gurtner C., Institute for Microbiology and Genetics, University of Vienna, Dr. Bohr-Gasse 9, 1030 Vienna, AUSTRIA  
 FEATURES  
 source  
 1. 510  
 /organism="uncultured fungus"  
 /db\_xref="taxon:175245"  
 /clone="GC-K27"  
 1. 510  
 /gene="18S rRNA"  
 <1..>510  
 /gene="18S rRNA"  
 /product="18S ribosomal RNA"  
 BASE COUNT 154 a 100 c 119 g 131 t 6 others  
 ORIGIN  
 Query Match 98.0%; Score 40.2; DB 8; Length 510;  
 Best Local Similarity 97.6%; Pred. No. 0.00034;  
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 DCCCGAAGGCGATGTTTATCTAATAAATACACCCC 41  
 :|||||  
 Db 198 GCCCGAAGGCGATGTTTATCTAATAAATACACCCC 158  
 RESULT 6  
 EMSMRNA01/c

LOCUS EMSMRNA01 519 bp DNA linear PLN 17-NOV-1995  
 DEFINITION Exophiala mansonii small subunit ribosomal RNA gene, 5' partial sequence.  
 ACCESSION U20382  
 VERSION U20382.1 GI:662816  
 KEYWORDS  
 SEGMENT  
 SOURCE  
 ORGANISM  
 1 of 2  
 Exophiala mansonii.  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Chaetothyriomycetes; Chaetothyriales; Herpoticheiales; Herpoticheiaceae; mitosporic Herpoticheiaceae; Exophiala.  
 REFERENCE 1 (bases 1 to 519)  
 AUTHORS Spatafora, J.W., Mitchell, T.G. and Vilgalys, R.  
 TITLE Analysis of genes coding for small-subunit rRNA sequences in studying phylogenetics of dematiaceous fungal pathogens  
 JOURNAL J. Clin. Microbiol. 33 (5), 1322-1326 (1995)  
 MEDLINE 95340770  
 PUBMED 7615749  
 REFERENCE 2 (bases 1 to 519)  
 AUTHORS Spatafora, J.W.  
 TITLE Direct Submission  
 JOURNAL Submitted (27-JAN-1995) Joseph W. Spatafora, Dept. of Botany & Plant Pathology, 2082 Cordley Hall, Oregon State University, Corvallis, OR 97331, USA  
 FEATURES  
 source  
 1. 519  
 /organism="Exophiala castellanii"  
 /db\_xref="taxon:91922"  
 <1..>519  
 /product="small subunit ribosomal RNA"  
 /note="approximately 400 bp separate the 3' end of segment 1 and the 5' end of segment 2"  
 BASE COUNT 152 a 107 c 125 g 135 t  
 ORIGIN  
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 Best Local Similarity 97.6%; Pred. No. 0.00034;  
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 DCCCGAAGGCGATGTTTATCTAATAAATACACCCC 41  
 :|||||  
 Db 192 GCCCGAAGGCGATGTTTATCTAATAAATACACCCC 152  
 RESULT 7  
 LOCUS UF0311484/c 526 bp RNA linear PLN 06-MAR-2002  
 DEFINITION Uncultured fungus partial 18S rRNA gene.  
 ACCESSION AJ311484  
 VERSION AJ311484.1 GI:18693088  
 KEYWORDS 18S ribosomal RNA; 18S rRNA gene.  
 SOURCE uncultured fungus.  
 ORGANISM Eukaryota; Fungi; environmental samples.  
 REFERENCE 1  
 Schabereiter-Gurtner, C., Pinar, G., Lubitz, W. and Roelcke, S.  
 TITLE Analysis of fungal communities on historical church window glass by denaturing gradient gel electrophoresis and phylogenetic 18S rDNA sequence analysis  
 JOURNAL J. Microbiol. Methods 47, 347-356 (2001)  
 REFERENCE 2 (bases 1 to 526)  
 AUTHORS Schabereiter-Gurtner, C.  
 TITLE Direct Submission  
 JOURNAL Submitted (14-FEB-2001) Schabereiter-Gurtner C., Institute for Microbiology and Genetics, University of Vienna, Dr. Bohr-Gasse 9, 1030 Vienna, AUSTRIA  
 FEATURES  
 source  
 1. 526  
 /organism="uncultured fungus"  
 /db\_xref="taxon:175245"  
 /clone="GC-K44"  
 1. 526

rRNA  
 /gene="18S rRNA"  
 <1. >526  
 /gene="18S rRNA"  
 /product="18S ribosomal RNA"  
 BASE COUNT 157 a 106 c 128 g 135 t  
 ORIGIN

Query Match 98.0%; Score 40.2; DB 8; Length 526;  
 Best Local Similarity 97.6%; Pred. No. 0.00034;  
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCGAAGGCGATTGTTTATCTAATAATACACCC 41  
 :|||||  
 Db 199 GCCCGAAGGCGATTGTTTATCTAATAATACACCC 159

RESULT 8  
 AF056370/c 544 bp DNA linear PLN 15-NOV-2001  
 LOCUS  
 DEFINITION Eusacomycetes sp. WB12 small subunit ribosomal RNA gene, partial  
 sequence.  
 ACCESSION AF056370  
 VERSION AF056370.1 GI:3088639  
 KEYWORDS  
 SOURCE eusacomycete sp. WB12.  
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; unclassified

REFERENCE  
 AUTHORS Jumpsonen, A. and Trappe, J.M.  
 TITLE Dark-septate endophytes: a review of facultative biotrophic  
 JOURNAL root-colonizing fungi  
 REFERENCE 2 (bases 1 to 544)  
 AUTHORS Jumpsonen, A. and Trappe, J.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (31-MAR-1998) Forest Science, Oregon State University,  
 3200 NW Jefferson Way, Corvallis, OR 97331, USA

FEATURES  
 source  
 1. 544  
 /organism="eusacomycete sp. WB12"  
 /strain="WB12"  
 /specific\_host="betula papyrifera"  
 /db\_xref="taxon:75492"  
 /note="gift of Kathleen Ann Johnson"  
 <1. >544  
 /product="small subunit ribosomal RNA"  
 BASE COUNT 159 a 112 c 129 g 140 t 4 others  
 ORIGIN

Query Match 98.0%; Score 40.2; DB 8; Length 544;  
 Best Local Similarity 97.6%; Pred. No. 0.00034;  
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCGAAGGCGATTGTTTATCTAATAATACACCC 41  
 :|||||  
 Db 177 GCCCGAAGGCGATTGTTTATCTAATAATACACCC 137

RESULT 9  
 AF056372/c 544 bp DNA linear PLN 15-NOV-2001  
 LOCUS  
 DEFINITION Eusacomycetes sp. A12b2 small subunit ribosomal RNA gene, partial  
 sequence.  
 ACCESSION AF056372  
 VERSION AF056372.1 GI:3088641  
 KEYWORDS  
 SOURCE eusacomycete sp. A12b2.  
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; unclassified

REFERENCE  
 AUTHORS 1 (bases 1 to 544)  
 Jumpsonen, A. and Trappe, J.M.

TITLE Dark-septate endophytes: a review of facultative biotrophic  
 JOURNAL root-colonizing fungi  
 REFERENCE 2 (bases 1 to 544)  
 AUTHORS Jumpsonen, A. and Trappe, J.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (31-MAR-1998) Forest Science, Oregon State University,  
 3200 NW Jefferson Way, Corvallis, OR 97331, USA

FEATURES  
 source  
 1. 544  
 /organism="eusacomycete sp. A12b2"  
 /strain="A12b2"  
 /specific\_host="Pinus sp."  
 /db\_xref="taxon:75494"  
 /note="Isolated at Kenai Fjords, Alaska"  
 <1. >544  
 /product="small subunit ribosomal RNA"  
 BASE COUNT 174 a 111 c 125 g 133 t 1 others  
 ORIGIN

Query Match 98.0%; Score 40.2; DB 8; Length 544;  
 Best Local Similarity 97.6%; Pred. No. 0.00034;  
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCGAAGGCGATTGTTTATCTAATAATACACCC 41  
 :|||||  
 Db 176 GCCCGAAGGCGATTGTTTATCTAATAATACACCC 136

RESULT 10  
 AF055885/c 546 bp DNA linear PLN 07-APR-1998  
 LOCUS  
 DEFINITION Phialocephala fortinii small subunit ribosomal RNA gene, partial  
 sequence.  
 ACCESSION AF055885  
 VERSION AF055885.1 GI:3025851  
 KEYWORDS  
 SOURCE Phialocephala fortinii.  
 ORGANISM Phialocephala fortinii.  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;  
 Helotiales; mitosporic Helotiales; Phialocephala.

REFERENCE  
 AUTHORS 1 (bases 1 to 546)  
 Jumpsonen, A. and Trappe, J.M.  
 TITLE Dark-septate endophytes: a review of facultative biotrophic  
 JOURNAL root-colonizing fungi  
 REFERENCE 2 (bases 1 to 546)  
 AUTHORS Jumpsonen, A. and Trappe, J.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-MAR-1998) Forest Science, Oregon State University,  
 3200 NW Jeffersonway, Corvallis, OR 97331, USA

FEATURES  
 source  
 1. 546  
 /organism="Phialocephala fortinii"  
 /strain="SE24"  
 /specific\_host="Lupinus latifolius (O'Dell et al. 1993,  
 New Phytologist 124: 93)"  
 /db\_xref="taxon:62722"  
 <1. >546  
 /product="small subunit ribosomal RNA"  
 BASE COUNT 162 a 112 c 129 g 142 t  
 ORIGIN

Query Match 98.0%; Score 40.2; DB 8; Length 546;  
 Best Local Similarity 97.6%; Pred. No. 0.00034;  
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCGAAGGCGATTGTTTATCTAATAATACACCC 41  
 :|||||  
 Db 178 GCCCGAAGGCGATTGTTTATCTAATAATACACCC 138

RESULT 11

AF056371/c  
LOCUS AF056371 551 bp DNA linear PLN 15-NOV-2001  
DEFINITION Euascomycetes sp. cc3 small subunit ribosomal RNA gene, partial  
sequence.  
ACCESSION AF056371  
VERSION AF056371.1 GI:3088640  
KEYWORDS  
SOURCE euascomycete sp. cc3.  
ORGANISM euascomycete sp. cc3.  
REFERENCE  
AUTHORS Eukaryota; Fungi; Ascomycota; Pezizomycotina; unclassified  
TITLE 1 (bases 1 to 551)  
JOURNAL Jumperon, A. and Trappe, J.M.  
REFERENCE Dark-septate endophytes: a review of facultative biotrophic  
AUTHORS root-colonizing fungi  
TITLE Unpublished  
JOURNAL 2 (bases 1 to 551)  
AUTHORS Jumperon, A. and Trappe, J.M.  
TITLE Direct Submission  
JOURNAL Submitted (31-MAR-1998) Forest Science, Oregon State University,  
3200 NW Jefferson Way, Corvallis, OR 97331, USA  
FEATURES  
source  
1. 551  
/organism="euascomycete sp. cc3"  
/strain="cc3"  
/specific-host="Carex sp."  
/db\_xref="taxon:75493"  
/note="gift of Kurt Haselwandter"  
<1..>551  
/product="small subunit ribosomal RNA"  
BASE COUNT 164 a 112 c 129 g 141 t 5 others  
ORIGIN  
Query Match 98.0%; Score 40.2; DB 8; Length 551;  
Best Local Similarity 97.6%; Pred. No. 0.00034;  
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 DCCCGAGGCGCATGTTTATCTAATAATACACCCC 41  
Db 181 GCCCGAGGCGCATGTTTATCTAATAATACACCCC 141  
RESULT 12  
LOCUS PM6A1B 657 bp DNA linear STS 09-MAR-2002  
DEFINITION Penicillium marneffei STS, clone pm6a1.b, sequence tagged site.  
ACCESSION AL686152  
VERSION AL686152.1 GI:19337074  
KEYWORDS STS.  
SOURCE Penicillium marneffei.  
ORGANISM Penicillium marneffei  
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
AUTHORS Eurotiates; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.  
TITLE 1  
JOURNAL Yuen, K.Y., Pascal, G., Wong, S., Glaser, P., Woo, P., Kunst, P.,  
Cheung, E., Medigue, C. and Danchin, A.  
REFERENCE Exploring the Penicillium marneffei genome  
AUTHORS 2 (bases 1 to 657)  
JOURNAL Danchin, A. and Pascal, G.  
TITLE Direct Submission  
JOURNAL Submitted (08-MAR-2002) Danchin A., HKU-Pasteur Research Centre,  
Dexter HC Man Building 8, Sassoon Road, Pokfulam, Hong Kong  
FEATURES  
source  
1. 657  
/organism="Penicillium marneffei"  
/db\_xref="taxon:37727"  
/clone="pm6a1.b"  
BASE COUNT 121 a 187 c 184 g 164 t 1 others  
ORIGIN  
Query Match 98.0%; Score 40.2; DB 11; Length 657;  
Best Local Similarity 97.6%; Pred. No. 0.00033;

Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 DCCCGAGGCGCATGTTTATCTAATAATACACCCC 41  
Db 574 GCCCGAGGCGCATGTTTATCTAATAATACACCCC 534  
RESULT 13  
LOCUS CNS01BMS 660 bp mRNA linear PLN 02-SEP-1999  
DEFINITION Botrytis cinerea strain T4 cDNA library under conditions of  
nitrogen deprivation.  
ACCESSION AL114405  
VERSION AL114405.1 GI:5829024  
KEYWORDS cDNA library; nitrogen deprivation.  
SOURCE Botryotinia fuckeliana.  
ORGANISM Botryotinia fuckeliana  
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;  
AUTHORS Helotiales; Sclerotiniaceae; Botryotinia.  
TITLE 1 (bases 1 to 660)  
JOURNAL Bitton, F., Levis, C., Fortini, D., Pradier, J.M. and Brygoo, Y.  
REFERENCE Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,  
78026 Versailles, France  
JOURNAL 2 (bases 1 to 660)  
REFERENCE Genoscope.  
AUTHORS Direct Submission  
TITLE Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :  
JOURNAL CP 5706 91057 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
COMMENT The cDNA library to be analyzed within the framework of this  
project was created using a Botrytis cinerea strain which was grown  
under conditions of nitrogen deprivation, which is the normal  
situation for B. cinerea during its development on its host plant.  
The library was produced in an oriented direction, in the pBS11  
vector.  
FEATURES  
source  
1. 660  
/organism="Botryotinia fuckeliana"  
/strain="T4"  
/db\_xref="taxon:40559"  
/note="Genoscope sequence ID : W72G041"  
BASE COUNT 196 a 176 c 119 g 169 t  
ORIGIN  
Query Match 98.0%; Score 40.2; DB 8; Length 660;  
Best Local Similarity 97.6%; Pred. No. 0.00033;  
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 DCCCGAGGCGCATGTTTATCTAATAATACACCCC 41  
Db 72 GCCCGAGGCGCATGTTTATCTAATAATACACCCC 112  
RESULT 14  
LOCUS PM8E3B 762 bp DNA linear STS 09-MAR-2002  
DEFINITION Penicillium marneffei STS, clone pm8e3.b, sequence tagged site.  
ACCESSION AL685346  
VERSION AL685346.1 GI:19336649  
KEYWORDS STS.  
SOURCE Penicillium marneffei.  
ORGANISM Penicillium marneffei  
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
AUTHORS Eurotiates; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.  
TITLE 1  
JOURNAL Yuen, K.Y., Pascal, G., Wong, S., Glaser, P., Woo, P., Kunst, P.,  
Cheung, E., Medigue, C. and Danchin, A.  
REFERENCE Exploring the Penicillium marneffei genome  
AUTHORS 2 (bases 1 to 762)  
JOURNAL Danchin, A. and Pascal, G.  
TITLE Direct Submission

JOURNAL Submitted (08-MAR-2002) Danchin A., HKU-Pasteur Research Centre,  
Dexter HC Man Building 8, Sassoon Road, Pokfulam, Hong Kong

FEATURES  
SOURCE  
1..762  
/organism="Penicillium marneffei"  
/db\_xref="taxon:37727"  
/clone="pm83.b"

BASE COUNT 148 a 207 c 220 g 183 t 4 others  
ORIGIN

Query Match 98.0%; Score 40.2; DB 11; Length 762;  
Best Local Similarity 97.6%; Pred. No. 0.00032;  
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DCCCGAAGGCATTGTTTATCTAATAATACACCC 41  
:|||||  
DB 574 GCCCGAAGGCATTGTTTATCTAATAATACACCC 534

RESULT 15  
PM8B7B/c

LOCUS PM8B7B 765 bp DNA linear STS 09-MAR-2002  
DEFINITION Penicillium marneffei STS, clone pm8b7.b, sequence tagged site.  
ACCESSION AL685282  
VERSION AL685282.1 GI:19336603

KEYWORDS STS.  
SOURCE Penicillium marneffei.  
ORGANISM Penicillium marneffei  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Eurotiales; Trichocomaceae; Mitosporic Trichocomaceae; Penicillium.

REFERENCE  
AUTHORS 1 Yuen,K.Y., Pascal,G., Wong,S., Glaser,P., Woo,P., Kunst,P.,  
Cheung,E., Medigue,C. and Danchin,A.  
TITLE Exploring the Penicillium marneffei genome  
JOURNAL Unpublished  
AUTHORS 2 (bases 1 to 765)  
TITLE Danchin,A. and Pascal,G.  
JOURNAL Direct Submission  
SUBMITTED (08-MAR-2002) Danchin A., HKU-Pasteur Research Centre,  
Dexter HC Man Building 8, Sassoon Road, Pokfulam, Hong Kong

FEATURES  
SOURCE  
1..765  
/organism="Penicillium marneffei"  
/db\_xref="taxon:37727"  
/clone="pm8b7.b"

BASE COUNT 146 a 208 c 226 g 183 t 2 others  
ORIGIN

Query Match 98.0%; Score 40.2; DB 11; Length 765;  
Best Local Similarity 97.6%; Pred. No. 0.00032;  
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DCCCGAAGGCATTGTTTATCTAATAATACACCC 41  
:|||||  
DB 574 GCCCGAAGGCATTGTTTATCTAATAATACACCC 534

Search completed: June 12, 2003, 02:33:53  
Job time : 622.827 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Comphen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 22:17:41 ; Search time 209.995 Seconds  
(without alignments)  
439,686 Million cell updates/sec

Title: US-09-674-195c-16

Perfect score: 41  
Sequence: 1 dccccgaaggcattggtt.....tattcataaacacccc 41

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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N\_Geneseq\_101002:\*

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- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:\*
- 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:\*
- 4: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:\*
- 5: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:\*
- 6: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:\*
- 7: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT:\*
- 8: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT:\*
- 9: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT:\*
- 10: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT:\*
- 11: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT:\*
- 12: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT:\*
- 13: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT:\*
- 14: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT:\*
- 15: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT:\*
- 16: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT:\*
- 17: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1996.DAT:\*
- 18: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT:\*
- 19: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:\*
- 20: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:\*
- 21: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:\*
- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:\*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:\*
- 24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	40.2	98.0	568	21	AAFL1545
C 2	40.2	98.0	1731	22	AA168286
C 3	40.2	98.0	1731	20	ABA01154
C 4	40.2	98.0	1731	24	AAZ00859
C 5	40.2	97.6	40	15	AAQ73434
C 6	37	90.2	570	21	AAFO8498
C 7	37	90.2	617	21	AAFL0913
C 8	37	90.2	1745	24	ABA01152
C 9	37	90.2	2293	23	AA516211

C 10	35.8	87.3	1771	19	AAV61668
C 11	32.2	78.5	1734	23	ABK49559
C 12	32.2	78.5	1793	19	AAV60107
C 13	32.2	78.5	1904	19	AAV60108
C 14	29.2	71.2	1024	21	AAFL1316
C 15	29	70.7	447	15	AAO71867
C 16	29	70.7	447	15	AAO71868
C 17	26.4	64.4	447	15	AAO71870
C 18	26.2	63.9	1750	21	AAV90818
C 19	26.2	63.9	1750	21	AAA46368
C 20	26	63.4	1776	22	AAE25849
C 21	26	63.4	1798	22	AAAD1404
C 22	26	63.4	1798	22	AAAD1407
C 23	26	63.4	1802	22	AAE23018
C 24	26	63.4	3420	24	ABA99033
C 25	25.8	62.9	1744	13	AAO31638
C 26	25.8	62.9	1744	13	AAO31323
C 27	25.8	62.9	1744	13	AAO31643
C 28	25.8	62.9	1747	22	AAE86243
C 29	25.8	62.9	1756	13	AAO31328
C 30	25.8	62.9	1756	13	AAO31647
C 31	25.8	62.4	1747	13	AAO31327
C 32	25.6	62.4	1747	13	AAO31643
C 33	25.6	60.5	29	20	AAE23834
C 34	24.8	60.0	1748	13	AAO31322
C 35	24.6	60.0	1748	13	AAO31469
C 36	24.6	60.0	1748	13	AAO31336
C 37	24.6	60.0	1748	13	AAO31336
C 38	24.4	59.5	1840	19	AAV61669
C 39	24.2	59.0	1756	13	AAO31326
C 40	24	58.5	1749	13	AAO31325
C 41	24	58.5	1749	13	AAO31472
C 42	24	58.5	1749	13	AAO31629
C 43	23.6	57.6	444	15	AAO71869
C 44	23.4	57.1	29	24	AAO38412
C 45	23.4	57.1	29	24	AAO38416

#### ALIGNMENTS

RESULT 1  
ID AAF11545 standard; cDNA; 568 BP.  
XX AAF11545;  
XX  
DT 13-MAR-2001 (first entry)  
XX  
DE Aspergillus niger EST SEQ ID NO:4068.  
XX  
XX Multiple gene expression; filamentous fungal cell; EST;  
KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;  
KW Aspergillus oryzae; Trichoderma reesei; Identification; recombination;  
KW culture condition; environmental stress; spore morphogenesis;  
KW metabolic pathway engineering; catabolic pathway engineering; ss.  
XX  
XX OS Aspergillus niger.  
XX  
XX WO200056762-A2.  
XX  
XX 28-SEP-2000.  
XX  
XX 22-MAR-2000; 2000WO-US07781.  
XX  
XX 22-MAR-1999; 99US-0273623.  
XX  
XX (NOVO ) NOVO NORDISK BIOTECH INC.  
XX (NOVO ) NOVO NORDISK AS.  
XX  
XX Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;  
XX WPI; 2000-594572/56.  
XX

Fusarium oxysporum  
putrefactive micro  
Rhizoctonia solani  
Rhizoctonia solani  
Aspergillus niger  
G. vesiculiferum s  
G. intraradices sm  
E. pisiiformis smal  
C. parvum 18S rRNA  
Nucleotide sequenc  
S. exiguus 18S rRN  
DNA to infer yeast  
Yeast DNA to infer  
Saccharomyces cere  
Elmeria brunetti s  
E. brunetti sRNA  
E. brunetti sRNA  
Consensus Cyclospo  
Cyclospora 16S-11  
E. tenella sRNA.  
Elmeria necatrix s  
E. praecox sRNA.  
Elmeria praecox ss  
Pan fungal PCR pri  
E. acervulina ssr  
E. acervulina ssr  
Elmeria acervulina  
Fusarium solani f.  
E. necatrix sRNA  
E. mitis sRNA.  
E. mitis sRNA.  
Elmeria mitis ssr  
G. margarita small  
Cryptosporidium pa  
Cryptosporidium pa

XX Monitoring differential expression of genes in filamentous fungal cells  
 PT uses fluorescence-labeled nucleic acids isolated from the cells and a  
 PT substrate of expressed sequence tags -  
 PS Claim 87; Page 1791-1792; 3161pp; English.  
 XX  
 CC The present invention describes a method for monitoring differential  
 CC expression of genes in a first filamentous fungal (FF) cell relative to  
 CC expression of the same genes in one or more second filamentous fungal  
 CC cells. The method uses fluorescence-labeled nucleic acids isolated from  
 CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs  
 CC are used in the methods for monitoring differential expression of genes  
 CC in a first filamentous fungal (FF) cell relative to expression of the  
 CC same genes in one or more second filamentous fungal cells. Monitoring  
 CC the global expression of genes from FF cells allows the production  
 CC potential of the microorganisms to be improved. New genes may be  
 CC discovered, possible functions of unknown open reading frames can be  
 CC identified and gene copy number variation and stability can be  
 CC monitored. The expression of genes can be used to study how FF cells  
 CC adapt to changes in culture conditions, environmental stress, spore  
 CC morphogenesis, recombination, metabolic or catabolic pathway  
 CC engineering. Using ESTs provides several advantages over genomic or  
 CC random cDNA clones including elimination of redundancy as one spot on an  
 CC array equals one gene or open reading frame, and organization of the  
 CC microarrays based on function of the gene products to facilitate  
 CC analysis of the results. AAF07478 to AAF11247 represents ESTs from  
 CC *Fusarium venenatum*; AAF11248 to AAF11853 represents ESTs from *Aspergillus*  
 CC *niger*; AAF11854 to AAF14878 represents ESTs from *Aspergillus oryzae*; and  
 CC AAF14879 to AAF15337 represents ESTs from *Trichoderma reesei*, which are  
 CC all specifically claimed in the present invention.  
 XX  
 SQ Sequence 568 BP; 155 A; 116 C; 141 G; 150 T; 6 other;  
 Query Match 98.0%; Score 40.2; DB 21; Length 568;  
 Best Local Similarity 97.6%; Pred. No. 4.3e-06;  
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DCCCGAAGGCATTGTTTTCATCTAATAATACACCCC 41  
 :|||||  
 DB 222 GCCCGAAGGCATTGTTTTCATCTAATAATACACCCC 182  
 RESULT 2  
 AAI68286/c  
 ID AAI68286 standard; DNA: 1731 BP.  
 AC AAI68286;  
 XX  
 DT 19-DEC-2001 (first entry)  
 XX  
 DE *Bulgaria inquinans* M-3 18S rDNA.  
 XX  
 KW *Bulgaria inquinans* M-3; 18S rDNA; Indole; M-3-A; antifungal;  
 XX Rice leaf spot; ds.  
 XX  
 OS *Bulgaria inquinans*.  
 XX  
 PN JP2001247566-A.  
 XX  
 PD 11-SEP-2001.  
 XX  
 PF 03-MAR-2000; 2000JP-0059685.  
 XX  
 PR 03-MAR-2000; 2000JP-0059685.  
 XX  
 PA (KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.  
 XX  
 DR WPI; 2001-621605/72.  
 XX  
 PT New indole derivative M-3-A, prepared by culture of *Ascomycetes* sp.  
 PT M-3, has antifungal activity -  
 XX

PS Claim 3; Page 6; 9pp; Japanese.  
 XX  
 CC The invention relates to a fungal derived indole derivative M-3-A with  
 CC antifungal activity useful in the treatment of leaf spot of rice with  
 CC M-3-A. The present sequence is that of the *Bulgaria inquinans* M-3 18S  
 CC rDNA sequence.  
 XX  
 SQ Sequence 1731 BP; 459 A; 351 C; 447 G; 474 T; 0 other;  
 Query Match 98.0%; Score 40.2; DB 22; Length 1731;  
 Best Local Similarity 97.6%; Pred. No. 4.9e-06;  
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DCCCGAAGGCATTGTTTTCATCTAATAATACACCCC 41  
 :|||||  
 DB 198 GCCCGAAGGCATTGTTTTCATCTAATAATACACCCC 158  
 RESULT 3  
 ABA01154/c  
 ID ABA01154 standard; DNA: 1731 BP.  
 XX  
 AC ABA01154;  
 XX  
 DT 24-JAN-2002 (first entry)  
 XX  
 DE *Deuteromycetes polynucleotide* SEQ ID 3.  
 XX  
 KM Aldonic acid; ds.  
 XX  
 OS *Deuteromycetes* sp.  
 XX  
 PN JP2001245657-A.  
 XX  
 PD 11-SEP-2001.  
 XX  
 PF 26-DEC-2000; 2000JP-0394766.  
 XX  
 PR 27-DEC-1999; 99JP-0369714.  
 XX  
 PA (TAKE-) TAKEHARA KAGAKU KOGYO KK.  
 XX  
 PA (OSAO) OSAKA CITY.  
 XX  
 DR WPI; 2002-002933/01.  
 XX  
 PT A new microbe for producing aldonic acid, comprises a new strain of  
 PT *Acinetobacter* or *Burkholderia* -  
 XX  
 PS Disclosure; Page 18-19; 22pp; Japanese.  
 XX  
 CC The present invention relates to a new microbe of *Acinetobacter* or  
 CC *Burkholderia* genus producing aldonic acid and oxidizing specifically the  
 CC hemiacetal hydroxy group of a saccharide having said hydroxy group.  
 CC Aldonic acid is used as a mineral reinforcing agent. The present sequence  
 CC was used to illustrate the present invention.  
 XX  
 SQ Sequence 1731 BP; 447 A; 366 C; 459 G; 459 T; 0 other;  
 Query Match 98.0%; Score 40.2; DB 24; Length 1731;  
 Best Local Similarity 97.6%; Pred. No. 4.9e-06;  
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DCCCGAAGGCATTGTTTTCATCTAATAATACACCCC 41  
 :|||||  
 DB 196 GCCCGAAGGCATTGTTTTCATCTAATAATACACCCC 156  
 RESULT 4  
 AA200859/c  
 ID AA200859 standard; DNA: 1733 BP.  
 AC AA200859;  
 XX

DT 11-OCT-1999 (first entry)  
 XX A. fumigatus 18S rRNA DNA.  
 DE  
 XX Detection: diagnosis; 18S rRNA; aspergilliosis; oncology;  
 KM Invasive infection; haematology; immune system suppression; ss.  
 XX Aspergillus fumigatus.  
 OS  
 XX DE19806274-A1.  
 XX  
 XX 19-AUG-1999.  
 PD  
 XX 16-FEB-1998; 98DE-1006274.  
 PF  
 XX 16-FEB-1998; 98DE-1006274.  
 PR  
 XX 16-FEB-1998; 98DE-1006274.  
 PA (BUCH/) BUCHHEIDT D.  
 PA (HEHL/) HEHLMANN R.  
 PA (SKLA/) SKLADNY H.  
 PI Buchheidt D, Hehlmann R, Skladny H;  
 XX WPI; 1999-470047/40.  
 DR  
 XX Detecting Aspergillus nucleic acid in body samples by two-step  
 PT polymerase chain reaction, for diagnosing aspergilliosis  
 PS  
 XX Claim 2; Fig 1; 16pp; German.  
 CC This invention describes a novel method for detecting Aspergillus nucleic  
 CC acid (I) in a body sample which comprises the isolation of (I) followed  
 CC by a two-step polymerase chain reaction (PCR) amplification of any  
 CC nucleic acid having a sequence essentially homologous to part of the  
 CC 3'-end of the Aspergillus 18S rRNA gene using primers used in the first  
 CC step that do not overlap with those in the second step. The method is  
 CC used for early diagnosis, and monitoring, of aspergilliosis, particularly  
 CC invasive infections in hematological-oncological patients with long-term  
 CC suppression of the immune system. Unlike the known method using  
 CC overlapping primers, this process provides efficient and reliable  
 CC detection of Aspergillus in clinical situations. It is specific for  
 CC Aspergillus (it detects the species terreus, niger, versicolor, clavatus,  
 CC flavus, and fumigatus, but not oryzae, nor bacteria or fungi from any  
 CC other genera). This sequence represents the DNA sequence of Aspergillus  
 CC fumigatus 18S rRNA.  
 CC  
 XX  
 SQ Sequence 1733 BP; 446 A; 374 C; 475 G; 438 T; 0 other;  
 Query Match 98.08; Score 40.2; DB 20; Length 1733;  
 Best Local Similarity 97.68; Pred. No. 4.9e-06;  
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DCCCGAAGGCGATGTTTATCTATATATAATACACCCC 41  
 Db 197 GCCCGAAGGCGATGTTTATCTATATATAATACACCCC 157  
 ID AAO73434 standard; DNA: 40 BP.  
 AC AAO73434;  
 XX  
 XX 18-MAY-1995 (first entry).  
 DE  
 XX Histoplasma capsulatum hybridisation helper probe #1.  
 XX  
 KM Probe: detection; Histoplasma capsulatum; 18S; rRNA; rDNA; hybridisation;  
 KM Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;  
 KM water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.  
 XX  
 OS Synthetic.  
 XX

PN US5352579-A.  
 XX  
 XX 04-OCT-1994.  
 PD  
 XX 28-JUN-1991; 91US-0720587.  
 PF  
 XX 28-JUN-1991; 91US-0720587.  
 PR  
 XX (GENP-) GEN-PROBE INC.  
 PA  
 XX M11man CL;  
 PI  
 XX WPI; 1994-316178/39.  
 DR  
 XX Hybridisation probe specific for Histoplasma capsulatum -  
 PT allowing differentiation from all other fungi for detection or  
 PT quantitation in body fluids, etc.  
 XX  
 XX Claim 6; Column 9; 8pp; English.  
 PS  
 XX A probe (AAO73433) or its complement (AAO73436) and corresponding RNA  
 CC sequences (AAO73437 and AAO86436) used for the specific detection of all  
 CC strains of Histoplasma capsulatum (H.c.). The probes are manufactured  
 CC complementary to the H.c. 18S rRNA or rDNA gene. This region also  
 CC corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.  
 CC The probe is specific for H.c. and can be used to distinguish the fungus  
 CC from all others, even its nearest phylogenetic neighbour Blastomyces  
 CC dermatitidis. Nucleic acid hybridisation of the specific probe is  
 CC enhanced by the use of helper probes (AAO73434-5). This method allows  
 CC the detection and/or the quantitation of H.c. from samples e.g. body  
 CC fluids, tissue samples, soil and water.  
 CC  
 XX  
 SQ Sequence 40 BP; 11 A; 11 C; 6 G; 12 T; 0 other;  
 Query Match 97.68; Score 40; DB 15; Length 40;  
 Best Local Similarity 100.08; Pred. No. 3.8e-06;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 CCCCAGGCGATGTTTATCTATATAATACACCCC 41  
 Db 1 CCCCAGGCGATGTTTATCTATATAATACACCCC 40  
 ID AAF08498 standard; CDNA: 570 BP.  
 AC AAF08498;  
 XX  
 XX 13-MAR-2001 (first entry)  
 DE  
 XX Fusarium venenatum EST SEQ ID NO:1021.  
 DE  
 XX Multiple gene expression; filamentous fungal cell; EST;  
 KM expressed sequence tag; Fusarium venenatum; Aspergillus niger;  
 KM Aspergillus oryzae; Trichoderma reesei; identification; recombination;  
 KM culture condition; environmental stress; spore morphogenesis;  
 KM metabolic pathway engineering; catabolic pathway engineering; ss.  
 XX  
 OS Fusarium venenatum.  
 XX  
 XX WO200056762-A2.  
 PN  
 XX 28-SEP-2000.  
 PD  
 XX 22-MAR-2000; 2000WO-US07781.  
 PF  
 XX 22-MAR-1999; 99US-0273623.  
 PR  
 XX (NOVO ) NOVO NORDISK BIOTECH INC.  
 PA (NOVO ) NOVO NORDISK AS.  
 PA  
 XX Berka RM, Rey MW, Shuster JR, Kaupinen S, Clausen IG, Olsen PB;  
 PI

XX WPI: 2000-594572/56.  
DR Monitoring differential expression of genes in filamentous fungal cells  
XX uses fluorescence-labeled nucleic acids isolated from the cells and a  
PT substrate of expressed sequence tags -  
XX  
PS Claim 86; Page 772; 3161pp; English.  
XX  
CC The present invention describes a method for monitoring differential  
CC expression of genes in a first filamentous fungal (FF) cell relative to  
CC expression of the same genes in one or more second filamentous fungal  
CC cells. The method uses fluorescence-labeled nucleic acids isolated from  
CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs  
CC are used in the methods for monitoring differential expression of genes  
CC in a first filamentous fungal (FF) cell relative to expression of the  
CC same genes in one or more second filamentous fungal cells. Monitoring  
CC the global expression of genes from FF cells allows the production  
CC potential of the microorganisms to be improved. New genes may be  
CC discovered, possible functions of unknown open reading frames can be  
CC identified and gene copy number variation and stability can be  
CC monitored. The expression of genes can be used to study how FF cells  
CC adapt to changes in culture conditions, environmental stress, spore  
CC morphogenesis, recombination, metabolic or catabolic pathway  
CC engineering. Using ESTs provides several advantages over genomic or  
CC random cDNA clones including elimination of redundancy as one spot on an  
CC array equals one gene or open reading frame, and organisation of the  
CC microarrays based on function of the gene products to facilitate  
CC analysis of the results. AAF07478 to AAF11247 represents ESTs from  
CC Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus  
CC niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and  
CC AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are  
CC all specifically claimed in the present invention.  
XX  
SQ Sequence 570 BP; 153 A; 136 C; 113 G; 166 T; 2 other;

Query Match 90.2%; Score 37; DB 21; Length 570;  
Best Local Similarity 92.7%; Pred. No. 7.4e-05;  
Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DCCCCGAAGGCGATTGTTTATCTAATAATACACCC 41  
:|||||  
DB 328 GCCCGAAGGCGATTGTTTATCTAATAATACATCCC 368

RESULT 7  
AAF10913/c  
ID AAF10913 standard; cDNA: 617 BP.  
XX  
AC AAF10913;  
XX  
DT 13-MAR-2001 (first entry)  
XX  
DE Fusarium venenatum EST SEQ ID NO:3436.  
XX  
KM Multiple gene expression; filamentous fungal cell; EST;  
KM expressed sequence tag; Fusarium venenatum; Aspergillus niger;  
KM Aspergillus oryzae; Trichoderma reesei; identification; recombination;  
KM culture condition; environmental stress; spore morphogenesis;  
KM metabolic pathway engineering; catabolic pathway engineering; ss.  
XX  
OS Fusarium venenatum.  
XX  
PN MO200056762-A2.  
XX  
PD 28-SEP-2000.  
XX  
PF 22-MAR-2000; 2000MO-US07781.  
XX  
PR 22-MAR-1999; 99US-0273623.  
XX  
PA (NOVO ) NOVO NORDISK BIOTECH INC.  
PA (NOVO ) NOVO NORDISK AS.

XX Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;  
PI WPI: 2000-594572/56.  
XX  
DR  
XX  
PT Monitoring differential expression of genes in filamentous fungal cells  
PT uses fluorescence-labeled nucleic acids isolated from the cells and a  
PT substrate of expressed sequence tags -  
XX  
PS Claim 86; Page 1589; 3161pp; English.  
XX  
CC The present invention describes a method for monitoring differential  
CC expression of genes in a first filamentous fungal (FF) cell relative to  
CC expression of the same genes in one or more second filamentous fungal  
CC cells. The method uses fluorescence-labeled nucleic acids isolated from  
CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs  
CC are used in the methods for monitoring differential expression of genes  
CC in a first filamentous fungal (FF) cell relative to expression of the  
CC same genes in one or more second filamentous fungal cells. Monitoring  
CC the global expression of genes from FF cells allows the production  
CC potential of the microorganisms to be improved. New genes may be  
CC discovered, possible functions of unknown open reading frames can be  
CC identified and gene copy number variation and stability can be  
CC monitored. The expression of genes can be used to study how FF cells  
CC adapt to changes in culture conditions, environmental stress, spore  
CC morphogenesis, recombination, metabolic or catabolic pathway  
CC engineering. Using ESTs provides several advantages over genomic or  
CC random cDNA clones including elimination of redundancy as one spot on an  
CC array equals one gene or open reading frame, and organisation of the  
CC microarrays based on function of the gene products to facilitate  
CC analysis of the results. AAF07478 to AAF11247 represents ESTs from  
CC Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus  
CC niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and  
CC AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are  
CC all specifically claimed in the present invention.  
XX  
SQ Sequence 617 BP; 155 A; 139 C; 140 G; 171 T; 12 other;

Query Match 90.2%; Score 37; DB 21; Length 617;  
Best Local Similarity 92.7%; Pred. No. 7.5e-05;  
Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DCCCCGAAGGCGATTGTTTATCTAATAATACACCC 41  
:|||||  
DB 219 GCCCGAAGGCGATTGTTTATCTAATAATACATCCC 179

RESULT 8  
ABA01152/c  
ID ABA01152 standard; DNA: 1745 BP.  
XX  
AC ABA01152;  
XX  
DT 24-JAN-2002 (first entry)  
XX  
DE Deuteromycetes polynucleotide SEQ ID 1.  
XX  
KM Aldonic acid; ds.  
KM Deuteromycetes sp.  
XX  
OS JP2001245657-A.  
XX  
PN 11-SEP-2001.  
XX  
PD 26-DEC-2000; 2000JP-0394766.  
XX  
PF 27-DEC-1999; 99JP-0369714.  
XX  
PR (TAKE-) TAKEHARA KAGAKU KOGYO KK.  
XX (OSAO ) OSAKA CITY.  
XX  
PA WPI: 2002-002933/01.  
DR

XX A new microbe for producing aldonic acid, comprises a new strain of  
 PT Acinetobacter or Burkholderis -  
 XX  
 PS Disclosure; Page 17; 22pp; Japanese.  
 CC The present invention relates to a new microbe of Acinetobacter or  
 CC Burkholderis genus producing aldonic acid and oxidizing specifically the  
 CC hemiacetal hydroxy group of a saccharide having said hydroxy group.  
 CC Aldonic acid is used as a mineral reinforcing agent. The present sequence  
 CC was used to illustrate the present invention.  
 XX  
 SQ Sequence 1745 BP; 448 A; 382 C; 465 G; 450 T; 0 other;  
 Query Match 90.2%; Score 37; DB 24; Length 1745;  
 Best Local Similarity 92.7%; Pred. No. 8.4e-05;  
 Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 OY 1 DCCCGAAGGCGATGTTTATCTAATAAATACACCCC 41  
 DB 211 GCCCGAAGGCGATGTTTATCTAATAAATACACCCC 171  
 RESULT 9  
 ID AAS16211/c  
 AC AAS16211; standard; DNA; 2293 BP.  
 XX  
 XX 29-JAN-2002 (first entry)  
 DE Fungus genomic DNA spanning 18S, 5.8S and 28S rRNA and ITS sequences.  
 XX  
 KM Gibberellin; 18S rRNA; internal transcribed spacer region; ITS1;  
 KM ITS2; 5.8S rRNA; LTB-1027; species differentiation; GA\_4; GA\_3; GA\_7;  
 KM flowering; fruit cell elongation; apple; pear; grape; fruit;  
 KM russet control; fungus; ds.  
 XX  
 OS Gibberella fujikuroi.  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_feature 1..1774  
 FT /\*tag= a  
 FT /note= "18S rRNA gene"  
 FT 1775..1921  
 FT /\*tag= b  
 FT /note= "ITS1 region"  
 FT 1922..2078  
 FT /\*tag= c  
 FT /note= "5.8S rRNA gene"  
 FT 2079..2243  
 FT /\*tag= d  
 FT /note= "ITS2 region"  
 FT 2244..2293  
 FT /\*tag= e  
 FT /note= "28S rRNA gene"  
 XX  
 XX US6287800-B1.  
 XX  
 PD 11-SEP-2001.  
 XX  
 XX 23-AUG-2000; 2000US-0645073.  
 PF  
 XX 31-AUG-1999; 99US-151770P.  
 PR  
 XX (GALL/) GALLAZZO J L.  
 PA (LEEM/) LEE M D.  
 XX  
 XX Gallazzo JL, Lee MD;  
 PI  
 XX WPI; 2001-662197/76.  
 DR  
 XX A new method for producing a mixture of gibberellins from Gibberella  
 PT

PT fujikuroi results in high titers of GA4 and GA7 useful to promote  
 PT flowering and fruit growth in the fruit growing industry -  
 XX  
 PS Example 4; Column 9-12; 7pp; English.  
 CC This sequence represents a genomic DNA sequence containing the 18S rRNA  
 CC gene, internal transcribed spacer regions 1 and 2 (ITS1, ITS2) and 5.8S  
 CC rRNA sequences from a mutant strain of Gibberella fujikuroi (LTB-1027)  
 CC of the invention. This region of DNA is highly variable and can be used  
 CC for species and strain differentiation. The LTB-1027 mutant produces a  
 CC mixture of gibberellins which is at least 70 % GA<sub>4</sub> and GA<sub>7</sub>.  
 CC Gibberellins GA<sub>4</sub> and GA<sub>7</sub> promote flowering and fruit cell elongation,  
 CC and are used by growers of apples, pears and grapes to produce larger  
 CC fruits and earlier harvests. The mixture of GA<sub>3</sub>, GA<sub>4</sub> and GA<sub>7</sub> achieved  
 CC using the method of this invention should be particularly useful in the  
 CC apple industry where GA<sub>4</sub> has been found to be particularly useful in the  
 CC control and in promoting fruit set. This method produces GA<sub>4</sub> and GA<sub>7</sub>  
 CC in much higher titers than prior art methods.  
 XX  
 SQ Sequence 2293 BP; 596 A; 527 C; 592 G; 578 T; 0 other;  
 Query Match 90.2%; Score 37; DB 23; Length 2293;  
 Best Local Similarity 92.7%; Pred. No. 8.7e-05;  
 Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 OY 1 DCCCGAAGGCGATGTTTATCTAATAAATACACCCC 41  
 DB 211 GCCCGAAGGCGATGTTTATCTAATAAATACACCCC 171  
 RESULT 10  
 ID AAV61668/c  
 AC AAV61668; standard; DNA; 1771 BP.  
 XX  
 XX 03-DEC-1998 (first entry)  
 DE Fusarium oxysporum f.sp. fragaria 18S rRNA DNA fragment.  
 XX  
 KM 18S rRNA; detection; identification; fungus; ss.  
 XX  
 OS Fusarium oxysporum.  
 XX  
 PN JP10234380-A.  
 XX  
 PD 08-SEP-1998.  
 XX  
 PF 28-FEB-1997; 97JP-0062104.  
 XX  
 PR 28-FEB-1997; 97JP-0062104.  
 XX  
 PA (SHIN-) SHINKINRUI KINO KAIHATSU KENKYUSHO KK.  
 XX  
 XX WPI; 1998-535034/46.  
 DR  
 XX Use of oligo:nucleotide for detecting and identification of fungus  
 PT of Fusarium genus - as primer or probe to detect of identify  
 PT microbes rapidly and exactly  
 XX  
 PS Example 1; Page 7-8; 20pp; Japanese.  
 XX  
 XX This DNA sequence encodes a fragment of a Fusarium oxysporum f.sp.  
 CC fragaria 18S rRNA gene which is used in a method for the detection  
 CC and identification of a fungus of Fusarium genus. The process can be  
 CC used to detect or identify microbes rapidly and exactly.  
 XX  
 SQ Sequence 1771 BP; 438 A; 377 C; 477 G; 461 T; 18 other;  
 Query Match 87.3%; Score 35.8; DB 19; Length 1771;  
 Best Local Similarity 94.9%; Pred. No. 0.00024;  
 Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 OY 1 DCCCGAAGGCGATGTTTATCTAATAAATACACCCC 41  
 DB 211 GCCCGAAGGCGATGTTTATCTAATAAATACACCCC 171



QY 5 CGAAGGCATTGTTTATCTAATAATACACCCC 41  
 DB 231 CGAAGGCATTGTTTATCTAATAATACACCCC 195

## RESULT 14

AAFI1316/c  
 ID AAF11316 standard; CDNA; 1024 BP.

AAFI1316;

DT 13-MAR-2001 (first entry)

DE Aspergillus niger EST SEQ ID NO:3839.

XX Multiple gene expression; filamentous fungal cell; EST;

KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;

KW Aspergillus oryzae; Trichoderma reesei; Identification; recombination;

KW culture condition; environmental stress; spore morphogenesis;

KW metabolic pathway engineering; catabolic pathway engineering; ss.

XX Aspergillus niger.

XX WO200056762-A2.

XX 28-SEP-2000.

XX 22-MAR-2000; 2000WO-US07781.

XX 22-MAR-1999; 99US-0273623.

XX (NOVO ) NOVO NORDISK BIOTECH INC.

XX (NOVO ) NOVO NORDISK AS.

XX Berka RM, Rey WM, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;

XX WPI, 2000-594572/56.

PT Monitoring differential expression of genes in filamentous fungal cells  
 PT uses fluorescence-labeled nucleic acids isolated from the cells and a  
 PT substrate of expressed sequence tags -

PS Claim 87; Page 1718; 3161pp; English.

CC The present invention describes a method for monitoring differential  
 CC expression of genes in a first filamentous fungal (FF) cell relative to  
 CC expression of the same genes in one or more second filamentous fungal  
 CC cells. The method uses fluorescence-labeled nucleic acids isolated from  
 CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs  
 CC are used in the methods for monitoring differential expression of genes  
 CC in a first filamentous fungal (FF) cell relative to expression of the  
 CC same genes in one or more second filamentous fungal cells. Monitoring  
 CC the global expression of genes from FF cells allows the production  
 CC potential of the microorganisms to be improved. New genes may be  
 CC discovered, possible functions of unknown open reading frames can be  
 CC identified and gene copy number variation and stability can be  
 CC monitored. The expression of genes can be used to study how FF cells  
 CC adapt to changes in culture conditions, environmental stress, spore  
 CC morphogenesis, recombination, metabolic or catabolic pathway  
 CC engineering. Using ESTs provides several advantages over genomic or  
 CC random cDNA clones including elimination of redundancy as one spot on an  
 CC array equals one gene or open reading frame, and organisation of the  
 CC microarrays based on function of the gene products to facilitate  
 CC analysis of the results. AAF04478 to AAF11247 represents ESTs from  
 CC Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus  
 CC niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and  
 CC AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are  
 CC all specifically claimed in the present invention.

SO Sequence 1024 BP; 275 A; 204 C; 275 G; 269 T; 1 other;

Query Match 71.2%; Score 29.2; DB 21; Length 1024;

Best Local Similarity 96.7%; Pred No. 0.08;  
 Matches 29; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCGAAGGCATTGTTTATCTAATAAT 30  
 DB 30 GCCCGAAGGCATTGTTTATCTAATAAT 1

## RESULT 15

AAO71867/c  
 ID AAO71867 standard; DNA; 447 BP.

AAO71867;

DT 23-MAR-1995 (first entry)

DE G. vesiculiferum small ribosomal subunit RNA.

XX Nuclear 18S ribosomal gene; SSU; probe; primer;

KW arbuscular endomycorrhizal fungi; plant; root; ds.

XX Glomus vesiculiferum.

XX CA2086136-A.

XX 24-JUN-1994.

XX 23-DEC-1992; 92CA-2086136.

XX 23-DEC-1992; 92CA-2086136.

XX (SIMO/) SIMON L.

XX Lalonde M, Simon L;

XX WPI; 1994-264577/33.

PT New oligonucleotide probes - used for the detection of arbuscular  
 PT endomycorrhizal fungi in plant root samples

PS Disclosure; Page 18; 40pp; English.

CC The gene sequence of the small ribosomal subunit RNA of arbuscular  
 CC endomycorrhizal fungi obtained from Glomus vesiculiferum, Glomus  
 CC intraradices and Gigaspora margarita were compared with that of a  
 CC non-arbuscular endomycorrhizal fungus, Endogone pisiformis,  
 CC in order to design taxon specific primers/probes.

SO Sequence 447 BP; 135 A; 86 C; 107 G; 118 T; 1 other;

Query Match 70.7%; Score 29; DB 15; Length 447;  
 Best Local Similarity 100.0%; Pred. No. 0.087;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 ATTGGTTTTTATCTAATAATACACCCC 41  
 DB 116 ATTGGTTTTTATCTAATAATACACCCC 88

Search completed: June 12, 2003, 01:44:09  
 Job time : 210.995 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 01:18:34 ; Search time 39.335 Seconds  
(without alignments)  
319,658 Million cell updates/sec

Title: US-09-674-195C-16

Perfect score: 41  
Sequence: 1 dccccgaaggcattggtt.....ttatctaataacaccccc 41

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_NA:\*  
1: /cgn2\_6/prodata/1/lna/5A.COMB.seq:\*  
2: /cgn2\_6/prodata/1/lna/5B.COMB.seq:\*  
3: /cgn2\_6/prodata/1/lna/6A.COMB.seq:\*  
4: /cgn2\_6/prodata/1/lna/6B.COMB.seq:\*  
5: /cgn2\_6/prodata/1/lna/PCFUS.COMB.seq:\*  
6: /cgn2\_6/prodata/1/lna/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	97.6	40	1	US-07-720-587A-3
2	37	90.2	2293	4	US-09-645-073-1
3	30	73.2	1788	2	US-08-867-820A-1
4	29	70.7	439	1	US-08-093-144-3
5	29	70.7	446	1	US-08-093-144-4
6	26.8	65.4	444	1	US-08-093-144-6
7	26.2	63.9	1750	3	US-08-949-170-1
8	26	63.4	703	4	US-08-998-416-178
9	26	63.4	709	4	US-08-998-416-281
10	26	63.4	723	4	US-08-998-416-952
11	25.8	62.9	1744	1	US-07-879-647A-25
12	25.8	62.9	1744	1	US-07-879-584A-25
13	25.8	62.9	1744	1	US-07-879-470A-25
14	25.8	62.9	1744	1	US-07-879-644A-25
15	25.8	62.9	1744	1	US-07-879-640A-25
16	25.8	62.9	1744	1	US-07-879-594A-25
17	25.8	62.9	1744	1	US-07-879-469A-25
18	25.8	62.9	1747	4	US-09-015-259-1
19	25.8	62.9	1747	4	US-09-015-259-2
20	25.8	62.9	1756	1	US-07-879-647A-28
21	25.8	62.9	1756	1	US-07-879-647A-30
22	25.8	62.9	1756	1	US-07-879-584A-28
23	25.8	62.9	1756	1	US-07-879-584A-30
24	25.8	62.9	1756	1	US-07-879-470A-28
25	25.8	62.9	1756	1	US-07-879-470A-30
26	25.8	62.9	1756	1	US-07-879-644A-28
27	25.8	62.9	1756	1	US-07-879-644A-30

C 28	25.8	62.9	1756	1	US-07-879-640A-28	Sequence 28, Appl
C 29	25.8	62.9	1756	1	US-07-879-640A-30	Sequence 30, Appl
C 30	25.8	62.9	1756	1	US-07-879-594A-28	Sequence 28, Appl
C 31	25.8	62.9	1756	1	US-07-879-594A-30	Sequence 30, Appl
C 32	25.8	62.9	1756	1	US-07-879-469A-28	Sequence 28, Appl
C 33	25.8	62.9	1756	1	US-07-879-469A-30	Sequence 30, Appl
C 34	25.6	62.4	1747	1	US-07-879-647A-29	Sequence 29, Appl
C 35	25.6	62.4	1747	1	US-07-879-647A-29	Sequence 29, Appl
C 36	25.6	62.4	1747	1	US-07-879-647A-29	Sequence 29, Appl
C 37	25.6	62.4	1747	1	US-07-879-647A-29	Sequence 29, Appl
C 38	25.6	62.4	1747	1	US-07-879-647A-29	Sequence 29, Appl
C 39	25.6	62.4	1747	1	US-07-879-647A-29	Sequence 29, Appl
C 40	25.6	62.4	1747	1	US-07-879-647A-29	Sequence 29, Appl
C 41	24.6	60.0	1748	1	US-07-879-647A-24	Sequence 24, Appl
C 42	24.6	60.0	1748	1	US-07-879-647A-24	Sequence 24, Appl
C 43	24.6	60.0	1748	1	US-07-879-647A-24	Sequence 24, Appl
C 44	24.6	60.0	1748	1	US-07-879-647A-24	Sequence 24, Appl
C 45	24.6	60.0	1748	1	US-07-879-647A-24	Sequence 24, Appl

#### ALIGNMENTS

RESULT 1  
US-07-720-587A-3  
Sequence 3, Application US/07720587A  
Patent No. 5352579

#### GENERAL INFORMATION:

APPLICANT: Curt L. Millman  
TITLE OF INVENTION: NUCLEIC ACIDS PROBES  
TITLE OF INVENTION: TO HISTOPLASMA CAPSULATUM  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017

#### COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM PS/2 Model 502 or 555X  
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
SOFTWARE: WordPerfect (Version 5.0)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07720,587A  
FILING DATE: 19910628

#### CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: Including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER:  
FILING DATE:

#### ATTORNEY/AGENT INFORMATION:

NAME: Walburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 193/121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

#### INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:  
LENGTH: 40  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-07-720-587A-3

Query Match 97.6%; Score 40; DB 1; Length 40;  
Best Local Similarity 100.0%; Pred. No. 1.4e-06;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CCCCCGAGGCGATGTTTTTATCTAATAATACACCCC 41  
|||||  
DB 1 CCCCCGAGGCGATGTTTTTATCTAATAATACACCCC 40

RESULT 2  
US-09-645-073-1/c  
Sequence 1, Application US/09645073  
Patent No. 6287800  
GENERAL INFORMATION:  
APPLICANT: Lee, May  
APPLICANT: Galazzo, Jorge  
TITLE OF INVENTION: Production of High Titers of Gibberellins GA4 and GA7  
FILE REFERENCE: L02-01MP  
CURRENT APPLICATION NUMBER: US/09/645,073  
CURRENT FILING DATE: 2000-08-25  
PRIOR APPLICATION NUMBER: US 60/151,770  
PRIOR FILING DATE: 1999-08-31  
NUMBER OF SEQ ID NOS: 1  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 1  
LENGTH: 2293  
TYPE: DNA  
ORGANISM: Gibberella fujikuroi  
US-09-645-073-1

Query Match 90.2%; Score 37; DB 4; Length 2293;  
Best Local Similarity 92.7%; Pred. No. 2.8e-05;  
Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DCCCCGAGGCGATGTTTTTATCTAATAATACACCCC 41  
|||||  
DB 211 CCCCCGAGGCGATGTTTTTATCTAATAATACACCCC 171

RESULT 3  
US-08-867-820A-1/c  
Sequence 1, Application US/08867820A  
Patent No. 5891685  
GENERAL INFORMATION:  
APPLICANT: YAMAGISHI Masahiro  
APPLICANT: TAKAI Yukie  
APPLICANT: MIKAWA Takashi  
APPLICANT: HARA Mari  
APPLICANT: UEDA Makoto  
APPLICANT: OHARA Akiko  
TITLE OF INVENTION: METHOD FOR PRODUCING ESTER OF (S)-HALOGENATED--HYDROXYBUTY  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: WENDEROFF, LIND & POMACK, L.L.P.  
STREET: 2033 K Street, N.W., Suite 800  
CITY: Washington, D.C.  
COUNTRY: USA  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/867,820A  
FILING DATE: June 3, 1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee Cheng  
REGISTRATION NUMBER: 40,949  
REFERENCE/DOCKET NUMBER: 1416/OP574US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1788 base pairs

TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
ORIGINAL SOURCE:  
ORGANISM: Candida albicans  
STRAIN: MUGL29800  
US-08-867-820A-1

Query Match 73.2%; Score 30; DB 2; Length 1788;  
Best Local Similarity 86.8%; Pred. No. 0.011;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 4 CCGAGGCGATGTTTTTATCTAATAATACACCCC 41  
|||||  
DB 234 CCGAGGCGATGTTTTTATCTAATAATACACCCC 197

RESULT 4  
US-08-093-144-3/c  
Sequence 3, Application US/08093144  
Patent No. 5434048  
GENERAL INFORMATION:  
APPLICANT: SIMON, LUC  
APPLICANT: LALONDE, MAURICE  
TITLE OF INVENTION: DNA PROBES FOR THE DETECTION OF  
TITLE OF INVENTION: ARBUSCULAR ENDOMYCORRHIZAL FUNGI  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN  
STREET: Eleventh Floor, 1615 L. Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20036-5601

COMPUTER READABLE FORM:  
MEDIUM TYPE: Tape  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/093,144  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,192  
FILING DATE: 15-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Hymo, Lawrence A.  
REGISTRATION NUMBER: 19,057  
REFERENCE/DOCKET NUMBER: LAH/3122/92223/MJW  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
TELEX: 6714627 CUSH

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 439 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-093-144-3

Query Match 70.7%; Score 29; DB 1; Length 439;  
Best Local Similarity 100.0%; Pred. No. 0.021;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 ATGGTTTTTATCTAATAATACACCCC 41  
|||||  
DB 114 ATGGTTTTTATCTAATAATACACCCC 86

RESULT 5

US-08-093-144-4/c  
; Sequence 4, Application US/08093144  
; Patent No. 5434048  
; GENERAL INFORMATION:  
; APPLICANT: SIMON, LUC  
; APPLICANT: LALONDE, MAURICE  
; TITLE OF INVENTION: DNA PROBES FOR THE DETECTION OF  
; TITLE OF INVENTION: ARBUSCULAR ENDOMYCORRHIZAL FUNGI  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN  
; STREET: Eleventh Floor, 1615 L. Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20036-5601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Tape  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/093,144  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/745,192  
; FILING DATE: 15-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hymo, Lawrence A.  
; REGISTRATION NUMBER: 19,057  
; REFERENCE/DOCKET NUMBER: LAH/3122/92223/MJW  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3000  
; TELEFAX: (202) 822-0944  
; TELEX: 6714627 CUSH  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 446 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; US-08-093-144-4  
Query Match 70.7%; Score 29; DB 1; Length 446;  
Best Local Similarity 100.0%; Pred. No. 0.021;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 13 ATTGGTTTATCTAATAATACACCCC 41  
DB 116 ATTGGTTTATCTAATAATACACCCC 88  
RESULT 6  
US-08-093-144-6/c  
; Sequence 6, Application US/08093144  
; Patent No. 5434048  
; GENERAL INFORMATION:  
; APPLICANT: SIMON, LUC  
; APPLICANT: LALONDE, MAURICE  
; TITLE OF INVENTION: DNA PROBES FOR THE DETECTION OF  
; TITLE OF INVENTION: ARBUSCULAR ENDOMYCORRHIZAL FUNGI  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN  
; STREET: Eleventh Floor, 1615 L. Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20036-5601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Tape  
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/093,144  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,192  
FILING DATE: 15-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Hymo, Lawrence A.  
REGISTRATION NUMBER: 19,057  
REFERENCE/DOCKET NUMBER: LAH/3122/92223/MJW  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
TELEX: 6714627 CUSH  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-093-144-6  
Query Match 65.4%; Score 26.8; DB 1; Length 444;  
Best Local Similarity 93.3%; Pred. No. 0.14;  
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 12 CATTGGTTTATCTAATAATACACCCC 41  
DB 117 CGTGGTTTATCTAATAATACACCCC 88  
RESULT 7  
US-08-949-770-1/c  
; Sequence 1, Application US/08949770  
; Patent No. 6063604  
; GENERAL INFORMATION:  
; APPLICANT: Wick, James F.  
; APPLICANT: Mueller, Reinhold  
; APPLICANT: Blassak, Michele  
; APPLICANT: Wilkosz, Richard K.  
; TITLE OF INVENTION: Target Nucleic Acid Sequence Amplification  
; PATENT NO. 6063604  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/949,770  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/617,045  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pochopien, Donald J.  
; REGISTRATION NUMBER: 32,167  
; REFERENCE/DOCKET NUMBER: 28003/33045  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856

```

: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1750 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: /- "18s rRNA gene of Cryptosporidium
: OTHER INFORMATION: parvum"
: US-08-949-770-1
:
: Query Match          63.9%; Score 26.2; DB 3; Length 1750;
: Best Local Similarity 79.5%; Pred. No. 0.27;
: Matches 31; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
:
: QY      3 CCGGAGGCGATGGTTTATCTAATAATACACCCC 41
: DB      235 CACCAATATATGTGTTCTTATCTAATAATACACCCC 197
:
: RESULT 8
: US-08-998-416-178
: Sequence 178, Application US/08998416
: Patent No. 6239264
: GENERAL INFORMATION:
: APPLICANT: Philippsen, Peter
: APPLICANT: Pohlmann, Rainer
: APPLICANT: Steiner, Sabine
: APPLICANT: Mohr, Christlne
: APPLICANT: Wendland, Jurgen
: APPLICANT: Knechtel, Philipp
: APPLICANT: Reibschung, Corinne
: TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSEYII
: TITLE OF INVENTION: AND USES THEREOF
: NUMBER OF SEQUENCES: 1152
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 6239264artis Corporation
: STREET: 3054 Cornwallis Road
: CITY: Research Triangle Park
: STATE: No. 6239264th Carolina
: COUNTRY: USA
: ZIP: 27709
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/998,416
: FILING DATE: 24-DEC-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: CH 0016/97
: FILING DATE: 31-DEC-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Meigs, J. Timothy
: REGISTRATION NUMBER: 38,241
: REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 919-541-8587
: TELEFAX: 919-541-8689
: INFORMATION FOR SEQ ID NO: 178:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 703 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: ORIGINAL SOURCE:
: ORGANISM: PAG1070RP
: US-08-998-416-178
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: Query Match          63.4%; Score 26; DB 4; Length 703;
: Best Local Similarity 85.3%; Pred. No. 0.29;
: Matches 29; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
:
: QY      8 AGGCGATGGTTTATCTAATAATACACCCC 41
: DB      450 AAGACATGATTTTATCTAATAATACATCTC 483
:
: RESULT 9
: US-08-998-416-281
: Sequence 281, Application US/08998416
: Patent No. 6239264
: GENERAL INFORMATION:
: APPLICANT: Philippsen, Peter
: APPLICANT: Pohlmann, Rainer
: APPLICANT: Steiner, Sabine
: APPLICANT: Mohr, Christlne
: APPLICANT: Wendland, Jurgen
: APPLICANT: Knechtel, Philipp
: APPLICANT: Reibschung, Corinne
: TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSEYII
: TITLE OF INVENTION: AND USES THEREOF
: NUMBER OF SEQUENCES: 1152
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 6239264artis Corporation
: STREET: 3054 Cornwallis Road
: CITY: Research Triangle Park
: STATE: No. 6239264th Carolina
: COUNTRY: USA
: ZIP: 27709
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/998,416
: FILING DATE: 24-DEC-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: CH 0016/97
: FILING DATE: 31-DEC-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Meigs, J. Timothy
: REGISTRATION NUMBER: 38,241
: REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 919-541-8587
: TELEFAX: 919-541-8689
: INFORMATION FOR SEQ ID NO: 281:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 709 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: ORIGINAL SOURCE:
: ORGANISM: PAG1237UP
: US-08-998-416-281
:
: Query Match          63.4%; Score 26; DB 4; Length 709;
: Best Local Similarity 85.3%; Pred. No. 0.29;
: Matches 29; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
:
: QY      8 AGGCGATGGTTTATCTAATAATACACCCC 41
: DB      451 AAGACATGATTTTATCTAATAATACATCTC 484
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: RESULT 10
: US-08-998-416-952
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Sequence 952, Application US/08998416  
Patent No. 6239264  
GENERAL INFORMATION:  
APPLICANT: Philippsen, Peter  
APPLICANT: Pohlmann, Rainer  
APPLICANT: Steiner, Sabine  
APPLICANT: Mohr, Christine  
APPLICANT: Wendland, Jürgen  
APPLICANT: Knechtel, Philipp  
APPLICANT: Reibischung, Corinne  
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPPII  
TITLE OF INVENTION: AND USES THEREOF  
NUMBER OF SEQUENCES: 1152  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6239264artis Corporation  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: No. 6239264th Carolina  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/998,416  
FILING DATE: 24-DEC-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: CH 0016/97  
FILING DATE: 31-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Meligs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8587  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 952:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 723 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORGANISM: PAG1588UP  
US-08-998-416-952

Query Match 63.4%; Score 26; DB 4; Length 723;  
Best Local Similarity 85.3%; Pred. No. 0.29;  
Matches 29; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 8 AGGCATGTTTATCTAATAATACACCC 41  
DB 450 AAGACATGATTTTATCTAATAATACATCTC 483

RESULT 11  
US-07-879-647A-25/c  
Sequence 25, Application US/07879647A  
Patent No. 526689  
GENERAL INFORMATION:  
APPLICANT: Chakraborty, P.R.  
APPLICANT: Dashkevich, M.  
APPLICANT: Elbrecht, A.  
APPLICANT: Feighner, S.D.  
APPLICANT: Liberator, P.A.  
APPLICANT: Profous-Juchelka, H.  
TITLE OF INVENTION: Elmeida Maxima DNA  
TITLE OF INVENTION: Probes  
NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: 126 Lincoln Avenue  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07065  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb  
MEDIUM TYPE: storage  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 6.0.4  
SOFTWARE: Microsoft Word 4.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/879,647A  
FILING DATE: 19920512  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/706,628  
FILING DATE: 29-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Tridble, Jack L.  
REGISTRATION NUMBER: 32,633  
REFERENCE/DOCKET NUMBER: 184201A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-5321  
TELEFAX: (908) 594-4720  
TELEX: 138825  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1744 bases  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-07-879-647A-25

Query Match 62.9%; Score 25.8; DB 1; Length 1744;  
Best Local Similarity 75.6%; Pred. No. 0.38;  
Matches 31; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 DCCCGAAGGCATGTTTATCTAATAATACACCC 41  
DB 215 TCCACAGGTGGTGGTTTGTATCTAATAAACACAGCCC 175

RESULT 12  
US-07-879-584A-25/c  
Sequence 25, Application US/07879584A  
Patent No. 5278298  
GENERAL INFORMATION:  
APPLICANT: Chakraborty, P.R.  
APPLICANT: Dashkevich, M.  
APPLICANT: Elbrecht, A.  
APPLICANT: Feighner, S.D.  
APPLICANT: Liberator, P.A.  
APPLICANT: Profous-Juchelka, H.  
TITLE OF INVENTION: Elmeida Brunetti DNA  
TITLE OF INVENTION: Probes  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: 126 Lincoln Avenue  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07065  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb  
MEDIUM TYPE: storage  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 6.0.4  
SOFTWARE: Microsoft Word 4.0  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/879,584A  
FILING DATE: 19920512  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/706,717  
FILING DATE: 29-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Tribble, Jack L.  
REGISTRATION NUMBER: 32,633  
REFERENCE/DOCKET NUMBER: .184191A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-5321  
TELEFAX: (908) 594-4720  
TELEX: 138825  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1744 bases  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-07-879-584A-25

Query Match 62.9%; Score 25.8; DB 1; Length 1744;  
Best Local Similarity 75.6%; Pred. No. 0.38;  
Matches 31; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 DCCCCAAGGCGATGTTTATCTAATAATACACCCC 41  
DB 215 TCACAAAGTGCGTGTGTTTATCTAATAATACACACCCC 175

RESULT 13  
US-07-879-470A-25/c  
Sequence 25, Application US/07879470A  
Patent No. 5286845  
GENERAL INFORMATION:  
APPLICANT: Chakraborty, P.R.  
APPLICANT: Dashkevicz, M.  
APPLICANT: Elbrecht, A.  
APPLICANT: Feigener, S.D.  
APPLICANT: Liberator, P.A.  
APPLICANT: Profous-Juchelka, H.  
TITLE OF INVENTION: Elmeria Necatrix DNA  
TITLE OF INVENTION: Probes  
NUMBER OF SEQUENCES: 50  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/879,470A  
FILING DATE: 19920512  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/706,351  
FILING DATE: 29-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Tribble, Jack L.  
REGISTRATION NUMBER: 32,633  
REFERENCE/DOCKET NUMBER: .184221A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-5321  
TELEFAX: (908) 594-4720  
TELEX: 138825

INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1744 bases  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-07-879-470A-25

Query Match 62.9%; Score 25.8; DB 1; Length 1744;  
Best Local Similarity 75.6%; Pred. No. 0.38;  
Matches 31; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 DCCCCAAGGCGATGTTTATCTAATAATACACCCC 41  
DB 215 TCACAAAGTGCGTGTGTTTATCTAATAATACACACCCC 175

RESULT 14  
US-07-879-644A-25/c  
Sequence 25, Application US/07879644A  
Patent No. 5298613  
GENERAL INFORMATION:

APPLICANT: Chakraborty, P.R.  
APPLICANT: Dashkevicz, M.  
APPLICANT: Elbrecht, A.  
APPLICANT: Feigener, S.D.  
APPLICANT: Liberator, P.A.  
APPLICANT: Profous-Juchelka, H.  
TITLE OF INVENTION: Elmeria Acetivulina DNA  
TITLE OF INVENTION: Probes  
NUMBER OF SEQUENCES: 50  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/879,644A  
FILING DATE: 19920512  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/706,817  
FILING DATE: 29-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Tribble, Jack L.  
REGISTRATION NUMBER: 32,633  
REFERENCE/DOCKET NUMBER: .184181A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-5321  
TELEFAX: (908) 594-4720  
TELEX: 138825  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1744 bases  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-07-879-644A-25

Query Match 62.9%; Score 25.8; DB 1; Length 1744;  
Best Local Similarity 75.6%; Pred. No. 0.38;  
Matches 31; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 DCCCCAAGGCGATGTTTATCTAATAATACACCCC 41  
DB 215 TCACAAAGTGCGTGTGTTTATCTAATAATACACACCCC 175

Query Match 62.9%; Score 25.8; DB 1; Length 1744;  
Best Local Similarity 75.6%; Pred. No. 0.38;  
Matches 31; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

DB 215 TCACACAGGTGGTTGGTTTGTATCTAATAAACAACAGCCC 175

RESULT 15

US-07-879-640A-25/C  
Sequence 25, Application US/07879640A  
Patent No. 5359050

GENERAL INFORMATION:

APPLICANT: Chakraborty, P.R.  
APPLICANT: Dashkevicz, M.  
APPLICANT: Elbrecht, A.  
APPLICANT: Feighner, S.D.  
APPLICANT: Liberator, P.A.  
APPLICANT: Profous-Juchelka, H.  
TITLE OF INVENTION: Elmeria Mils DNA  
TITLE OF INVENTION: Probes  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: 126 Lincoln Avenue  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07065

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 800 KB  
MEDIUM TYPE: Storage  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 6.0.4  
SOFTWARE: Microsoft Word 4.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/879,640A  
FILING DATE: 19920512  
CLASSIFICATION: 336  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/706,355  
FILING DATE: 29-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Tribble, Jack L.  
REGISTRATION NUMBER: 32,633  
REFERENCE/DOCKET NUMBER: .184211A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-5321  
TELEFAX: (908) 594-4720  
TELEX: 138825  
INFORMATION FOR SEQ. ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1744 bases  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-07-879-640A-25

Query Match

Best Local Similarity 62.9%; Score 25.8; DB 1; Length 1744;  
Pred. No. 0.38;  
Matches 31; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 DCCCCAGGCGATGGTTTATCTAATAAATACACCC 41  
DB 215 TCACACAGGTGGTTGGTTTGTATCTAATAAACAACAGCCC 175

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Job time : 40.335 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 01:27:04 ; Search time 239.548 Seconds  
(without alignments)  
239.539 Million cell updates/sec

Title: US-09-674-195C-16

Perfect score: 41  
Sequence: 1 dccccgaaggcattggtt.....ttatctaataacacccc 41

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Gapop 10.0 , Gapext 1.0

Searched: 870385 segs, 699768693 residues

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008  
Listing first 45 summaries

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Published Applications, NA.\*  
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3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
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13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	23.4	57.1	29	10	US-09-954-695-36
3	23.4	57.1	29	10	US-09-954-695-40
4	23.4	57.1	29	10	US-09-954-695-44
5	23.4	57.1	29	10	US-09-954-586-32
6	23.4	57.1	29	10	US-09-954-586-36
7	23.4	57.1	29	10	US-09-954-586-40
8	23.4	57.1	29	10	US-09-954-586-44
9	21.4	52.2	2499	10	US-09-732-665-4
10	21.4	51.2	1130	9	US-10-167-015-26
11	21.4	51.2	1747	9	US-09-957-995A-1
12	20.6	50.2	300	9	US-09-294-093B-1219
13	20.6	50.2	17276	9	US-09-870-759-83
14	20.4	49.8	23	10	US-09-954-695-31
15	20.4	49.8	23	10	US-09-954-695-35
16	20.4	49.8	23	10	US-09-954-695-39
17	20.4	49.8	23	10	US-09-954-695-43
18	20.4	49.8	23	10	US-09-954-586-31
19	20.4	49.8	23	10	US-09-954-586-35

20	20.4	49.8	23	10	US-09-954-586-39	Sequence 39, Appl
21	20.4	49.8	23	10	US-09-954-586-43	Sequence 43, Appl
22	20.4	49.8	2207	7	US-08-779-460B-9	Sequence 9, Appl1
23	20.4	49.8	173808	12	US-10-003-806-10	Sequence 10, Appl
24	20.4	49.8	1830121	9	US-10-329-960-1	Sequence 1, Appl1
25	20.2	49.3	180	9	US-10-083-357-17	Sequence 17, Appl1
26	20.2	49.3	249	9	US-10-083-357-605	Sequence 605, App
27	20.2	49.3	460	9	US-09-918-995-36295	Sequence 36295, A
28	20.2	49.3	483	9	US-09-918-995-6515	Sequence 6515, App
29	20.2	49.3	943	10	US-09-939-980-34	Sequence 1750, Appl
30	20.2	48.8	430	10	US-09-954-456-1150	Sequence 1750, App
31	20.2	48.8	724	9	US-10-092-154-228	Sequence 228, App
32	20.2	48.8	724	10	US-09-764-847-228	Sequence 228, Appl
33	20.2	48.8	1808	10	US-09-771-935B-17	Sequence 17, Appl
34	20.2	48.8	2000	9	US-09-938-842B-3456	Sequence 3456, App
35	20.2	48.8	2000	10	US-09-887-576-82	Sequence 82, Appl
36	20.2	48.8	3156	9	US-09-974-298-70	Sequence 70, Appl
37	20.2	48.8	3156	9	US-09-919-172-86	Sequence 86, Appl
38	20.2	48.8	3190	9	US-10-270-595-3	Sequence 3, Appl1
39	20.2	48.8	3362	10	US-09-735-705-167	Sequence 167, App
40	20.2	48.8	3362	10	US-09-850-716A-167	Sequence 167, App
41	20.2	48.8	3362	10	US-09-897-778-167	Sequence 167, App
42	20.2	48.8	3951	10	US-09-735-705-160	Sequence 160, App
43	20.2	48.8	3951	10	US-09-850-716A-160	Sequence 160, App
44	20.2	48.8	3951	10	US-09-897-778-160	Sequence 160, App
45	20.2	48.8	14649	9	US-10-239-676-122	Sequence 122, App

#### ALIGNMENTS

RESULT 1  
US-09-954-695-32/c  
; Sequence 32, Application US/09954695  
; Patent No. US20020055116A1  
; GENERAL INFORMATION:  
; APPLICANT: CUNNINGHAM, Melissa M.  
; APPLICANT: STULL, Paul D.  
; APPLICANT: WEISBURG, William G.  
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF  
; TIME OF INVENTION: CRIPSPORIDIUM ORGANISMS IN A TEST SAMPLE  
; FILE REFERENCE: GP116-02-UT  
; CURRENT APPLICATION NUMBER: US/09/954, 695  
; PRIOR FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/232,028  
; NUMBER OF SEQ ID NOS: 69  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 32  
; LENGTH: 29  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-09-954-695-32  
Query Match 57.1%; Score 23.4; DB 10; Length 29;  
Best Local Similarity 96.0%; Pred. No. 14;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 13 ATTGGTTTATCTATATAATACA 37  
DB 26 ATGGTCTTATCTATATAATACA 2  
RESULT 2  
US-09-954-695-36/c  
; Sequence 36, Application US/09954695  
; Patent No. US20020055116A1  
; GENERAL INFORMATION:  
; APPLICANT: CUNNINGHAM, Melissa M.  
; APPLICANT: STULL, Paul D.  
; APPLICANT: WEISBURG, William G.

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; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; FILE REFERENCE: GP116-02.UT
; CURRENT APPLICATION NUMBER: US/09/954,695
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 29
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-695-36

Query Match      57.1%; Score 23.4; DB 10; Length 29;
Best Local Similarity 96.0%; Pred. No. 14;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB      26 ATTGGTCTTATCTAATAAATACA 2

RESULT 3
US-09-954-695-40
; Sequence 40, Application US/09954695
; Patent No. US20020055116A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STOLL, Paul D.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; FILE REFERENCE: GP116-02.UT
; CURRENT APPLICATION NUMBER: US/09/954,695
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-695-40

Query Match      57.1%; Score 23.4; DB 10; Length 29;
Best Local Similarity 96.0%; Pred. No. 14;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      13 ATTGGTTTATCTAATAAATACA 37
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DB      4 ATTGGTCTTATCTAATAAATACA 28

RESULT 4
US-09-954-695-44
; Sequence 44, Application US/09954695
; Patent No. US20020055116A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STOLL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; FILE REFERENCE: GP116-02.UT
; CURRENT APPLICATION NUMBER: US/09/954,695
; CURRENT FILING DATE: 2001-09-11
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; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 29
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-695-44

Query Match      57.1%; Score 23.4; DB 10; Length 29;
Best Local Similarity 52.0%; Pred. No. 14;
Matches 13; Conservative 11; Mismatches 1; Indels 0; Gaps 0;

QY      13 ATTGGTTTATCTAATAAATACA 37
        |::||::|::|::|::|::|::|
DB      4 AUGCUCUUCUUUAUUAUUAUUAUACA 28

RESULT 5
US-09-954-586-32/C
; Sequence 32, Application US/09954586
; Patent No. US20020146717A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STOLL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; FILE REFERENCE: GP116-03.UT
; CURRENT APPLICATION NUMBER: US/09/954,586
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-586-32

Query Match      57.1%; Score 23.4; DB 10; Length 29;
Best Local Similarity 96.0%; Pred. No. 14;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      13 ATTGGTTTATCTAATAAATACA 37
        ||||||| ||||||| ||||||| |||
DB      26 ATTGGTCTTATCTAATAAATACA 2

RESULT 6
US-09-954-586-36/C
; Sequence 36, Application US/09954586
; Patent No. US20020146717A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STOLL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; FILE REFERENCE: GP116-03.UT
; CURRENT APPLICATION NUMBER: US/09/954,586
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
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LENGTH: 29  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Construct  
US-09-954-586-36

Query Match  
Best Local Similarity 57.1%; Score 23.4; DB 10; Length 29;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 13 ATGGTTTCTTACTAATAATACA 37  
Db 26 ATGGTTCTTACTAATAATACA 2

RESULT 7  
US-09-954-586-40  
Sequence 40, Application US/09954586  
Patent No. US20020146717A1  
GENERAL INFORMATION:  
APPLICANT: CONNINGHAM, Melissa M.  
APPLICANT: STULL, Paul D.  
TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF  
FILE REFERENCE: GP116-03.07  
CURRENT APPLICATION NUMBER: US/09/954,586  
PRIOR FILING DATE: 2001-09-11  
PRIOR APPLICATION NUMBER: US 60/232,028  
NUMBER OF SEQ ID NOS: 69  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 40  
LENGTH: 29  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Construct  
US-09-954-586-40

Query Match  
Best Local Similarity 57.1%; Score 23.4; DB 10; Length 29;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 13 ATGGTTTCTTACTAATAATACA 37  
Db 4 ATGGTTCTTACTAATAATACA 28

RESULT 8  
US-09-954-586-44  
Sequence 44, Application US/09954586  
Patent No. US20020146717A1  
GENERAL INFORMATION:  
APPLICANT: CONNINGHAM, Melissa M.  
APPLICANT: STULL, Paul D.  
TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF  
FILE REFERENCE: GP116-03.07  
CURRENT APPLICATION NUMBER: US/09/954,586  
PRIOR FILING DATE: 2001-09-11  
PRIOR APPLICATION NUMBER: US 60/232,028  
NUMBER OF SEQ ID NOS: 69  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 44  
LENGTH: 29  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Construct

US-09-954-586-44

Query Match  
Best Local Similarity 57.1%; Score 23.4; DB 10; Length 29;  
Matches 13; Conservative 11; Mismatches 1; Indels 0; Gaps 0;  
QY 13 ATGGTTTCTTACTAATAATACA 37  
Db 4 AUGGUCUUCUUACUAAUAAUACA 28

RESULT 9  
US-09-732-665-4  
Sequence 4, Application US/09732665  
Patent No. US20010034018A1  
GENERAL INFORMATION:  
APPLICANT: Roche Diagnostics Corporation  
TITLE OF INVENTION: Hepatitis Sentinel Virus I  
FILE REFERENCE: RDID 0069  
CURRENT APPLICATION NUMBER: US/09/732,665  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 4  
LENGTH: 2499  
TYPE: DNA  
ORGANISM: VIRUS  
US-09-732-665-4

Query Match  
Best Local Similarity 52.2%; Score 21.4; DB 10; Length 2499;  
Matches 25; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 8 AGGCGATTGGTTTCTTACTAATAATACAC 38  
Db 1669 AGGCGAAAGTTTCTTACTAATAAACAACAC 1699

RESULT 10  
US-10-167-015-26  
Sequence 26, Application US/10167015  
Publication No. US20030056249A1  
GENERAL INFORMATION:  
APPLICANT: Simmons, Carl R.  
APPLICANT: Gordon-Kamm, William J.  
APPLICANT: Johal, Gurmukh  
APPLICANT: Acevedo, Pedro A. Navarro  
TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use  
FILE REFERENCE: Thereof  
CURRENT APPLICATION NUMBER: US/10/167,015  
PRIOR FILING DATE: 2002-06-11  
PRIOR APPLICATION NUMBER: US 60/297,478  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 26  
LENGTH: 1130  
TYPE: DNA  
ORGANISM: glycine max  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (109)...(837)  
US-10-167-015-26

Query Match  
Best Local Similarity 51.2%; Score 21; DB 9; Length 1130;  
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;  
QY 1 DCCCGAAGGCAGTGGTTTCTTACTAATAATACACCC 41  
Db 182 GCCCGAAGTGGCTGCTTCTTACTAGAAAAGTACTCC 222

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Patent No. US20010051335A1
GENERAL INFORMATION:
APPLICANT: Ialigudi, Raghunath, V.
APPLICANT: Ito, Laura, Y.
APPLICANT: Sherman, Bradley, K.
FILE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
FILE REFERENCE: PL-0009 US
CURRENT APPLICATION NUMBER: US/09/294,093B
CURRENT FILING DATE: 1999-04-16
PRIORITY APPLICATION NUMBER: 60/082,567
PRIORITY FILING DATE: April 21, 1998
NUMBER OF SEQ ID NOS: 6207
SOFTWARE: PERL Program
SEQ ID NO 1219
LENGTH: 300
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: incyte ID No. US20010051335A1 700343964H1
US-09-294-093B-1219

Query Match
Best Local Similarity 50.2%; Score 20.6; DB 10; Length 300;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 9 GGGCATGGTTTTCATCTAATAATA 35
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Db 44 GGGCATTTGTGTTTATGTAATGATA 70

RESULT 13
US-09-870-759-83
Sequence 83, Application us/09870759
Patent No. US20020177551A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
FILE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 870759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIORITY APPLICATION NUMBER: 60/208,128
PRIORITY FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: PatentIn version 3.1
SEQ ID NO 83
LENGTH: 17276
TYPE: DNA
ORGANISM: Streptococcus agalactiae
FEATURE:
NAME/KEY: CDS
LOCATION: (7062)..(8207)
OTHER INFORMATION:
US-09-870-759-83

Query Match
Best Local Similarity 50.2%; Score 20.6; DB 9; Length 17276;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 4 CCGAAGGCATGGTTTTCATCTAATAATACAC 38
||||| ||| ||| ||| ||| ||| |||
Db 15996 CCGAAGGCGGCTATTTCATCTAATAAGAAAC 16030

RESULT 14
US-09-954-695-31/C
Sequence 31, Application US/09954695
Patent No. US20020055116A1
GENERAL INFORMATION:
APPLICANT: CUNNINGHAM, Melissa M.
APPLICANT: STULL, Paul D.
APPLICANT: WEISBURG, William G.
TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF

```

; TITLE OF INVENTION: CRYPTOSPORIDIUM ORGANISMS IN A TEST SAMPLE  
; FILE REFERENCE: GP116-02.UT  
; CURRENT APPLICATION NUMBER: US/09/954,695  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/232,028  
; PRIOR FILING DATE: 2000-09-12  
; NUMBER OF SEQ ID NOS: 69  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 31  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-09-954-695-31

Query Match 49.8%; Score 20.4; DB 10; Length 23;  
Best Local Similarity 95.5%; Pred. No. 1.6e+02;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 16 GGTTTTTATCTAATAAATACA 37  
Db 23 GGTTCTTTATCTAATAAATACA 2

RESULT 15  
US-09-954-695-35/G  
; Sequence 35, Application US/09954695  
; Patent No. US2002005116A1  
; GENERAL INFORMATION:  
; APPLICANT: CUNNINGHAM, Melissa M.  
; APPLICANT: STULL, Paul D.  
; APPLICANT: WEISBURG, William G.  
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF  
; FILE REFERENCE: GP116-02.UT  
; CURRENT APPLICATION NUMBER: US/09/954,695  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/232,028  
; PRIOR FILING DATE: 2000-09-12  
; NUMBER OF SEQ ID NOS: 69  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 35  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-09-954-695-35

Query Match 49.8%; Score 20.4; DB 10; Length 23;  
Best Local Similarity 95.5%; Pred. No. 1.6e+02;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 16 GGTTTTTATCTAATAAATACA 37  
Db 23 GGTTCTTTATCTAATAAATACA 2

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GenCore version 5.1.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 00:35:54 ; Search time 1504.93 Seconds  
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Title: US-09-674-195c-16

Perfect score: 41

Sequence: 1 dcccgaaggcattggtt.....ttatctaataatacacccc 41

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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C 2	40.2	98.0	362	12	BF251811	BF251811 EST419073
C 3	40.2	98.0	377	12	BF251964	BF251964 EST419226
C 4	40.2	98.0	391	12	BF251561	BF251561 EST418910
C 5	40.2	98.0	488	12	BF251704	BF251704 EST418888
C 6	40.2	98.0	502	12	BF252581	BF252581 EST419843

C 7	40.2	98.0	518	12	BF251715	BF251715 EST418899
C 8	40.2	98.0	541	12	BF252371	BF252371 EST419633
C 9	40.2	98.0	546	12	BF253171	BF253171 EST445866
C 10	40.2	98.0	567	12	BF252094	BF252094 EST419356
C 11	40.2	98.0	568	12	BF252878	BF252878 EST420141
C 12	40.2	98.0	570	12	BF251284	BF251284 EST418544
C 13	40.2	98.0	572	12	BF252095	BF252095 EST419357
C 14	40.2	98.0	605	12	BF252135	BF252135 EST419397
C 15	40.2	98.0	679	12	BF251385	BF251385 EST418646
C 16	40.2	98.0	679	12	BF251001	BF251001 EST418258
C 17	40.2	98.0	701	12	BF251666	BF251666 EST418850
C 18	40.2	98.0	836	12	BF250962	BF250962 EST418219
C 19	38.6	94.1	122	9	AA783903	AA783903 c8h04a1.f
C 20	38.6	94.1	244	9	AI212196	AI212196 w9f07a1.f
C 21	38.6	94.1	250	9	AA784878	AA784878 g3a04a1.f
C 22	38.6	94.1	252	9	AI211979	AI211979 v7h05a1.f
C 23	38.6	94.1	260	9	AI329914	AI329914 c1e02ne.f
C 24	38.6	94.1	268	9	AA783154	AA783154 c1f02a1.f
C 25	38.6	94.1	269	9	AA966666	AA966666 w7f12a1.f
C 26	38.6	94.1	273	9	AA966294	AA966294 v7h05a1.f
C 27	38.6	94.1	280	9	AA965352	AA965352 e9d08a1.f
C 28	38.6	94.1	293	9	AA783904	AA783904 c8h04a1.f
C 29	38.6	94.1	294	10	AA722519	AA722519 c1d05nm.f
C 30	38.6	94.1	295	9	AA788074	AA788074 r4f04a1.f
C 31	38.6	94.1	295	9	AI327731	AI327731 10c01a1.f
C 32	38.6	94.1	308	9	AA785043	AA785043 g4e05a1.f
C 33	38.6	94.1	317	9	AA785195	AA785195 g5f07a1.f
C 34	38.6	94.1	320	12	BF252882	BF252882 EST420145
C 35	38.6	94.1	321	9	AA966439	AA966439 w5a05a1.f
C 36	38.6	94.1	329	9	AA965722	AA965722 o4e03a1.f
C 37	38.6	94.1	332	9	AA788075	AA788075 r4f04a1.f
C 38	38.6	94.1	333	9	AI327845	AI327845 j0d11a1.f
C 39	38.6	94.1	342	9	AA966525	AA966525 w5h08a1.f
C 40	38.6	94.1	343	9	AI210348	AI210348 10c01a1.f
C 41	38.6	94.1	352	9	AI210317	AI210317 h4g07a1.f
C 42	38.6	94.1	354	9	AI212309	AI212309 w9g08a1.f
C 43	38.6	94.1	356	9	AA786224	AA786224 j7g07a1.f
C 44	38.6	94.1	357	9	AA966771	AA966771 s9a12a1.f
C 45	38.6	94.1	364	9	AI212192	AI212192 w9f02a1.f

#### ALIGNMENTS

RESULT 1  
BF251693/C  
LOCUS BF251693 351 bp mRNA linear EST 15-NOV-2001  
DEFINITION EST418877 Coccidioides immitis spherule cDNA library Coccidioides immitis cDNA clone CIAAK21 5' sequence, mRNA sequence.  
ACCESSION BF251693  
VERSION BF251693.1 GI:16931759  
KEYWORDS EST.  
SOURCE Coccidioides immitis.  
ORGANISM Coccidioides immitis.  
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; mitosporic Onygenales; Coccidioides.  
AUTHORS Gardner M.J. and Kirkland, T.  
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library  
JOURNAL Unpublished (2000)  
COMMENT Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardneretigr.org  
Location/Qualifiers  
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/organism="Coccidioides immitis"  
/db\_xref="taxon:5501"  
/clone="CIAAK21"  
/clone\_lib="Coccidioides immitis spherule cDNA library"

Thu Jun 12 08:47:47 2003

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REFERENCE
AUTHORS      Gardner,M.J. and Kirkland,T.
TITLE        Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL      Unpublished (2000)
COMMENT      Contact: Malcolm J. Gardner
              Department of Eukaryotic Genomics
              The Institute for Genomic Research
              9712 Medical Center Drive, Rockville, MD 20850, USA
              Tel: 301 838 3519
              Fax: 301 838 0208
              Email: gardner@tigr.org.

BASE COUNT   97 a    69 c    81 g    104 t
ORIGIN

Query Match  98.0%; Score 40.2; DB 12; Length 351;
Best Local Similarity 97.6%; Pred. No. 0.0031;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCGAAGGCGATGTTTTTATCTAATAATACACCCC 41
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Db 220 GCCCGAAGGCGATGTTTTTATCTAATAATACACCCC 180

RESULT 2
BF251811/c 362 bp mRNA linear EST 15-NOV-2001
LOCUS      immitis spherule cDNA library Coccidioides
DEFINITION immitis cDNA clone CIAAM73 5' sequence, mRNA sequence.
ACCESSION  BF251811
VERSION     BF251811.1 GI:16931954
KEYWORDS    EST.
SOURCE      Coccidioides immitis.
ORGANISM    Coccidioides immitis.
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Onygenales; Mitosporic Onygenales; Coccidioides.
REFERENCE   1 (bases 1 to 362)
AUTHORS     Gardner,M.J. and Kirkland,T.
TITLE       Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL     Unpublished (2000)
COMMENT     Contact: Malcolm J. Gardner
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301 838 3519
            Fax: 301 838 0208
            Email: gardner@tigr.org.

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/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT   98 a    69 c    84 g    111 t
ORIGIN

Query Match  98.0%; Score 40.2; DB 12; Length 362;
Best Local Similarity 97.6%; Pred. No. 0.0031;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCGAAGGCGATGTTTTTATCTAATAATACACCCC 41
   :|||||
Db 215 GCCCGAAGGCGATGTTTTTATCTAATAATACACCCC 175

RESULT 3
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LOCUS      immitis spherule cDNA library Coccidioides
DEFINITION immitis cDNA clone CIAAP15 5' sequence, mRNA sequence.
ACCESSION  BF251964
VERSION     BF251964.1 GI:16932107
KEYWORDS    EST.
SOURCE      Coccidioides immitis.
ORGANISM    Coccidioides immitis.
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Onygenales; Mitosporic Onygenales; Coccidioides.

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1 (bases 1 to 377)
Gardner,M.J. and Kirkland,T.
Generation of ESTs from Coccidioides immitis spherule cDNA library
Unpublished (2000)
Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org.

FEATURES
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/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT   103 a    85 c    94 g    95 t
ORIGIN

Query Match  98.0%; Score 40.2; DB 12; Length 377;
Best Local Similarity 97.6%; Pred. No. 0.0031;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCGAAGGCGATGTTTTTATCTAATAATACACCCC 41
   :|||||
Db 119 GCCCGAAGGCGATGTTTTTATCTAATAATACACCCC 79

RESULT 4
BF251561/c 391 bp mRNA linear EST 15-NOV-2001
LOCUS      immitis spherule cDNA library Coccidioides
DEFINITION immitis cDNA clone CIAAK57 5' sequence, mRNA sequence.
ACCESSION  BF251561
VERSION     BF251561.1 GI:16931792
KEYWORDS    EST.
SOURCE      Coccidioides immitis.
ORGANISM    Coccidioides immitis.
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Onygenales; Mitosporic Onygenales; Coccidioides.
REFERENCE   1 (bases 1 to 391)
AUTHORS     Gardner,M.J. and Kirkland,T.
TITLE       Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL     Unpublished (2000)
COMMENT     Contact: Malcolm J. Gardner
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301 838 3519
            Fax: 301 838 0208
            Email: gardner@tigr.org.

FEATURES
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/organism="Coccidioides immitis"
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/clone="CIAAK57"
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/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT   107 a    76 c    96 g    112 t
ORIGIN

Query Match  98.0%; Score 40.2; DB 12; Length 391;
Best Local Similarity 97.6%; Pred. No. 0.0031;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DCCCGAAGGCGATGTTTATCTATAATAATACACCC 41  
 Db :|||||  
 220 GCCCGAAGGCGATGTTTATCTATAATAATACACCC 180

## RESULT 5

BF251704/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF251704 488 bp mRNA linear EST 15-NOV-2001  
 EST418898 Coccidioides immitis spherule cDNA library Coccidioides  
 immitis cDNA clone CIAAK33 5' sequence, mRNA sequence.

BF251704  
 BF251704.1 GI:16931770  
 EST.  
 Coccidioides immitis.  
 Coccidioides immitis.  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 Onygenales; mitosporic Onygenales; Coccidioides.  
 1 (bases 1 to 488)  
 Gardner, M.J. and Kirkland, T.  
 Generation of ESTs from Coccidioides immitis spherule cDNA library  
 Unpublished (2000)  
 Contact: Malcolm J. Gardner  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301 838 3519  
 Fax: 301 838 0208  
 Email: gardner@tigr.org.

Location/Qualifiers  
 1..488  
 /organism="Coccidioides immitis"  
 /db\_xref="taxon:5501"  
 /clone="CIAAK33"  
 /clone\_lib="Coccidioides immitis spherule cDNA library"  
 /dev\_stage="spherule"  
 /lab\_host="SOLR"  
 /note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
 XhoI"

BASE COUNT 129 a 97 c 126 g 136 t

ORIGIN

Query Match 98.0%; Score 40.2; DB 12; Length 488;  
 Best Local Similarity 97.6%; Pred. No. 0.003;  
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCGAAGGCGATGTTTATCTATAATAATACACCC 41  
 Db :|||||  
 220 GCCCGAAGGCGATGTTTATCTATAATAATACACCC 180

RESULT 6

BF252581/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF252581 502 bp mRNA linear EST 15-NOV-2001  
 EST419843 Coccidioides immitis spherule cDNA library Coccidioides  
 immitis cDNA clone CIAAK35 5' sequence, mRNA sequence.

BF252581  
 BF252581.1 GI:16932724  
 EST.  
 Coccidioides immitis.  
 Coccidioides immitis.  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 Onygenales; mitosporic Onygenales; Coccidioides.  
 1 (bases 1 to 502)  
 Gardner, M.J. and Kirkland, T.  
 Generation of ESTs from Coccidioides immitis spherule cDNA library  
 Unpublished (2000)  
 Contact: Malcolm J. Gardner  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301 838 3519  
 Fax: 301 838 0208  
 Email: gardner@tigr.org.

Location/Qualifiers  
 1..502  
 /organism="Coccidioides immitis"  
 /db\_xref="taxon:5501"  
 /clone="CIAAK35"  
 /clone\_lib="Coccidioides immitis spherule cDNA library"  
 /dev\_stage="spherule"  
 /lab\_host="SOLR"  
 /note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
 XhoI"

BASE COUNT 141 a 104 c 133 g 140 t

ORIGIN

Query Match 98.0%; Score 40.2; DB 12; Length 518;  
 Best Local Similarity 97.6%; Pred. No. 0.003;  
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCGAAGGCGATGTTTATCTATAATAATACACCC 41  
 Db :|||||  
 220 GCCCGAAGGCGATGTTTATCTATAATAATACACCC 180

RESULT 7

BF251715/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF251715 518 bp mRNA linear EST 15-NOV-2001  
 EST418899 Coccidioides immitis spherule cDNA library Coccidioides  
 immitis cDNA clone CIAAK45 5' sequence, mRNA sequence.

BF251715  
 BF251715.1 GI:16931781  
 EST.  
 Coccidioides immitis.  
 Coccidioides immitis.  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 Onygenales; mitosporic Onygenales; Coccidioides.  
 1 (bases 1 to 518)  
 Gardner, M.J. and Kirkland, T.  
 Generation of ESTs from Coccidioides immitis spherule cDNA library  
 Unpublished (2000)  
 Contact: Malcolm J. Gardner  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301 838 3519  
 Fax: 301 838 0208  
 Email: gardner@tigr.org.

Location/Qualifiers  
 1..518  
 /organism="Coccidioides immitis"  
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 /clone="CIAAK45"  
 /clone\_lib="Coccidioides immitis spherule cDNA library"  
 /dev\_stage="spherule"  
 /lab\_host="SOLR"  
 /note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
 XhoI"

BASE COUNT 142 a 101 c 126 g 133 t

ORIGIN

Query Match 98.0%; Score 40.2; DB 12; Length 502;  
 Best Local Similarity 97.6%; Pred. No. 0.003;  
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCGAAGGCGATGTTTATCTATAATAATACACCC 41  
 Db :|||||  
 223 GCCCGAAGGCGATGTTTATCTATAATAATACACCC 183

RESULT 8

BF252371/c

LOCUS

DEFINITION

ACCESSION

BF252371 541 bp mRNA linear EST 15-NOV-2001  
 EST419633 Coccidioides immitis spherule cDNA library Coccidioides  
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## FEATURES

source

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 /dev\_stage="spherule"  
 /lab\_host="SOLR"  
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 XhoI"

BASE COUNT 142 a 101 c 126 g 133 t

ORIGIN

Query Match 98.0%; Score 40.2; DB 12; Length 502;  
 Best Local Similarity 97.6%; Pred. No. 0.003;  
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCGAAGGCGATGTTTATCTATAATAATACACCC 41  
 Db :|||||  
 223 GCCCGAAGGCGATGTTTATCTATAATAATACACCC 183

RESULT 7

BF251715/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF251715 518 bp mRNA linear EST 15-NOV-2001  
 EST418899 Coccidioides immitis spherule cDNA library Coccidioides  
 immitis cDNA clone CIAAK45 5' sequence, mRNA sequence.

BF251715  
 BF251715.1 GI:16931781  
 EST.  
 Coccidioides immitis.  
 Coccidioides immitis.  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 Onygenales; mitosporic Onygenales; Coccidioides.  
 1 (bases 1 to 518)  
 Gardner, M.J. and Kirkland, T.  
 Generation of ESTs from Coccidioides immitis spherule cDNA library  
 Unpublished (2000)  
 Contact: Malcolm J. Gardner  
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 The Institute for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301 838 3519  
 Fax: 301 838 0208  
 Email: gardner@tigr.org.

Location/Qualifiers  
 1..518  
 /organism="Coccidioides immitis"  
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 /clone="CIAAK45"  
 /clone\_lib="Coccidioides immitis spherule cDNA library"  
 /dev\_stage="spherule"  
 /lab\_host="SOLR"  
 /note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
 XhoI"

BASE COUNT 141 a 104 c 133 g 140 t

ORIGIN

Query Match 98.0%; Score 40.2; DB 12; Length 518;  
 Best Local Similarity 97.6%; Pred. No. 0.003;  
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCGAAGGCGATGTTTATCTATAATAATACACCC 41  
 Db :|||||  
 220 GCCCGAAGGCGATGTTTATCTATAATAATACACCC 180

RESULT 8

BF252371/c

LOCUS

DEFINITION

ACCESSION

BF252371 541 bp mRNA linear EST 15-NOV-2001  
 EST419633 Coccidioides immitis spherule cDNA library Coccidioides  
 immitis cDNA clone CIAAV41 5' sequence, mRNA sequence.

Thu Jun 12 08:47:47 2003

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VERSION      BF25371.1  GI:16932514
KEYWORDS
SOURCE
ORGANISM      Coccidioides immitis.
               Coccidioides immitis
               Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
               Onygenales; mitosporic Onygenales; Coccidioides.

REFERENCE
AUTHORS      Gardner,M.J. and Kirkland,T.
TITLE        Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL      Unpublished (2000)
COMMENT      Contact: Malcolm J. Gardner
               The Institute for Genomic Research
               9712 Medical Center Drive, Rockville, MD 20850, USA
               Tel: 301 838 3519
               Fax: 301 838 0208
               Email: gardner@tigr.org.

FEATURES
source
location/Qualifiers
1..541
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIAV41"
/clone_lib="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT   157 a 109 c 133 g 142 t
ORIGIN

Query Match      98.0%; Score 40.2; DB 12; Length 541;
Best Local Similarity 97.6%; Pred. No. 0.0029;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY      1  DCCCGGAGGCATTGGTTTTTATCTAATAATACACCC 41
          :|||||
DB      219 GCCCGGAGGCATTGGTTTTTATCTAATAATACACCC 179
          :|||||

RESULT 9
BF253171/c
LOCUS
DEFINITION    BF253171
               546 bp mRNA linear EST 15-NOV-2000
               EST445666 Coccidioides immitis spherule cDNA library Coccidioides
               immitis cDNA clone CIGAB68 5' sequence, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM      Coccidioides immitis.
               Coccidioides immitis
               Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
               Onygenales; mitosporic Onygenales; Coccidioides.

REFERENCE
AUTHORS      Gardner,M.J. and Kirkland,T.
TITLE        Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL      Unpublished (2000)
COMMENT      Other ESTs: EST445665
               Contact: Malcolm J. Gardner
               Department of Eukaryotic Genomics
               The Institute for Genomic Research
               9712 Medical Center Drive, Rockville, MD 20850, USA
               Tel: 301 838 3519
               Fax: 301 838 0208
               Email: gardner@tigr.org.

FEATURES
source
location/Qualifiers
1..546
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIGAB68"
/clone_lib="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

```

## COMMENT

Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org.

FEATURES  
source

Location/Qualifiers  
1..368  
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/clone="CIAAB97"  
/clone\_lib="Coccidioides immitis spherule cDNA library"  
/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI"

BASE COUNT 162 a 117 c 143 g 146 t  
ORIGIN

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Best Local Similarity 97.6%; Pred. No. 0.0029;  
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCCCGAAGGCATGGTGTATCTAATAATACACCC 41  
Db 226 GCCCGAAGGCATGGTGTATCTAATAATACACCC 186

## RESULT 12

BF251284/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF251284 570 bp mRNA linear EST 15-NOV-2001  
EST418344 Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone CIAAF16 5' sequence, mRNA sequence.

BF251284

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF251284 570 bp mRNA linear EST 15-NOV-2001  
EST418344 Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone CIAAF16 5' sequence, mRNA sequence.

BF251284

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF251284 570 bp mRNA linear EST 15-NOV-2001  
EST418344 Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone CIAAF16 5' sequence, mRNA sequence.

BF251284

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF251284 570 bp mRNA linear EST 15-NOV-2001  
EST418344 Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone CIAAF16 5' sequence, mRNA sequence.

BF251284

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF251284 570 bp mRNA linear EST 15-NOV-2001  
EST418344 Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone CIAAF16 5' sequence, mRNA sequence.

BF251284

VERSION

KEYWORDS

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ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF251284 570 bp mRNA linear EST 15-NOV-2001  
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BF251284

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF251284 570 bp mRNA linear EST 15-NOV-2001  
EST418344 Coccidioides immitis spherule cDNA library Coccidioides  
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BF251284

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF251284 570 bp mRNA linear EST 15-NOV-2001  
EST418344 Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone CIAAF16 5' sequence, mRNA sequence.

BF251284

VERSION

KEYWORDS

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ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

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BF251284 570 bp mRNA linear EST 15-NOV-2001  
EST418344 Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone CIAAF16 5' sequence, mRNA sequence.

BF251284

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF251284 570 bp mRNA linear EST 15-NOV-2001  
EST418344 Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone CIAAF16 5' sequence, mRNA sequence.

BF251284

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF251284 570 bp mRNA linear EST 15-NOV-2001  
EST418344 Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone CIAAF16 5' sequence, mRNA sequence.

BF251284

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF251284 570 bp mRNA linear EST 15-NOV-2001  
EST418344 Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone CIAAF16 5' sequence, mRNA sequence.

BF251284

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF251284 570 bp mRNA linear EST 15-NOV-2001  
EST418344 Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone CIAAF16 5' sequence, mRNA sequence.

BF251284

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF251284 570 bp mRNA linear EST 15-NOV-2001  
EST418344 Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone CIAAF16 5' sequence, mRNA sequence.

BF251284

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF251284 570 bp mRNA linear EST 15-NOV-2001  
EST418344 Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone CIAAF16 5' sequence, mRNA sequence.

BF251284

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF251284 570 bp mRNA linear EST 15-NOV-2001  
EST418344 Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone CIAAF16 5' sequence, mRNA sequence.

BF251284

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF251284 570 bp mRNA linear EST 15-NOV-2001  
EST418344 Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone CIAAF16 5' sequence, mRNA sequence.

BF251284

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF251284 570 bp mRNA linear EST 15-NOV-2001  
EST418344 Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone CIAAF16 5' sequence, mRNA sequence.

BF251284

VERSION

KEYWORDS

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ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF251284 570 bp mRNA linear EST 15-NOV-2001  
EST418344 Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone CIAAF16 5' sequence, mRNA sequence.

BF251284

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF251284 570 bp mRNA linear EST 15-NOV-2001  
EST418344 Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone CIAAF16 5' sequence, mRNA sequence.

BF251284

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

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BF251284 570 bp mRNA linear EST 15-NOV-2001  
EST418344 Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone CIAAF16 5' sequence, mRNA sequence.

BF251284

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF251284 570 bp mRNA linear EST 15-NOV-2001  
EST418344 Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone CIAAF16 5' sequence, mRNA sequence.

BF251284

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF251284 570 bp mRNA linear EST 15-NOV-2001  
EST418344 Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone CIAAF16 5' sequence, mRNA sequence.

BF251284

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF251284 570 bp mRNA linear EST 15-NOV-2001  
EST418344 Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone CIAAF16 5' sequence, mRNA sequence.

BF251284

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF251284 570 bp mRNA linear EST 15-NOV-2001  
EST418344 Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone CIAAF16 5' sequence, mRNA sequence.

BF251284

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

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BF251284 570 bp mRNA linear EST 15-NOV-2001  
EST418344 Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone CIAAF16 5' sequence, mRNA sequence.

BF251284

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

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XhoI"
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BASE COUNT 160 a 149 c 125 g 170 t 1 others  
ORIGIN

Query Match 98.0%; Score 40.2; DB 12; Length 605;  
Best Local Similarity 97.6%; Pred. No. 0.0029;  
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DCCCGAAGGCATTGGTTTTTATCTAATAAATACACCCC 41  
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Db 387 GCCCGAAGGCATTGGTTTTTATCTAATAAATACACCCC 427

## RESULT 15

BF251385/c

## LOCUS

BF251385 679 bp mRNA linear EST 15-NOV-2001  
DEFINITION EST418646 Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone CIAAG36 5' sequence, mRNA sequence.

ACCESSION BF251385

VERSION BF251385.1 GI:16931528

KEYWORDS EST.

SOURCE

ORGANISM

Coccidioides immitis.

Coccidioides immitis

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Onygenales; mitosporic Onygenales; Coccidioides.

1 (bases 1 to 679)

Gardner, M.J. and Kirkland, T.

Generation of ESTs from Coccidioides immitis spherule cDNA library

Unpublished (2000)

Contact: Malcolm J. Gardner

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301 838 3519

Fax: 301 838 0208

Email: gardner@tigr.org

## FEATURES

source

1..679

/organism="Coccidioides immitis"

/db\_xref="taxon:5501"

/clone="CIAAG36"

/clone\_lib="Coccidioides immitis spherule cDNA library"

/dev\_stage="spherule"

/lab\_host="SOLR"

/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:

XhoI"

BASE COUNT 175 a 167 c 153 g 184 t

## ORIGIN

Query Match 98.0%; Score 40.2; DB 12; Length 679;  
Best Local Similarity 97.6%; Pred. No. 0.0029;  
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DCCCGAAGGCATTGGTTTTTATCTAATAAATACACCCC 41  
:|||||  
Db 205 GCCCGAAGGCATTGGTTTTTATCTAATAAATACACCCC 165

Search completed: June 12, 2003, 04:35:05

Job time : 1507.64 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 22:21:06 ; Search time 348.269 Seconds  
(without alignments)  
1921.975 Million cell updates/sec

Title: US-09-674-195c-17  
Perfect score: 23  
Sequence: 1 dgaagtcgaggttcagcatg 23

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl.\*

- 1: gb.ba.\*
- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sv.\*
- 13: gb.un.\*
- 14: gb.vi.\*
- 15: em.ba.\*
- 16: em.fun.\*
- 17: em.hum.\*
- 18: em.in.\*
- 19: em.mu.\*
- 20: em.om.\*
- 21: em.or.\*
- 22: em.ov.\*
- 23: em.pat.\*
- 24: em.ph.\*
- 25: em.pl.\*
- 26: em.ro.\*
- 27: em.sts.\*
- 28: em.un.\*
- 29: em.vi.\*
- 30: em.htg\_hum.\*
- 31: em.htg\_inv.\*
- 32: em.htg\_other.\*
- 33: em.htg\_mus.\*
- 34: em.htg\_pln.\*
- 35: em.htg\_rtd.\*
- 36: em.htg\_mam.\*
- 37: em.htg\_vrt.\*
- 38: em.sy.\*
- 39: em.htgo\_hum.\*
- 40: em.htgo\_mus.\*
- 41: em.htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	22	95.7	1704	8	HCC18SRN	275306 H.capsulatu
C 2	22	95.7	1704	8	HCC18SRN	X58572 H.capsulatu
C 3	22	95.7	1713	8	HCC18SR	AF320009 Ajellomyc
C 4	22	95.7	1726	8	AF320009	AB030916 Aspergill
C 5	20.4	88.7	494	8	AB030916	AF088252 Teloschis
C 6	20.4	88.7	786	8	AF088252	AF113712 Dibaeis b
C 7	20.4	88.7	969	8	AF113712	AF107345 Dibaeis b
C 8	20.4	88.7	990	8	AF107345	AF203458 Cyclaneus
C 9	20.4	88.7	1031	8	AF203458	AB030917 Aspergill
C 10	20.4	88.7	1054	8	AB030917	U45438 Amylocarpus
C 11	20.4	88.7	1479	8	AEU45438	U72712 Siphula cer
C 12	20.4	88.7	1648	8	SCU72712	X78538 A.niger (ls
C 13	20.4	88.7	1673	8	AN18SR	Y13996 Paecilomyce
C 14	20.4	88.7	1678	8	PV13996	AF113713 Dibaeis b
C 15	20.4	88.7	1866	8	AF113713	AF113710 Siphula p
C 16	20.4	88.7	1887	8	AF184749	AF113711 Siphula p
C 17	20.4	88.7	1692	8	AF113710	AF085473 Dibaeis b
C 18	20.4	88.7	1701	8	AF085473	AF242259 Acrosporm
C 19	20.4	88.7	1721	8	AF242259	AB008408 Aspergill
C 20	20.4	88.7	1732	8	AB008408	AB008397 Aspergill
C 21	20.4	88.7	1733	8	AB008397	AB008413 Aspergill
C 22	20.4	88.7	1733	8	AB008413	D63697 Aspergillus
C 23	20.4	88.7	1733	8	D63697	D63697 Aspergillus
C 24	20.4	88.7	1733	8	D63697	AB006716 Talaromyc
C 25	20.4	88.7	1734	8	AB006716	AB033479 Leveillul
C 26	20.4	88.7	1734	8	AB033479	AF053726 Kirschste
C 27	20.4	88.7	1746	8	AF053726	AF02079 Aspergill
C 28	20.4	88.7	1746	8	AF02079	AF02079 Aspergill
C 29	20.4	88.7	1771	8	AF02079	AF02079 Aspergill
C 30	20.4	88.7	1771	8	AF02079	AF02079 Aspergill
C 31	20.4	88.7	1772	8	AF053729	AF053729 Helicascu
C 32	20.4	88.7	1774	8	AB003947	AB003947 Talaromyc
C 33	20.4	88.7	1776	8	AB003947	AB003946 Penicilli
C 34	20.4	88.7	1777	8	AB003946	AB003808 Aspergill
C 35	20.4	88.7	1777	8	AB003808	AJ301706 Capnobotr
C 36	20.4	88.7	1989	8	CSF301706	AB003945 Penicilli
C 37	20.4	88.7	2150	8	AB003945	AJ421692 Anaptychi
C 38	20.4	88.7	2734	8	ARU421692	AJ421689 Physconia
C 39	19.4	84.3	1759	8	AB005561	AB005561 Kockovael
C 40	19	82.6	913	8	AF006722	AF006722 Antennari
C 41	18.8	81.7	144	8	AB046947	AB046947 Endophyte
C 42	18.8	81.7	144	8	AB046948	AB046948 Endophyte
C 43	18.8	81.7	144	8	AB046949	AB046949 Endophyte
C 44	18.8	81.7	192	8	AF062662	AF062662 Endophyte
C 45	18.8	81.7	192	8	AF062664	AF062664 Endophyte

ALIGNMENTS

RESULT 1  
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LOCUS H.capsulatum ssp. duboisii 18S rRNA gene.  
DEFINITION H.capsulatum ssp. duboisii 18S rRNA gene.  
ACCESSION 275306  
VERSION 275306.1 GI:1419549  
KEYWORDS 18S ribosomal RNA; 18S rRNA gene; small subunit ribosomal RNA.  
SOURCE Ajellomyces capsulatus.  
ORGANISM Ajellomyces capsulatus  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; Onygenaceae; Ajellomyces.  
REFERENCE 1 (bases 1 to 1704)  
AUTHORS Okeke,C.N., Kappe,R., Zakikhani,S., Nolte,O. and Sonntag,H.G.  
TITLE Ribosomal genes of Histoplasma capsulatum var. duboisii and var. farciminosum

JOURNAL Mycoses 41 (9-10), 355-362 (1998)  
 MEDLINE 99114487  
 PUBMED 9916456  
 REFERENCE 2 (bases 1 to 1704)  
 AUTHORS Kappe,R.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-JUL-1996) Reinhard Kappe, Hygiene & Med.  
 Microbiology, University of Heidelberg, Hygiene Institute, Im  
 Neuenheimer Feld 324, Heidelberg, D-69120, Germany  
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 /db\_xref="taxon:5037"  
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 /product="18S ribosomal RNA"  
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 BASE COUNT 432 a 365 c 470 g 437 t  
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 Best Local Similarity 100.0%; Pred. No. 1.7;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 CGAAGTCGAGCGTTTCAGCATG 23  
 Db 133 CGAAGTCGAGCGTTTCAGCATG 112  
 RESULT 2  
 HCF18SRN/c  
 LOCUS HCF18SRN 1704 bp DNA linear PLN 10-DEC-1999  
 DEFINITION H. capsulatum spp. farciminosum 18S rRNA gene.  
 ACCESSION Z75307  
 VERSION Z75307.1 GI:1419550  
 KEYWORDS 18S ribosomal RNA; 18S rRNA gene; small subunit ribosomal RNA.  
 SOURCE Ajellomyces capsulatus.  
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 Onygenales; Onygenaceae; Ajellomyces.  
 REFERENCE 1 (bases 1 to 1704)  
 AUTHORS Okeke,C.N., Kappe,R., Zakikhani,S., Nolte,O. and Sonntag,H.G.  
 TITLE Ribosomal genes of Histoplasma capsulatum var. duboisii and var.  
 farciminosum  
 JOURNAL Mycoses 41 (9-10), 355-362 (1998)  
 MEDLINE 99114487  
 PUBMED 9916456  
 REFERENCE 2 (bases 1 to 1704)  
 AUTHORS Kappe,R.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-JUL-1996) Reinhard Kappe, Hygiene & Med.  
 Microbiology, University of Heidelberg, Hygiene Institute, Im  
 Neuenheimer Feld 324, Heidelberg, D-69120, Germany  
 FEATURES Location/Qualifiers  
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 /strain="CBS205.35, CBS478.64"  
 /sub\_species="farciminosum"  
 /db\_xref="taxon:5037"  
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 BASE COUNT 432 a 364 c 471 g 437 t  
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 Best Local Similarity 100.0%; Pred. No. 1.7;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGAAGTCGAGCGTTTCAGCATG 23  
 Db 133 CGAAGTCGAGCGTTTCAGCATG 112  
 RESULT 3  
 HCF18SR/c  
 LOCUS HCF18SR 1713 bp DNA linear PLN 30-JUN-1993  
 DEFINITION H. capsulatum DNA for 18S.ribosomal RNA, partial.  
 ACCESSION X58572 S45469  
 VERSION X58572.1 GI:2759  
 KEYWORDS 18S ribosomal RNA.  
 SOURCE Ajellomyces capsulatus.  
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 Onygenales; Onygenaceae; Ajellomyces.  
 REFERENCE 1 (bases 1 to 1713)  
 AUTHORS Bowman,B.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (19-MAR-1991) B.H. Bowman, Roche Molecular Systems, 1145  
 Atlantic Avenue, Alameda CA 94501, USA  
 REFERENCE 2 (bases 1 to 1713)  
 AUTHORS Bowman,B.H., Taylor,J.W. and White,T.J.  
 TITLE Molecular evolution of the fungi: human pathogens  
 JOURNAL Mol. Biol. Evol. 9 (5), 893-904 (1992)  
 MEDLINE 92408455  
 PUBMED 1528111  
 REFERENCE 3 (bases 1 to 1713)  
 AUTHORS Berbee,M.L. and Taylor,J.W.  
 TITLE Convergence in ascospore discharge mechanism among pyrenomycete  
 fungi based on 18S ribosomal RNA gene sequence  
 JOURNAL Mol. Phylogenet. Evol. 1 (1), 59-71 (1992)  
 MEDLINE 94115689  
 PUBMED 1342925  
 REMARK Location/Qualifiers  
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 /strain="ATCC 11408"  
 /db\_xref="taxon:5037"  
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 /product="18S ribosomal RNA"  
 /note="missing approx. 38 bases from 5' and 49 from 3'  
 end of coding region"  
 BASE COUNT 434 a 368 c 473 g 438 t  
 ORIGIN  
 Query Match 95.78; Score 22; DB 8; Length 1713;  
 Best Local Similarity 100.0%; Pred. No. 1.7;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 CGAAGTCGAGCGTTTCAGCATG 23  
 Db 153 CGAAGTCGAGCGTTTCAGCATG 132  
 RESULT 4  
 AF320009/c  
 LOCUS AF320009 1726 bp DNA linear PLN 13-FEB-2001  
 DEFINITION Ajellomyces capsulatus ATCC26032 18S ribosomal RNA gene, partial  
 sequence.  
 ACCESSION AF320009  
 VERSION AF320009  
 KEYWORDS AF320009.1 GI:12751371  
 SOURCE Ajellomyces capsulatus.  
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 Onygenales; Onygenaceae; Ajellomyces.  
 REFERENCE 1 (bases 1 to 1726)  
 AUTHORS Kasuga,T., White,T.J. and Taylor,J.W.  
 TITLE The Molecular Clock in Fungi in the Class Plecomycetes  
 JOURNAL Unpublished

```

REFERENCE
AUTHORS      2 (bases 1 to 1726)
TITLE        Kasuga,T., White,T.J. and Taylor,J.W.
JOURNAL      Direct Submission
FEATURES     Submitted (07-NOV-2000) Roche Molecular Systems, 1145 Atlantic
SOURCE       Ave., Alameda, CA 94501, USA
             Location/Qualifiers
             1..1726
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             /strain="ATCC26032; G217B"
             /db_xref="ATCC:26032"
             /db_xref="taxon:5037"
             /note="class 2 North American population"
             <1..>1726
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             /product="18S ribosomal RNA"
BASE COUNT   440 a 371 c 475 g 440 t
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Query Match 95.7%; Score 22; DB 8; Length 1726;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTCAGCATG 23
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Db 153 CGAAGTCGAGGCTTTCAGCATG 132

RESULT 5
AB030916/c
LOCUS       AB030916             494 bp DNA linear PLN 19-AUG-1999
DEFINITION Aspergillus niger gene for 18S rRNA, partial sequence.
ACCESSION   AB030916
VERSION     AB030916.1 GI:5738920
KEYWORDS    18S rRNA; 18S ribosomal RNA.
SOURCE      Aspergillus niger (strain:IEF1) DNA.
ORGANISM    Aspergillus niger
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
            1' (bases 1 to 494)
            Shintani,T. and Matsumoto,Y.
            Aspergillus niger gene for 18S rRNA, partial sequence
            Published Only in DataBase (1999)
            2 (bases 1 to 494)
            Shintani,T. and Matsumoto,Y.
            Direct Submission
            Submitted (10-AUG-1999) Tomoyoshi Shintani, Industrial Research
            Center of Ehime Prefecture, Laboratory of Food Process; 487-2
            Kumebota, Matsuyama, Ehime 791-1101, Japan
            (E-mail:shintani@eri.pref.ehime.jp, URL:www.iri.pref.ehime.jp,
            Tel:81-89-976-7612, Fax:81-89-976-7313)
FEATURES     Location/Qualifiers
             1..494
             /organism="Aspergillus niger"
             /strain="IEF1"
             /db_xref="taxon:5061"
             <1..>494
             /product="18S ribosomal RNA"
BASE COUNT   141 a 100 c 121 g 131 t
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Query Match 88.7%; Score 20.4; DB 8; Length 494;
Best Local Similarity 95.5%; Pred. No. 11;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTCAGCATG 23
    |||||||
Db 171 CGAAGTCGAGGCTTTCAGCATG 150

RESULT 6
AF088252/c
LOCUS       AF088252             786 bp DNA linear PLN 17-JUN-1999
DEFINITION Teloschistes cf. chrysophthalmus Feige and Mies ESS-6640 18S
            ribosomal RNA, partial sequence.

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ACCESSION   AF088252
VERSION     AF088252.1 GI:4731142
KEYWORDS    Teloschistes cf. chrysophthalmus Feige and Mies ESS-6640.
SOURCE      Teloschistes cf. chrysophthalmus Feige and Mies ESS-6640
ORGANISM    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;
            Lecanorales; Teloschistaceae; Teloschistaceae; Teloschistes.
REFERENCE   1 (bases 1 to 786)
AUTHORS     Stenroos,S.K. and DePriest,P.T.
TITLE       SSU rDNA phylogeny of cladoniiform lichens
JOURNAL     Am. J. Bot. 85, 1548-1559 (1998)
REFERENCE   2 (bases 1 to 786)
AUTHORS     DePriest,P.T., Ivanova,N. and Gargas,A.
TITLE       Direct Submission
JOURNAL     Submitted (31-AUG-1998) Department of Botany, NHB-166, Smithsonian
            Institution, National Museum of Natural History, 10th &
            Constitution Avenue NW, Washington, DC 20560-0166, USA
FEATURES     Location/Qualifiers
             1..786
             /organism="Teloschistes cf. chrysophthalmus Feige and Mies
             ESS-6640"
             /specimen_voucher="Feige & Mies Ess-6640 (US)"
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             /country="Cape Verde:Santo Antao, 1988"
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             /note="small subunit ribosomal RNA"
BASE COUNT   208 a 161 c 198 g 219 t
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Query Match 88.7%; Score 20.4; DB 8; Length 786;
Best Local Similarity 95.5%; Pred. No. 11;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTCAGCATG 23
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Db 134 CGAAGTCGAGGCTTTCAGCATG 113

RESULT 7
AF113712/c
LOCUS       AF113712             969 bp DNA linear PLN 06-DEC-1999
DEFINITION Dibaeis baecomyces small subunit ribosomal RNA gene, partial
            sequence.
ACCESSION   AF113712
VERSION     AF113712.1 GI:6502558
KEYWORDS    Dibaeis baecomyces.
SOURCE      Dibaeis baecomyces
ORGANISM    Dibaeis baecomyces
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;
            Lecanoromycetes incertae sedis; Icmadophyllaceae; Dibaeis.
            1 (bases 1 to 969)
            Platt,J.L. and Spatafora,J.W.
            Evolutionary relationships of nonsexual lichenized fungi: molecular
            phylogenetic hypotheses for the genera Siphula and Thamnolia from
            SSU and LSU rDNA analyses
            Unpublished
            2 (bases 1 to 969)
            Platt,J.L. and Spatafora,J.W.
            Direct Submission
            Submitted (16-DEC-1998) Department of Botany & Plant Pathology,
            Oregon State University, 2082 Cordley Hall, Corvallis, OR
            97331-2902, USA
FEATURES     Location/Qualifiers
             1..969
             /organism="Dibaeis baecomyces"
             /db_xref="taxon:83478"
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             /product="small subunit ribosomal RNA"
BASE COUNT   268 a 189 c 243 g 268 t
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Best Local Similarity 95.5%; Pred. No. 11;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTTCAGCATG 23
Db 128 CGAAGTCGAGGCTTTTCAGCATG 107

RESULT 8
AF107345/c
LOCUS
DEFINITION
Dibaeis baecomycetes small subunit ribosomal RNA gene, partial
sequence.
ACCESSION
AF107345
VERSION
AF107345.1 GI:6318520
KEYWORDS
Dibaeis baecomycetes.
ORGANISM
Dibaeis baecomycetes
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;
Lecanoromycetes incertae sedis; Icmadophylaceae; Dibaeis.
1 (bases 1 to 990)
Platt, J.L., Camacho, F.J. and Spatafora, J.W.
Evolution of the lichen symbiosis within the Leotiales; molecular
phylogenetic hypotheses for Dibaeis and Baecomycetes
Unpublished
2 (bases 1 to 990)
Platt, J.L. and Spatafora, J.W.
Direct Submission
JOURNAL
Submitted (18-NOV-1998) Botany & Plant Pathology, Oregon State
University, 2082 Cordley Hall, Corvallis, OR 97331, USA
FEATURES
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/isolate="OSC56400"
/db_xref="taxon:83478"
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269 a 189 c 248 g 284 t

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BASE COUNT
269 a 189 c 248 g 284 t
ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 990;
Best Local Similarity 95.5%; Pred. No. 11;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTTCAGCATG 23
Db 117 CGAAGTCGAGGCTTTTCAGCATG 96

RESULT 9
AF203458/c
LOCUS
DEFINITION
Cyclaneusma minus small subunit ribosomal RNA gene, partial
sequence.
ACCESSION
AF203458
VERSION
AF203458.1 GI:9622908
KEYWORDS
Cyclaneusma minus.
ORGANISM
Cyclaneusma minus
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Rhytismatales; Rhytismataceae; Cyclaneusma.
1 (bases 1 to 1031)
Gerhardt, D.S., Platt, J.L., Stone, J.K., Spatafora, J.W.,
Holst-Jensen, A., Hamelin, R.C. and Kohn, L.M.
Phylogenetics of Helotiales and Rhytismatales based on partial
small subunit nuclear ribosomal DNA sequences
Mycologia 93 (5) 915-933 (2001)
2 (bases 1 to 1031)
Gerhardt, D.S., Platt, J.L., Stone, J.K., Spatafora, J.W.,
Holst-Jensen, A., Hamelin, R.C. and Kohn, L.M.
Direct Submission
JOURNAL
Submitted (12-NOV-1999) Department of Botany and Plant Pathology,
Oregon State University, 2082 Cordley Hall, Corvallis, OR

Best Local Similarity 95.5%; Pred. No. 11;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTTCAGCATG 23
Db 117 CGAAGTCGAGGCTTTTCAGCATG 96

RESULT 10
AB030917/c
LOCUS
DEFINITION
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ACCESSION
AB030917
VERSION
AB030917.1 GI:5738921
KEYWORDS
18S rRNA; 18S ribosomal RNA.
SOURCE
Aspergillus niger var. awamori (strain: IEF2) DNA.
ORGANISM
Aspergillus awamori
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
1 (bases 1 to 1054)
Shintani, T. and Matsumoto, Y.
Aspergillus awamori gene for 18S rRNA, partial sequence
Published Only in DataBase (1999)
2 (bases 1 to 1054)
Shintani, T. and Matsumoto, Y.
Direct Submission
JOURNAL
Submitted (10-AUG-1999) Tomoyoshi Shintani, Industrial Research
Center of Ehime Prefecture, Laboratory of Food Process; 487-2
Kumekubota, Matsuyama, Ehime 791-1101, Japan
(E-mail: shintani@iri.pref.ehime.jp, URL: www.iri.pref.ehime.jp,
Tel: 81-89-976-7612, Fax: 81-89-976-7313)
FEATURES
Location/Qualifiers
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/db_xref="taxon:105351"
/note="synonym: Aspergillus awamori"
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/product="18S ribosomal RNA"
288 a 215 c 274 g 277 t

rRNA
BASE COUNT
288 a 215 c 274 g 277 t
ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 1054;
Best Local Similarity 95.5%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTTCAGCATG 23
Db 155 CGAAGTCGAGGCTTTTCAGCATG 134

RESULT 11
AEU45438/c
LOCUS
DEFINITION
Amylocarpus encephaloides small subunit rRNA gene.
ACCESSION
U45438
VERSION
U45438.1 GI:1736923
KEYWORDS
Amylocarpus encephaloides.
SOURCE
Amylocarpus encephaloides.
ORGANISM
Amylocarpus encephaloides.
1479 bp DNA linear
PLN 17-DEC-1996

```

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes; Helotiales; Helotiales incertae sedis; Amylocarpus.

1 (bases 1 to 1479)

Landvik, S., Shailer, N.F.J. and Eriksson, O.E.

SSU rDNA sequences support for a close relationship between the Elaphomycetales and the Eurotiales and Onygenales

Mycoscience 37, 237-241 (1996)

2 (bases 1 to 1479)

Landvik, S., Shailer, N.F.J. and Eriksson, O.E.

Direct Submission

Submitted (11-JAN-1996) Sara Landvik, Ecological Botany, Umea, S-90187, Sweden

FEATURES

Location/Qualifiers

1..1479

/organism="Amylocarpus encephaloides"

/strain="UME 29765"

/db\_xref="taxon:45428"

1..1479

/product="small subunit ribosomal RNA"

BASE COUNT 382 a 300 c 399 g 398 t

ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 1479;

Best Local Similarity 95.5%; Pred. No. 12;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CGAAGTCGAGGCTTTCAGCATG 23

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Db 108 CGAAGTCGAGGCTTTAGCATG 87

RESULT 12

SCU72712/c

LOCUS SCU72712 1648 bp DNA linear PLN 30-JUL-1997

DEFINITION Siphula ceratites 18S small subunit ribosomal RNA gene, complete sequence.

ACCESSION U72712

VERSION U72712.1 GI:2286071

KEYWORDS

SOURCE Siphula ceratites.

ORGANISM Siphula ceratites.

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes; Lecanoromycetes incertae sedis; Icmadophilaaceae; Siphula.

1 (bases 1 to 1648)

Stenroos, S., Lohlander, K. and Tehler, A.

Direct Submission

Submitted (27-SEP-1996) Botany, National Museum of Natural History, Smithsonian Institution, NHB-166, 10th St. & Constitution Ave., Washington, DC 20560, USA

FEATURES

Location/Qualifiers

1..1648

/organism="Siphula ceratites"

/db\_xref="taxon:53373"

1..1648

/product="18S small subunit ribosomal RNA"

BASE COUNT 424 a 343 c 442 g 439 t

ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 1648;

Best Local Similarity 95.5%; Pred. No. 12;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CGAAGTCGAGGCTTTCAGCATG 23

|||||

Db 110 CGAAGTCGAGGCTTTCAGCATG 89

RESULT 13

AN18SRR/c

LOCUS AN18SRR 1673 bp DNA linear PLN 13-MAR-1995

DEFINITION A.niger (Isolate CBS102.12) 18S rRNA gene.

ACCESSION X78538

VERSION X78538.1 GI:469079

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Aspergillus niger.

Aspergillus niger.

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

1 (bases 1 to 1673)

Melchers, W.J., Verweij, P.E., van den Hurk, P., van Belkum, A., De Pauw, B.E., Hoogkamp-Korstanje, J.A. and Meis, J.F.

General primer-mediated PCR for detection of Aspergillus species

J. Clin. Microbiol. 32 (7), 1710-1717 (1994)

95014936

7929762

2 (bases 1 to 1673)

Melchers, W.J.G.

Direct Submission

Submitted (25-MAR-1994) W.J.G. Melchers, Department of Medical Microbiology, University of Nijmegen, P O Box 9101, 6500 HB Nijmegen, NETHERLANDS

FEATURES

Location/Qualifiers

1..1673

/organism="Aspergillus niger"

/isolate="CBS102.12"

/db\_xref="taxon:5061"

<1..>1673

/product="18S ribosomal RNA"

/evidence="experimental"

BASE COUNT 423 a 365 c 458 g 426 t

ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 1673;

Best Local Similarity 95.5%; Pred. No. 12;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CGAAGTCGAGGCTTTCAGCATG 23

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Db 131 CGAAGTCGAGGCTTTCAGCATG 110

RESULT 14

PVY13996/c

LOCUS PVY13996 1678 bp DNA linear PLN 23-JUL-1997

DEFINITION Paecilomyces variotii 18S rRNA gene.

ACCESSION Y13996

VERSION Y13996.1 GI:2224834

KEYWORDS 18S ribosomal RNA; 18S rRNA gene.

SOURCE Paecilomyces variotii.

ORGANISM Paecilomyces variotii.

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Paecilomyces.

1 (bases 1 to 1678)

Zakikhani, S., Okeke, C.N. and Kappe, R.

18S rDNA sequence of Paecilomyces variotii CBS339.51

Unpublished

2 (bases 1 to 1678)

Kappe, R.

Direct Submission

Submitted (24-JUN-1997) Kappe R., Hygiene Institute, University of Heidelberg, Im Neuenheimer Feld 324 D-69120 GERMANY

FEATURES

Location/Qualifiers

1..1678

/organism="Paecilomyces variotii"

/strain="CBS339.51"

/isolate="Man, sputum"

/db\_xref="taxon:45996"

1..1678

/gene="18S rRNA"

/product="18S ribosomal RNA"

/evidence="experimental"

BASE COUNT 422 a 363 c 467 g 426 t

ORIGIN

18S ribosomal RNA.

Aspergillus niger.

Aspergillus niger.

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

1 (bases 1 to 1673)

Melchers, W.J., Verweij, P.E., van den Hurk, P., van Belkum, A., De Pauw, B.E., Hoogkamp-Korstanje, J.A. and Meis, J.F.

General primer-mediated PCR for detection of Aspergillus species

J. Clin. Microbiol. 32 (7), 1710-1717 (1994)

95014936

7929762

2 (bases 1 to 1673)

Melchers, W.J.G.

Direct Submission

Submitted (25-MAR-1994) W.J.G. Melchers, Department of Medical Microbiology, University of Nijmegen, P O Box 9101, 6500 HB Nijmegen, NETHERLANDS

FEATURES

Location/Qualifiers

1..1673

/organism="Aspergillus niger"

/isolate="CBS102.12"

/db\_xref="taxon:5061"

<1..>1673

/product="18S ribosomal RNA"

/evidence="experimental"

BASE COUNT 423 a 365 c 458 g 426 t

ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 1673;

Best Local Similarity 95.5%; Pred. No. 12;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CGAAGTCGAGGCTTTCAGCATG 23

|||||

Db 131 CGAAGTCGAGGCTTTCAGCATG 110

RESULT 14

PVY13996/c

LOCUS PVY13996 1678 bp DNA linear PLN 23-JUL-1997

DEFINITION Paecilomyces variotii 18S rRNA gene.

ACCESSION Y13996

VERSION Y13996.1 GI:2224834

KEYWORDS 18S ribosomal RNA; 18S rRNA gene.

SOURCE Paecilomyces variotii.

ORGANISM Paecilomyces variotii.

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Paecilomyces.

1 (bases 1 to 1678)

Zakikhani, S., Okeke, C.N. and Kappe, R.

18S rDNA sequence of Paecilomyces variotii CBS339.51

Unpublished

2 (bases 1 to 1678)

Kappe, R.

Direct Submission

Submitted (24-JUN-1997) Kappe R., Hygiene Institute, University of Heidelberg, Im Neuenheimer Feld 324 D-69120 GERMANY

FEATURES

Location/Qualifiers

1..1678

/organism="Paecilomyces variotii"

/strain="CBS339.51"

/isolate="Man, sputum"

/db\_xref="taxon:45996"

1..1678

/gene="18S rRNA"

/product="18S ribosomal RNA"

/evidence="experimental"

BASE COUNT 422 a 363 c 467 g 426 t

ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 1678;  
 Best Local Similarity 95.5%; Pred. No. 12;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTCAGCATG 23  
 |||||  
 Db 105 CGAAGTCGAGGCTTTCAGCATG 84

RESULT 15  
 AF113713/c  
 LOCUS 1686 bp DNA linear PLN 06-DEC-1999  
 DEFINITION Dibaels baecomyces isolate OSC53939 small subunit ribosomal RNA  
 gene, partial sequence.  
 ACCESSION AF113713  
 VERSION AF113713.1 GI:6502559  
 KEYWORDS  
 SOURCE Dibaels baecomyces.  
 ORGANISM Dibaels baecomyces  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;  
 Lecanoromycetes Incertae sedis; Icmadophilaceae; Dibaels.  
 REFERENCE 1 (bases 1 to 1686)  
 AUTHORS Platt, J. L. and Spatafora, J. W.  
 TITLE Evolutionary relationships of nonsexual lichenized fungi: molecular  
 phylogenetic hypotheses for the genera siphula and Thamnolia from  
 SSU and LSU rDNA analyses  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1686)  
 AUTHORS Platt, J. L. and Spatafora, J. W.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-DEC-1998) Department of Botany & Plant Pathology,  
 Oregon State University, 2082 Cordley Hall, Corvallis, OR  
 97331-2902, USA

FEATURES  
 source  
 1..1686  
 /organism="Dibaels baecomyces"  
 /isolate="OSC53939"  
 /db\_xref="taxon:83478"  
 <1..>1686  
 /product="small subunit ribosomal RNA"  
 BASE COUNT 441 a 346 c 438 g 460 t 1 others  
 ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 1686;  
 Best Local Similarity 95.5%; Pred. No. 12;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTCAGCATG 23  
 |||||  
 Db 128 CGAAGTCGAGGCTTTCAGCATG 107

Search completed: June 12, 2003, 02:33:53  
 Job time : 348.269 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 22:17:41 ; Search time 117.802 Seconds  
(without alignments)  
439.686 Million cell updates/sec

Title: US-09-674-195C-17

Perfect score: 23

Sequence: 1 degaagtcagagcttcagcatg 23

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_101002.\*

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4:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	95.7	22	15	AAQ73433
2	22	95.7	22	15	AAQ73436
3	22	95.7	22	15	AAQ73437
4	22	95.7	22	15	AAQ86436
5	20.4	88.7	568	21	AAFI1545
6	18.8	81.7	1733	20	AAZ00859
7	17.4	75.7	4403765	22	RAI199683
8	17.4	75.7	4411529	22	RAI199682
9	17.2	74.8	1745	24	ABA01152
					Histoplasma capsul
					Histoplasma capsul
					Histoplasma capsul
					Aspergillus niger
					A. fumigatus 18S r
					Mycobacterium tube
					Mycobacterium tube
					Deuteromycetes pol

c 10	16.8	73.0	454	22	AB444550	Human breast cell
c 11	16.8	73.0	454	22	ABA54997	Human foetal liver
c 12	16.8	73.0	454	22	ABA24760	Probe #3226 for ge
c 13	16.8	73.0	454	22	AAK03266	Human brain expres
c 14	16.8	73.0	454	22	AAK28719	Human bone marrow
c 15	16.8	73.0	454	22	AAI13296	Probe #3229 for ge
c 16	16.8	73.0	454	22	AAI34650	Probe #3336 used t
c 17	16.8	73.0	454	22	AAI03197	Probe #3188 used t
c 18	16.8	73.0	454	22	ABS03233	Human genome-deriv
c 19	16.8	73.0	492	23	AA365314	DNA encoding novel
c 20	16.4	71.3	891	19	AAV37154	DNA sequence used
c 21	16.4	71.3	891	19	AAH01747	Fibrobacter succin
c 22	16.4	71.3	1097	24	AAK72888	Bacillus lichenifo
c 23	16.2	70.4	351	21	AAC04990	Human secreted pro
c 24	16.2	70.4	1932	23	AA567693	DNA encoding novel
c 25	16.2	70.4	9228	23	ABLI1660	Drosophila melanog
c 26	16.2	69.6	7584	20	AAI19362	Rhodococcus corall
c 27	16	69.6	7600	21	AAA51878	Rhodococcus sp. OH
c 28	15.8	68.7	397	24	ABL85432	Human ovarian canc
c 29	15.8	68.7	550	21	AA294343	Cat flea head and
c 30	15.8	68.7	654	21	AA253824	Neisseria gonorrhoe
c 31	15.8	68.7	695	22	AAK91828	Human cDNA 5'-end
c 32	15.8	68.7	695	22	AAK93228	Human cDNA clone r
c 33	15.8	68.7	738	14	AAQ43293	Sequence encoding
c 34	15.8	68.7	738	15	AAQ66841	CC49 VL / 217 / 4-
c 35	15.8	68.7	738	20	AAK04747	DNA encoding a pro
c 36	15.8	68.7	738	20	AAV99764	Fusion polypeptide
c 37	15.8	68.7	738	21	AAA95090	DNA encoding bival
c 38	15.8	68.7	738	21	AAA59622	DNA encoding a sin
c 39	15.8	68.7	738	21	AA257095	4-4-20 Vh region a
c 40	15.8	68.7	738	21	AA290344	DNA (SEQ ID NO:22)
c 41	15.8	68.7	738	21	AA237393	Antibody CC49/anti
c 42	15.8	68.7	744	14	AAQ43288	Sequence encoding
c 43	15.8	68.7	744	20	AAK04742	DNA encoding a pro
c 44	15.8	68.7	744	21	AAA95085	Bivalent antigen b
c 45	15.8	68.7	744	21	AAA59617	DNA encoding a het

## ALIGNMENTS

RESULT 1  
AAQ73433  
ID AAQ73433 standard; DNA; 22 BP.  
XX  
AC AAQ73433;  
XX  
DT 18-MAY-1995 (first entry)  
XX  
DE Histoplasma capsulatum-specific DNA hybridisation probe.  
XX  
KW Probe; detection; Histoplasma capsulatum; 18S; rRNA; rDNA; hybridisation;  
KW Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;  
KW water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.  
XX  
OS Synthetic.  
XX  
PN US5352579-A.  
XX  
PD 04-OCT-1994.  
XX  
PF 28-JUN-1991; 91US-0720587.  
XX  
PR 28-JUN-1991; 91US-0720587.  
XX  
(GENP-) GEN-PROBE INC.  
XX  
PI Milliman CL;  
XX  
DR WPI; 1994-316178/39.  
XX  
PT Hybridisation probe specific for Histoplasma capsulatum -  
PT allowing differentiation from all other fungi for detection or

```

PT quantitation in body fluids, etc.
PS Claim 4; Column 11; 8pp; English.
XX
XX A probe (AAQ73433) or its complement (AAQ73436) and corresponding RNA
XX sequences (AAQ73437 and AAQ86436) used for the specific detection of all
XX strains of Histoplasma capsulatum (H.c.). The probes are manufactured
XX complementary to the H.c. 18S rRNA or rDNA gene. This region also
XX corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.
XX The probe is specific for H.c. and can be used to distinguish the fungus
XX from all others, even its nearest phylogenetic neighbour Blastomyces
XX dermatitidis. Nucleic acid hybridisation of the specific probe is
XX enhanced by the use of helper probes (AAQ73434-5). This method allows
XX the detection and/or the quantitation of H.c. from samples e.g. body
XX fluids, tissue samples, soil and water.
XX Sequence 22 BP; 5 A; 5 C; 7 G; 5 T; 0 other;

Query Match 95.7%; Score 22; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTCAGCATG 23
DB 1 CGAAGTCGAGGCTTTCAGCATG 22

RESULT 2
AAQ73436/C
ID AAQ73436 standard; DNA; 22 BP.
XX
AC AAQ73436;
XX
XX 18-MAY-1995 (first entry)
XX
XX Histoplasma capsulatum specific DNA probe, complementary sequence.
XX
XX Probe; detection; Histoplasma capsulatum; 18S; rRNA; rDNA; hybridisation;
XX KW. Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;
XX KW water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.
XX
XX Synthetic.
XX
XX US5352579-A.
XX
XX 04-OCT-1994.
XX
XX 28-JUN-1991; 91US-0720587.
XX
XX 28-JUN-1991; 91US-0720587.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Milliman CL;
XX
XX WPI; 1994-316178/39.
XX
XX Hybridisation probe specific for Histoplasma capsulatum -
XX allowing differentiation from all other fungi for detection or
XX quantitation in body fluids, etc.
XX
XX Claim 9; Column 12; 8pp; English.
XX
XX A probe (AAQ73433) or its complement (AAQ73436) and corresponding RNA
XX sequences (AAQ73437 and AAQ86436) used for the specific detection of all
XX strains of Histoplasma capsulatum (H.c.). The probes are manufactured
XX complementary to the H.c. 18S rRNA or rDNA gene. This region also
XX corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.
XX The probe is specific for H.c. and can be used to distinguish the fungus
XX from all others, even its nearest phylogenetic neighbour Blastomyces
XX dermatitidis. Nucleic acid hybridisation of the specific probe is
XX enhanced by the use of helper probes (AAQ73434-5). This method allows
XX the detection and/or the quantitation of H.c. from samples e.g. body
XX fluids, tissue samples, soil and water.
XX Sequence 22 BP; 5 A; 5 C; 7 G; 5 T; 0 other;

Query Match 95.7%; Score 22; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTCAGCATG 23
DB 1 CGAAGTCGAGGCTTTCAGCATG 22

RESULT 2
AAQ73436/C
ID AAQ73436 standard; DNA; 22 BP.
XX
AC AAQ73436;
XX
XX 18-MAY-1995 (first entry)
XX
XX Histoplasma capsulatum specific DNA probe, complementary sequence.
XX
XX Probe; detection; Histoplasma capsulatum; 18S; rRNA; rDNA; hybridisation;
XX KW. Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;
XX KW water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.
XX
XX Synthetic.
XX
XX US5352579-A.
XX
XX 04-OCT-1994.
XX
XX 28-JUN-1991; 91US-0720587.
XX
XX 28-JUN-1991; 91US-0720587.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Milliman CL;
XX
XX WPI; 1994-316178/39.
XX
XX Hybridisation probe specific for Histoplasma capsulatum -
XX allowing differentiation from all other fungi for detection or
XX quantitation in body fluids, etc.
XX
XX Claim 9; Column 12; 8pp; English.
XX
XX A probe (AAQ73433) or its complement (AAQ73436) and corresponding RNA
XX sequences (AAQ73437 and AAQ86436) used for the specific detection of all
XX strains of Histoplasma capsulatum (H.c.). The probes are manufactured
XX complementary to the H.c. 18S rRNA or rDNA gene. This region also
XX corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.
XX The probe is specific for H.c. and can be used to distinguish the fungus
XX from all others, even its nearest phylogenetic neighbour Blastomyces
XX dermatitidis. Nucleic acid hybridisation of the specific probe is
XX enhanced by the use of helper probes (AAQ73434-5). This method allows
XX the detection and/or the quantitation of H.c. from samples e.g. body
XX fluids, tissue samples, soil and water.
XX Sequence 22 BP; 5 A; 5 C; 7 G; 5 T; 0 other;

Query Match 95.7%; Score 22; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTCAGCATG 23
DB 2 CGAAGTCGAGGCTTTCAGCATG 1

RESULT 4
AAQ73437/C
ID AAQ73437 standard; RNA; 22 BP.
XX
AC AAQ73437;
XX
XX 18-MAY-1995 (first entry)
XX
XX Histoplasma capsulatum-specific RNA hybridisation probe.
XX
XX Probe; detection; Histoplasma capsulatum; 18S; rRNA; rDNA; hybridisation;
XX KW. Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;
XX KW water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.
XX
XX Synthetic.
XX
XX US5352579-A.
XX
XX 04-OCT-1994.
XX
XX 28-JUN-1991; 91US-0720587.
XX
XX 28-JUN-1991; 91US-0720587.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Milliman CL;
XX
XX WPI; 1994-316178/39.
XX
XX Hybridisation probe specific for Histoplasma capsulatum -
XX allowing differentiation from all other fungi for detection or
XX quantitation in body fluids, etc.
XX
XX Claim 9; Column 12-13; 8pp; English.
XX
XX A probe (AAQ73433) or its complement (AAQ73436) and corresponding RNA
XX sequences (AAQ73437 and AAQ86436) used for the specific detection of all
XX strains of Histoplasma capsulatum (H.c.). The probes are manufactured
XX complementary to the H.c. 18S rRNA or rDNA gene. This region also
XX corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.
XX The probe is specific for H.c. and can be used to distinguish the fungus
XX from all others, even its nearest phylogenetic neighbour Blastomyces
XX dermatitidis. Nucleic acid hybridisation of the specific probe is
XX enhanced by the use of helper probes (AAQ73434-5). This method allows
XX the detection and/or the quantitation of H.c. from samples e.g. body
XX fluids, tissue samples, soil and water.
XX Sequence 22 BP; 5 A; 7 C; 5 G; 5 U; 0 other;

Query Match 95.7%; Score 22; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTCAGCATG 23
DB 22 CGAAGTCGAGGCTTTCAGCATG 1

RESULT 4

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AAQ86436  
ID AAQ86436 standard; RNA; 22 BP.  
XX  
AC AAQ86436;  
XX  
DT 18-MAY-1995 (first entry)  
XX  
XX  
DE Histoplasma capsulatum-specific complementary RNA hybridisation probe.  
XX  
KW Probe; detection: Histoplasma capsulatum; 18S; rRNA; rDNA; hybridisation;  
KW Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;  
KW water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.  
XX  
OS Synthetic.  
XX  
PN US5352579-A.  
XX  
PD 04-OCT-1994.  
XX  
PF 28-JUN-1991; 91US-0720587.  
XX  
PR 28-JUN-1991; 91US-0720587.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Milliman CL;  
XX  
DR WPI; 1994-316178/39.  
XX  
DT Hybridisation probe specific for Histoplasma capsulatum -  
PT allowing differentiation from all other fungi for detection or  
PT quantitation in body fluids, etc.  
XX  
PS Claim 9; Column 13; 8pp; English.  
XX  
CC A probe (AAQ73433) or its complement (AAQ73436) and corresponding RNA  
CC sequences (AAQ73437 and AAQ86436) used for the specific detection of all  
CC strains of Histoplasma capsulatum (H.c.). The probes are manufactured  
CC complementary to the H.c. 18S rRNA or rDNA gene. This region also  
CC corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.  
CC The probe is specific for H.c. and can be used to distinguish the fungus  
CC from all others, even its nearest phylogenetic neighbour Blastomyces  
CC dermatitidis. Nucleic acid hybridisation of the specific probe is  
CC enhanced by the use of helper probes (AAQ73434-5). This method allows  
CC the detection and/or the quantitation of H.c. from samples e.g. body  
CC fluids, tissue samples, soil and water.  
XX  
SQ Sequence 22 BP; 5 A; 5 C; 7 G; 5 U; 0 other;

Query Match 95.7%; Score 22; DB 15; Length 22;  
Best Local Similarity 77.3%; Pred. No. 0.14;  
Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTCAGCATG 23  
|||||:|||||:|||||:|  
Db 1 CGAAGTCGAGGCTTTCAGCATG 22

RESULT 5  
AAFL1545/c  
ID AAFL1545 standard; cDNA; 568 BP.  
XX  
AC AAFL1545;  
XX  
DT 13-MAR-2001 (first entry)  
XX  
DE Aspergillus niger EST SEQ ID NO:4068.  
XX  
KW Multiple gene expression; filamentous fungal cell; EST;  
KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;  
KW Aspergillus oryzae; Trichoderma reesei; identification; recombination;  
KW culture condition; environmental stress; spore morphogenesis;  
KW metabolic pathway engineering; catabolic pathway engineering; ss.

XX Aspergillus niger.  
OS  
XX WO200056762-A2.  
PN  
XX 28-SEP-2000.  
PD  
XX 22-MAR-2000; 2000WO-US07781.  
PF  
XX 22-MAR-1999; 99US-0273623.  
PR  
XX (NOVO ) NOVO NORDISK BIOTECH INC.  
PA (NOVO ) NOVO NORDISK AS.  
XX  
PI Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;  
XX WPI; 2000-594572/56.  
DR  
XX Monitoring differential expression of genes in filamentous fungal cells  
PT uses fluorescence-labeled nucleic acids isolated from the cells and a  
PT substrate of expressed sequence tags -  
XX  
PS Claim 87; Page 1791-1792; 3161pp; English.  
XX  
CC The present invention describes a method for monitoring differential  
CC expression of genes in a first filamentous fungal (FF) cell relative to  
CC expression of the same genes in one or more second filamentous fungal  
CC cells. The method uses fluorescence-labeled nucleic acids isolated from  
CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs  
CC are used in the methods for monitoring differential expression of genes  
CC in a first filamentous fungal (FF) cell relative to expression of the  
CC same genes in one or more second filamentous fungal cells. Monitoring  
CC the global expression of genes from FF cells allows the production  
CC potential of the microorganisms to be improved. New genes may be  
CC discovered, possible functions of unknown open reading frames can be  
CC identified and gene copy number variation and stability can be  
CC monitored. The expression of genes can be used to study how FF cells  
CC adapt to changes in culture conditions, environmental stress, spore  
CC morphogenesis, recombination, metabolic or catabolic pathway  
CC engineering. Using ESTs provides several advantages over genomic or  
CC random cDNA clones including elimination of redundancy as one spot on an  
CC array equals one gene or open reading frame, and organisation of the  
CC microarrays based on function of the gene products to facilitate  
CC analysis of the results. AAF07478 to AAF11247 represents ESTs from  
CC Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus  
CC niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and  
CC AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are  
CC all specifically claimed in the present invention.  
XX  
SQ Sequence 568 BP; 155 A; 116 C; 141 G; 150 T; 6 other;

Query Match 88.7%; Score 20.4; DB 21; Length 568;  
Best Local Similarity 95.5%; Pred. No. 1.4;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTCAGCATG 23  
|||||:|||||:|||||:|  
Db 178 CGAAGTCGAGGCTTTCAGCATG 157

RESULT 6  
AAZ00859/c  
ID AAZ00859 standard; DNA; 1733 BP.  
XX  
AC AAZ00859;  
XX  
DT 11-OCT-1999 (first entry)  
XX  
DE A. fumigatus 18S rRNA DNA.  
XX  
KW Detection; diagnosis; 18S rRNA; aspergillosis; oncology;  
KW invasive infection; haematology; immune system suppression; ss.  
XX

OS Aspergillus fumigatus.  
 PN DE19806274-A1.  
 XX 19-AUG-1999.  
 XX 16-FEB-1998; 98DE-1006274.  
 XX 16-FEB-1998; 98DE-1006274.  
 XX (BUCH/) BUCHHEIDT D.  
 PA (HEHL/) HEHLMANN R.  
 PA (SKLA/) SKLADNY H.  
 XX Buchheidt D, Hehlmann R, Skladny H;  
 PI WPI; 1999-470047/40.  
 XX  
 DR Detecting Aspergillus nucleic acid in body samples by two-step  
 XX polymerase chain reaction, for diagnosing aspergillosis  
 PT  
 PT Claim 2; Fig 1; 16pp; German.  
 XX  
 CC This invention describes a novel method for detecting Aspergillus nucleic  
 CC acid (i) in a body sample which comprises the isolation of (i) followed  
 CC by a two-step polymerase chain reaction (PCR) amplification of any  
 CC nucleic acid having a sequence essentially homologous to part of the  
 CC 3'-end of the Aspergillus 18S rRNA gene using primers used in the first  
 CC step that do not overlap with those in the second step. The method is  
 CC used for early diagnosis, and monitoring, of aspergillosis, particularly  
 CC invasive infections in hematological-oncological patients with long-term  
 CC suppression of the immune system. Unlike the known method using  
 CC overlapping primers, this process provides efficient and reliable  
 CC detection of Aspergillus in clinical situations. It is specific for  
 CC Aspergillus (it detects the species terreus, niger, versicolor, clavatus,  
 CC flavus, and fumigatus, but not oryzae, nor bacteria or fungi from any  
 CC other genera). This sequence represents the DNA sequence of Aspergillus  
 CC fumigatus 18S rRNA.  
 XX  
 SQ Sequence 1733 BP; 446 A; 374 C; 475 G; 438 T; 0 other;  
 Query Match 81.7%; Score 18.8; DB 20; Length 1733;  
 Best Local Similarity 90.9%; Pred. No. 10;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 CGAAGTCGAGGCTTTCAGCATG 23  
 Db 153 CGAAGTCGAGGCTTTCAGCATG 132  
 RESULT 7  
 AA199683  
 ID AA199683 standard; DNA; 4403765 BP.  
 AC AA199683;  
 XX  
 DT 15-JAN-2002 (first entry)  
 XX  
 DE Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 2.  
 XX  
 KW Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome;  
 XX variation; epidemiology; patient treatment; epidemic monitoring; ds.  
 OS Mycobacterium tuberculosis.  
 XX  
 PN US6294328-B1.  
 XX  
 PD 25-SEP-2001.  
 XX  
 DE 24-JUN-1998; 98US-0103840.  
 XX  
 KW 24-JUN-1998; 98US-0103840.  
 XX  
 PR 24-JUN-1998; 98US-0103840.  
 XX  
 XX

(GENO-) INST GENOMIC RES.  
 Fleischmann RD, White OR, Fraser CM, Venter JC;  
 WPI; 2001-647261/74.  
 Evaluating strain variation of Mycobacterium tuberculosis, comprises  
 determining the nucleotide sequence of the strain at positions in the  
 genome corresponding to positions where M. tuberculosis strains CDC  
 1551 and H37Rv differ  
 Claim 4; SEQ ID NO 2; 3pp + Sequence Listing; English.  
 The invention relates to evaluating strain variation within and between  
 different populations of the tuberculosis bacterial pathogen,  
 Mycobacterium tuberculosis or related Mycobacterium by determining the  
 nucleotide sequence of the first strain at positions in the complete  
 sequence of the genome that correspond to positions that differ in the  
 nucleotide sequences of M. tuberculosis strains CDC 1551 (AA199683) and  
 H37Rv (AA199682). The method is useful for evaluating strain variation of  
 M. tuberculosis and has valuable application in the fields of  
 tuberculosis genetics, epidemiology, patient treatment and epidemic  
 monitoring.  
 Note: The sequence data for this patent did not form part of the printed  
 specification, but was obtained in electronic format directly from USPTO  
 at seqdata.uspto.gov/sequence.html?DocID=6294328B1.  
 Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189 other;  
 Query Match 75.7%; Score 17.4; DB 22; Length 4403765;  
 Best Local Similarity 82.6%; Pred. No. 1.1e+02;  
 Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 DCGAAGTCGAGGCTTTCAGCATG 23  
 Db 172049 TCGCTGTCGAGGCTTTCAGCATG 172071  
 RESULT 8  
 AA199682  
 ID AA199682 standard; DNA; 4411529 BP.  
 AC AA199682;  
 XX  
 DT 15-JAN-2002 (first entry)  
 XX  
 DE Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 1.  
 XX  
 KW Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome;  
 XX variation; epidemiology; patient treatment; epidemic monitoring; ds.  
 OS Mycobacterium tuberculosis.  
 XX  
 PN US6294328-B1.  
 XX  
 PD 25-SEP-2001.  
 XX  
 DE 24-JUN-1998; 98US-0103840.  
 XX  
 KW 24-JUN-1998; 98US-0103840.  
 XX  
 PR (GENO-) INST GENOMIC RES.  
 XX  
 PI Fleischmann RD, White OR, Fraser CM, Venter JC;  
 XX WPI; 2001-647261/74.  
 XX  
 PT Evaluating strain variation of Mycobacterium tuberculosis, comprises  
 PT determining the nucleotide sequence of the strain at positions in the  
 PT genome corresponding to positions where M. tuberculosis strains CDC  
 PT 1551 and H37Rv differ  
 XX Claim 3; SEQ ID NO 1; 3pp + Sequence Listing; English.

XX The invention relates to evaluating strain variation within and between  
 CC different populations of the tuberculosis bacterial pathogen,  
 CC Mycobacterium tuberculosis or related Mycobacterium by determining the  
 CC nucleotide sequence of the first strain at positions that differ in the  
 CC sequence of the genome that correspond to positions that differ in the  
 CC nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and  
 CC H37Rv (AAI99682). The method is useful for evaluating strain variation of  
 CC M. tuberculosis and has valuable application in the fields of  
 CC tuberculosis genetics, epidemiology, patient treatment and epidemic  
 CC monitoring.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from USPTO  
 CC at [seqdata.uspto.gov/sequence.html?DocID=6294328B1](http://seqdata.uspto.gov/sequence.html?DocID=6294328B1).  
 XX  
 SQ Sequence 4411529 BP; 758565 A; 1449983 C; 1444602 G; 758379 T; 0 other;

Query Match 75.7%; Score 17.4; DB 22; Length 4411529;  
 Best Local Similarity 82.6%; Pred. No. 1.1e+02;  
 Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DCGAAGTCGAGGCTTTCAGCATG 23  
 :|| ||||| ||||| |||||  
 DB 171880 TCGCTGTCGAGGCTTTCACCATG 171902

RESULT 9  
 ABA01152/c  
 ID ABA01152 standard; DNA; 1745 BP.  
 XX  
 AC ABA01152;  
 XX  
 DT 24-JAN-2002 (first entry)  
 XX  
 DE Deuteromycetes polynucleotide SEQ ID 1.  
 XX  
 KW Aldonic acid; ds.  
 XX  
 OS Deuteromycetes sp.  
 XX  
 PN JP2001245657-A.  
 XX  
 PD 11-SEP-2001.

XX  
 PF 26-DEC-2000; 2000JP-0394766.  
 XX  
 PR 27-DEC-1999; 99JP-0369714.  
 XX  
 PA (TAKE-) TAKEHARA KAGAKU KOGYO KK.  
 PA (OSAKA) OSAKA CITY.  
 XX  
 DR WPI; 2002-002933/01.

XX A new microbe for producing aldonic acid, comprises a new strain of  
 PT Acinetobacter or Burkholderis -  
 PT  
 PS Disclosure; Page 17; 22pp; Japanese.  
 XX  
 CC The present invention relates to a new microbe of Acinetobacter or  
 CC Burkholderis genus producing aldonic acid and oxidizing specifically the  
 CC hemiacetal hydroxy group of a saccharide having said hydroxy group.  
 CC Aldonic acid is used as a mineral reinforcing agent. The present sequence  
 CC was used to illustrate the present invention.  
 XX

XX Sequence 1745 BP; 448 A; 382 C; 465 G; 450 T; 0 other;  
 Query Match 74.8%; Score 17.2; DB 24; Length 1745;  
 Best Local Similarity 86.4%; Pred. No. 66;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTCAGCATG 23  
 ||||| ||||| ||||| |||||  
 DB 167 CGAAGTCGGGGTTTTCAGCATG 146

RESULT 10  
 ABA44550/c  
 ID ABA44550 standard; DNA; 454 BP.  
 XX  
 AC ABA44550;  
 XX  
 DT 01-FEB-2002 (first entry)  
 XX  
 DE Human breast cell single exon nucleic acid probe #3245.

XX  
 KW Human; microarray; single exon probe; gene expression; breast;  
 KW disease; cancer; ss.  
 XX  
 OS Homo sapiens.

XX WO200157271-A2.  
 XX  
 PD 09-AUG-2001.  
 XX

XX 30-JAN-2001; 2001WO-US00662.  
 XX  
 PR 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI; 2001-496933/54.

XX  
 PT New spatially-addressable set of single exon nucleic acid probes,  
 PT useful for measuring gene expression in sample derived from human  
 PT breast, comprises number of single exon nucleic acid probes -  
 XX  
 PS Claim 1; SEQ ID NO 3245; 327pp + sequence listing; English.

XX The invention relates to a spatially-addressable set of single exon  
 CC nucleic acid probes for measuring gene expression in a sample derived  
 CC from human breast and BT 474 cells. The method involves contacting  
 CC the probes with a collection of detectably labelled nucleic acids  
 CC derived from mRNA of human breast, and then measuring the label  
 CC bound to each probe of the microarray. The probes are useful for  
 CC verifying the expression of regions of genomic DNA predicted to  
 CC encode proteins. They are useful for gene discovery, and for  
 CC determining predisposition and/or prognosing breast disease. Gene  
 CC expression analysis is useful for assessing the toxicity of chemical  
 CC agents on cells. The microarray of this invention presents a far greater  
 CC diversity of probes for measuring gene expression, with far less bias  
 CC than expressed sequence tag microarrays. The method is suitable for  
 CC rapid production of functional information from genomic sequence. The  
 CC present sequence is a single exon nucleic acid probe of the invention.  
 CC Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences).  
 XX

SQ Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;

Query Match 73.0%; Score 16.8; DB 22; Length 454;  
 Best Local Similarity 90.0%; Pred. No. 90;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AAGTCGAGGCTTTCAGCATG 23  
 ||||| ||||| ||||| |||||  
 DB 201 AAGTAGAGGCTTTCAGCATG 182

```

RESULT 11
ABA54997/C
ID ABA54997 standard; DNA; 454 BP.
XX AC
XX ABA54997;
XX DT
XX 01-FEB-2002 (first entry)
XX DE
XX Human foetal liver single exon nucleic acid probe #3302.
XX KW
XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX OS
XX Homo sapiens.
XX PN
XX WO200157277-A2.
XX PD
XX 09-AUG-2001.
XX PF
XX 30-JAN-2001; 2001WO-US00669.
XX PR
XX 04-FEB-2000; 2000US-0180312.
XX PR
XX 26-MAY-2000; 2000US-0207456.
XX PR
XX 30-JUN-2000; 2000US-0608408.
XX PR
XX 03-AUG-2000; 2000US-0632366.
XX PR
XX 21-SEP-2000; 2000US-0234687.
XX PR
XX 27-SEP-2000; 2000US-0236359.
XX PR
XX 04-OCT-2000; 2000GB-0024263.
XX PA
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX PI
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX X
XX WPI; 2001-483447/52.
XX DR
XX Human genome-derived single exon nucleic acid probes useful for
XX PT analyzing gene expression in human fetal liver.
XX PS
XX Claim 1; SEQ ID NO 3302; 639pp + sequence listing; English.
XX CC
XX The invention relates to a single exon nucleic acid probe for
XX CC measuring human gene expression in a sample derived from human
XX CC liver. The single exon nucleic acid probes may be used for predicting,
XX CC measuring and displaying gene expression in samples derived from human
XX CC fetal liver. The present sequence is a single exon nucleic acid
XX CC probe of the invention.
XX CC Note: The sequence data for this patent did not form part of the
XX CC printed specification, but was obtained in electronic format directly
XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ
XX Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;

Query Match 73.0%; Score 16.8; DB 22; Length 454;
Best Local Similarity 90.0%; Pred. No. 90;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AAGTCGAGGCTTTCAGCATG 23
DB 201 AAGTAGAGGCTTTCGCATG 182

RESULT 12
ABA24760/C
ID ABA24760 standard; DNA; 454 BP.
XX AC
XX ABA24760;
XX DT
XX 23-JAN-2002 (first entry)
XX DE
XX Probe #3226 for gene expression analysis in human heart cell sample.
XX KW
XX Human; gene expression; heart; microarray; vascular system; probe;
XX KW cardiovascular disease; hypertension; cardiac arrhythmia;
XX KW congenital heart disease; ss.

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XX OS Homo sapiens.
XX PN WO200157274-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US00666.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX X
XX WPI; 2001-488899/53.
XX DR
XX Single exon nucleic acid probes for analyzing gene expression in human
XX PT hearts.
XX PS
XX Claim 1; SEQ ID No 3226; 530pp; English.
XX CC
XX The present invention relates to single exon nucleic acid probes for
XX CC measuring human gene expression in a sample derived from human heart. The
XX CC present sequence is one such probe. The probes may be used for
XX CC predicting, measuring and displaying gene expression in samples derived
XX CC from the human heart via microarrays. By measuring gene expression, the
XX CC probes are useful for predicting, diagnosing, grading, staging,
XX CC monitoring and prognosing diseases of the human heart and vascular system
XX CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX CC congenital heart disease.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ
XX Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;

Query Match 73.0%; Score 16.8; DB 22; Length 454;
Best Local Similarity 90.0%; Pred. No. 90;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AAGTCGAGGCTTTCAGCATG 23
DB 201 AAGTAGAGGCTTTCGCATG 182

RESULT 13
AAK03266/C
ID AAK03266 standard; DNA; 454 BP.
XX AC
XX AAK03266;
XX DT
XX 05-NOV-2001 (first entry)
XX DE
XX Human brain expressed single exon probe SEQ ID NO: 3257.
XX KW
XX Human; brain expressed exon; gene expression analysis; probe;
XX KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
XX KW epilepsy; cancer; ss.
XX OS Homo sapiens.
XX PN WO200157275-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US00667.

```



CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;

Query Match 73.0%; Score 16.8; DB 22; Length 454;

Best Local Similarity 90.0%; Pred. No. 90;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 4 AAGTCGAGGCTTTCAGCATG 23

|||||

Db 201 AAGTAGAGGCTTTCAGCATG 182

Search completed: June 12, 2003, 01:44:26

Job time : 134.802 secs

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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 01:18:34 ; Search time 22.066 Seconds  
(without alignments)  
319.658 Million cell updates/sec

Title: US-09-674-195c-17

Perfect score: 23  
Sequence: 1 dcaagtcgaggttcagcatg 23

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PTCUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	95.7	22	1	US-07-720-587A-1
2	17.4	75.7	4403765	4	US-09-103-840A-2
3	17.4	75.7	4411529	4	US-09-103-840A-1
C 4	15.8	68.7	738	2	US-08-224-591-13
C 5	15.8	68.7	738	2	US-08-392-338A-22
C 6	15.8	68.7	738	2	US-08-926-789-13
C 7	15.8	68.7	738	3	US-09-166-750-22
C 8	15.8	68.7	738	3	US-09-166-093-22
C 9	15.8	68.7	738	3	US-09-172-019-22
C 10	15.8	68.7	738	3	US-09-166-094-22
C 11	15.8	68.7	738	5	PCT-US93-11138-13
C 12	15.8	68.7	744	2	US-08-392-338A-12
C 13	15.8	68.7	744	3	US-09-166-750-12
C 14	15.8	68.7	744	3	US-09-166-093-12
C 15	15.8	68.7	744	3	US-09-172-019-12
C 16	15.8	68.7	744	3	US-09-166-094-12
C 17	15.8	68.7	758	4	US-09-069-821-1
C 18	15.8	68.7	782	4	US-09-420-592A-1
C 19	15.8	68.7	797	1	US-08-323-445A-3
C 20	15.8	68.7	797	1	US-08-515-903A-3
C 21	15.8	68.7	797	5	PCT-US95-12840-3
C 22	15.8	68.7	803	1	US-08-323-445A-7
C 23	15.8	68.7	803	1	US-08-515-903A-7
C 24	15.8	68.7	803	5	PCT-US95-12840-7
C 25	15.8	68.7	818	4	US-09-420-592A-3
C 26	15.8	68.7	1460	2	US-08-392-338A-18
C 27	15.8	68.7	1460	3	US-09-166-750-18

C 28	15.8	68.7	1460	3	US-09-166-093-18	Sequence 18, Appl
C 29	15.8	68.7	1460	3	US-09-172-019-18	Sequence 18, Appl
C 30	15.8	68.7	1460	3	US-09-166-094-18	Sequence 18, Appl
C 31	15.8	68.7	1722	1	US-08-055-945-1	Sequence 1, Appl
C 32	15.6	67.8	2033	1	US-08-148-910-14	Sequence 14, Appl
C 33	15.6	67.8	2033	1	US-08-448-937A-14	Sequence 14, Appl
C 34	15.6	67.8	2293	4	US-09-645-073-1	Sequence 1, Appl
C 35	15.4	67.0	870	1	US-08-411-706-1	Sequence 1, Appl
C 36	15.4	67.0	9515	1	US-08-920-812-13	Sequence 13, Appl
C 37	15.4	67.0	9515	1	US-08-920-827-13	Sequence 13, Appl
C 38	15.4	67.0	9515	1	US-08-921-177-13	Sequence 13, Appl
C 39	15.4	67.0	9515	1	US-08-362-577C-13	Sequence 13, Appl
C 40	15.4	67.0	9515	2	US-08-920-828-13	Sequence 13, Appl
C 41	15.4	67.0	12412	1	US-08-390-878-18	Sequence 18, Appl
C 42	15.4	67.0	4403765	4	US-09-103-840A-2	Sequence 2, Appl
C 43	15.2	66.1	522	4	US-09-221-017B-1065	Sequence 1065, Ap
C 44	15.2	66.1	709	4	US-08-998-416-281	Sequence 281, App
C 45	14.8	64.3	1029	2	US-08-899-011-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1  
US-07-720-587A-1  
; Sequence 1, Application US/07720587A  
; Patent No. 5352579  
; GENERAL INFORMATION:  
; APPLICANT: Curt L. Millman  
; TITLE OF INVENTION: NUCLEIC ACIDS PROBES  
; TITLE OF INVENTION: TO HISTOPLASMA CAPSULATUM  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM PS/2 Model 502 or 55SX  
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
; SOFTWARE: WordPerfect (Version 5.0)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/720,587A  
; FILING DATE: 19910628  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION DATA: including application  
; PRIOR APPLICATION DATA: described below:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 193/121  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 22  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-07-720-587A-1

Query Match 95.7%; Score 22; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGAAGTCGAGGCTTTCAGCATG 23  
Db 1 CGAAGTCGAGGCTTTCAGCATG 22

RESULT 2  
US-09-103-840A-2  
; Sequence 2, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; FILE REFERENCE: 24366-20007.00  
; CURRENT APPLICATION NUMBER: US/09/103,840A  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 4403765  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; FEATURE:  
; OTHER INFORMATION: CDC 1551  
; OTHER INFORMATION: "n" bases at various positions throughout the sequence  
; OTHER INFORMATION: represent a, t, c or g  
US-09-103-840A-2

Query Match 75.7%; Score 17.4; DB 4; Length 4403765;  
Best Local Similarity 82.6%; Pred. No. 21;  
Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DCGAAGTCGAGGCTTTCAGCATG 23  
Db 172049 TCGCTGTCGAGGCTTTCACCATG 172071

RESULT 3  
US-09-103-840A-1  
; Sequence 1, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; FILE REFERENCE: 24366-20007.00  
; CURRENT APPLICATION NUMBER: US/09/103,840A  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 4411529  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; OTHER INFORMATION: H37Rv  
US-09-103-840A-1

Query Match 75.7%; Score 17.4; DB 4; Length 4411529;  
Best Local Similarity 82.6%; Pred. No. 21;  
Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DCGAAGTCGAGGCTTTCAGCATG 23  
Db 171880 TCGCTGTCGAGGCTTTCACCATG 171902

RESULT 4

US-08-224-591-13/c  
; Sequence 13, Application US/08224591  
; Patent No. 5856456  
; GENERAL INFORMATION:  
; APPLICANT: Whitlow, Marc  
; APPLICANT: Filpula, David  
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/224,591  
; FILING DATE: Herewith  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/002,845  
; FILING DATE: 15-JAN-1993  
; APPLICATION NUMBER: US 07/980,529  
; FILING DATE: 20-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0977.1920002/JAG  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 738 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: join(1..726)  
US-08-224-591-13

Query Match 68.7%; Score 15.8; DB 2; Length 738;  
Best Local Similarity 89.5%; Pred. No. 44;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAAGTCGAGGCTTTCAGCA 21  
Db 350 GAAGTCGAGGCTTTCAGCA 332

RESULT 5  
US-08-392-338A-22/c  
; Sequence 22, Application US/08392338A  
; Patent No. 5869620  
; GENERAL INFORMATION:  
; APPLICANT: Whitlow, Marc  
; APPLICANT: Wood, James F.  
; APPLICANT: Hardman, Karl  
; APPLICANT: Bird, Robert  
; APPLICANT: Filpula, David  
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, NW  
; CITY: Washington  
; STATE: D.C.

COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/392,338A  
FILING DATE: 22-FEB-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/989,846  
FILING DATE: 20-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/796,936  
FILING DATE: 25-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.0030007  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 738 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..726  
US-08-392-338A-22

Query Match 68.7%; Score 15.8; DB 2; Length 738;  
Best Local Similarity 89.5%; Pred. No. 44;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGCGCTTCAGCA 21  
||||| ||| |||||  
Db 350 GAAGTAGAGCGCTTCAGCA 332

RESULT 6  
US-08-926-789-13/C  
Sequence 13, Application US/08926789  
Patent No. 5990275  
GENERAL INFORMATION:  
APPLICANT: Whitlow, Marc  
APPLICANT: Filpula, David  
TITLE OF INVENTION: Linker For Linked Fusion Polypeptides  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/926,789  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/724,591  
FILING DATE:  
APPLICATION NUMBER: US 08/002,845

FILING DATE: 15-JAN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/980,529  
FILING DATE: 20-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.1920002/JAG  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 738 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: CDS  
LOCATION: Join(1..726)  
US-08-926-789-13

Query Match 68.7%; Score 15.8; DB 2; Length 738;  
Best Local Similarity 89.5%; Pred. No. 44;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGCGCTTCAGCA 21  
||||| ||| |||||  
Db 350 GAAGTAGAGCGCTTCAGCA 332

RESULT 7  
US-09-166-750-22/C  
Sequence 22, Application US/09166750  
Patent No. 6025165  
GENERAL INFORMATION:  
APPLICANT: Whitlow, Marc  
APPLICANT: Wood, James F.  
APPLICANT: Hardman, Karl  
APPLICANT: Bird, Robert  
APPLICANT: Filpula, David  
APPLICANT: Rollence, Michelle  
TITLE OF INVENTION: Methods for Producing Multivalent Antigen-Binding  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, NW  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/166,750  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/392,338  
FILING DATE: 22-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/989,846  
FILING DATE: 20-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/796,936  
FILING DATE: 25-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021

REFERENCE/DOCKET NUMBER: 0977.003000C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 738 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..726  
US-09-166-750-22

Query Match 68.7%; Score 15.8; DB 3; Length 738;  
Best Local Similarity 89.5%; Pred. No. 44;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGCGCTTTCAGCA 21  
||||| ||| |||||  
DB 350 GAAGTAGAGCGCTTTCAGCA 332

RESULT 8  
US-09-166-093-22/c  
; Sequence 22, Application US/09166093  
; Patent No. 6027725  
; GENERAL INFORMATION:  
; APPLICANT: Whitlow, Marc  
; APPLICANT: Wood, James F.  
; APPLICANT: Hardman, Karl  
; APPLICANT: Bird, Robert  
; APPLICANT: Filpula, David  
; APPLICANT: Rollence, Michelle  
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, NW  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/166.093  
; FILING DATE: Herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/392,338  
; FILING DATE: 22-FEB-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/989,846  
; FILING DATE: 20-NOV-1992  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 07/796,936  
; FILING DATE: 25-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0977.003000B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 738 base pairs  
; TYPE: nucleic acid

STRANDEDNESS: both  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..726  
US-09-166-093-22  
Query Match 68.7%; Score 15.8; DB 3; Length 738;  
Best Local Similarity 89.5%; Pred. No. 44;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGCGCTTTCAGCA 21  
||||| ||| |||||  
DB 350 GAAGTAGAGCGCTTTCAGCA 332

RESULT 9  
US-09-172-019-22/c  
; Sequence 22, Application US/09172019  
; Patent No. 6103889  
; GENERAL INFORMATION:  
; APPLICANT: Whitlow, Marc  
; APPLICANT: Hardman, Karl  
; APPLICANT: Bird, Robert  
; APPLICANT: Filpula, David  
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Single-Chain  
; Antigen-Binding Proteins (As Amended)  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, NW  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/172.019  
; FILING DATE: Herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/392,338  
; FILING DATE: 22-FEB-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/989,846  
; FILING DATE: 20-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/796,936  
; FILING DATE: 25-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0977.003000D  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 738 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..726  
US-09-172-019-22  
Query Match 68.7%; Score 15.8; DB 3; Length 738;  
Best Local Similarity 89.5%; Pred. No. 44;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGGCTTTCAGCA 21  
||||| ||| |||||||||  
Db 350 GAAGTAGAGCCTTTCAGCA 332

## RESULT 10

US-09-166-094-22/c  
; Sequence 22, Application US/09166094  
; Patent No. 6121424  
; GENERAL INFORMATION:  
; APPLICANT: Whitlow, Marc  
; APPLICANT: Wood, James F.  
; APPLICANT: Hardman, Karl  
; APPLICANT: Bird, Robert  
; APPLICANT: Filpula, David  
; APPLICANT: Rolence, Michelle  
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, NW  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/09166,094  
; FILING DATE: Herewith

CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/392,338  
; FILING DATE: 22-FEB-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/989,846  
; FILING DATE: 20-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/796,936  
; FILING DATE: 25-NOV-1991

ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0977.003000A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 738 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..726  
US-09-166-094-22

Query Match 68.7%; Score 15.8; DB 3; Length 738;  
Best Local Similarity 89.5%; Pred. No. 44;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGGCTTTCAGCA 21  
||||| ||| |||||||||  
Db 350 GAAGTAGAGCCTTTCAGCA 332

## RESULT 11

PCT-US93-11138-13/c  
; Sequence 13, Application PC/TUS9311138  
; GENERAL INFORMATION:  
; APPLICANT: Enzon, Inc.  
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-3934

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/11138  
; FILING DATE: Herewith

CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/980,529  
; FILING DATE: 20-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/002,845  
; FILING DATE: 15-JAN-1993

ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0977.2006604/JAG  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 738 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..738

PCT-US93-11138-13

Query Match 68.7%; Score 15.8; DB 5; Length 738;  
Best Local Similarity 89.5%; Pred. No. 44;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGGCTTTCAGCA 21  
||||| ||| |||||||||  
Db 350 GAAGTAGAGCCTTTCAGCA 332

## RESULT 12

US-08-392-338A-12/c  
; Sequence 12, Application US/08392338A  
; Patent No. 5869820  
; GENERAL INFORMATION:  
; APPLICANT: Whitlow, Marc  
; APPLICANT: Wood, James F.  
; APPLICANT: Hardman, Karl  
; APPLICANT: Bird, Robert  
; APPLICANT: Filpula, David  
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, NW  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.

ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/392,338A  
FILING DATE: 22-FEB-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/989,846  
FILING DATE: 20-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/796,936  
FILING DATE: 25-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.0030007  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 744 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..732  
US-08-392-338A-12

Query Match 68.7%; Score 15.8; DB 2; Length 744;  
Best Local Similarity 89.5%; Pred. No. 44;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGCGCTTCAGCA 21  
||||| ||| |||||  
DB 350 GAAGTAGAGCGCTTCAGCA 332

RESULT 13  
US-09-166-750-12/c  
Sequence 12, Application US/09166750  
Patent No. 6025165  
GENERAL INFORMATION:  
APPLICANT: Whitlow, Marc  
APPLICANT: Wood, James F.  
APPLICANT: Hardman, Karl  
APPLICANT: Bird, Robert  
APPLICANT: Filpula, David  
APPLICANT: Rollence, Michelle  
TITLE OF INVENTION: Methods for Producing Multivalent Antigen-Binding  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, NW  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/166,750  
FILING DATE: Herewith  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/392,338  
FILING DATE: 22-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/989,846  
FILING DATE: 20-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/796,936  
FILING DATE: 25-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.003000C  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 744 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..732  
US-09-166-750-12

Query Match 68.7%; Score 15.8; DB 3; Length 744;  
Best Local Similarity 89.5%; Pred. No. 44;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGCGCTTCAGCA 21  
||||| ||| |||||  
DB 350 GAAGTAGAGCGCTTCAGCA 332

RESULT 14  
US-09-166-093-12/c  
Sequence 12, Application US/09166093  
Patent No. 6027725  
GENERAL INFORMATION:  
APPLICANT: Whitlow, Marc  
APPLICANT: Wood, James F.  
APPLICANT: Hardman, Karl  
APPLICANT: Bird, Robert  
APPLICANT: Filpula, David  
APPLICANT: Rollence, Michelle  
TITLE OF INVENTION: Multivalent Antigen-Binding Proteins  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, NW  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/166,093  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/392,338  
FILING DATE: 22-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/989,846  
FILING DATE: 20-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/796,936

; FILING DATE: 25-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0977.003000B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 744 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..732  
US-09-166-093-12

Query Match 68.7%; Score 15.8; DB 3; Length 744;  
Best Local Similarity 89.5%; Pred. No. 44;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGCCTTCAGCA 21  
||||| ||| |||||  
Db 350 GAAGTAGAGCCTTCAGCA 332

## RESULT 15

US-09-172-019-12/c  
; Sequence 12, Application US/09172019  
; Patent No. 6103889

## ; GENERAL INFORMATION:

; APPLICANT: Whitlow, Marc  
; APPLICANT: Hardman, Karl  
; APPLICANT: Bird, Robert  
; APPLICANT: Filipula, David  
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Single-Chain  
; TITLE OF INVENTION: Antigen-Binding Proteins (As Amended)  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, NW  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005

## ; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/172,019  
; FILING DATE: Herewith

## ; CLASSIFICATION:

## ; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/392,338  
; FILING DATE: 22-FEB-1995

## ; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/989,846  
; FILING DATE: 20-NOV-1992

## ; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/796,936  
; FILING DATE: 25-NOV-1991

## ; ATTORNEY/AGENT INFORMATION:

; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0977.003000D  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 12:

## ; SEQUENCE CHARACTERISTICS:

; LENGTH: 744 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both

## ; FEATURE:

; NAME/KEY: CDS  
; LOCATION: 1..732  
US-09-172-019-12

Query Match 68.7%; Score 15.8; DB 3; Length 744;  
Best Local Similarity 89.5%; Pred. No. 44;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGCCTTCAGCA 21  
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Db 350 GAAGTAGAGCCTTCAGCA 332

Search completed: June 12, 2003, 04:39:26  
Job time : 53.066 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 01:27:04 ; Search time 134.381 Seconds  
(without alignments)  
239.539 Million cell updates/sec

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Perfect score: 23  
Sequence: 1 dcaagtcgagcgtttcagcatg 23

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*  
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pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	17.2	74.8	1691139	9	US-10-067-514-1
2	16.8	73.0	454	10	US-09-864-761-3226
3	16.4	71.3	891	9	US-09-989-643-155
4	16.4	71.3	1097	10	US-09-974-300-179
5	15.8	68.7	310	10	US-09-878-574-665
6	15.8	68.7	375	10	US-09-878-574-3603
7	15.8	68.7	397	10	US-09-867-701-8410
8	15.8	68.7	550	9	US-09-991-936-838
9	15.8	68.7	723	10	US-09-791-578-5
10	15.8	68.7	723	10	US-09-791-540-5
11	15.8	68.7	758	9	US-09-956-086-1
12	15.8	68.7	758	9	US-09-956-087-1
13	15.8	68.7	782	9	US-09-985-442-1
14	15.8	68.7	782	10	US-09-791-578-3
15	15.8	68.7	782	10	US-09-791-540-3
16	15.8	68.7	782	10	US-09-983-580-1
17	15.8	68.7	818	9	US-09-985-442-3
18	15.8	68.7	818	10	US-09-983-580-3
19	15.8	68.7	933	9	US-09-938-842A-536

c	20	15.8	68.7	981	10	US-09-770-445-271	Sequence 271, App
	21	15.8	68.7	1279	9	US-10-165-603-19	Sequence 19, Appli
	22	15.8	68.7	177556	9	US-09-952-213D-6	Sequence 6, Appli
c	23	15.6	67.8	2036	10	US-09-954-456-552	Sequence 552, App
c	24	15.6	67.8	2036	10	US-09-880-107-1612	Sequence 1612, Ap
c	25	15.6	67.8	20556	10	US-09-880-107-3945	Sequence 3945, Ap
c	26	15.4	67.0	1413	9	US-09-894-844-25	Sequence 25, Appli
c	27	15.4	67.0	1579	10	US-09-822-849A-139	Sequence 139, App
c	28	15.4	67.0	3119	10	US-09-867-701-10873	Sequence 10873, A
	29	15.4	67.0	34094	9	US-10-199-550-1	Sequence 1, Appli
	30	15.4	67.0	1503841	9	US-09-946-807-1	Sequence 1, Appli
	31	15.4	67.0	1503841	10	US-09-795-668-1	Sequence 1, Appli
	32	15.4	67.0	1503841	10	US-09-795-668-1	Sequence 1, Appli
	33	15.2	66.1	365	10	US-09-783-590-10265	Sequence 10265, A
	34	15.2	66.1	768	10	US-09-910-943-408	Sequence 408, App
c	35	15.2	66.1	843	9	US-10-164-433-1	Sequence 1, Appli
c	36	15.2	66.1	1014	10	US-09-815-242-7828	Sequence 7828, Ap
c	37	15.2	66.1	1186	9	US-09-925-299-98	Sequence 98, Appli
c	38	15.2	66.1	1186	10	US-09-925-299-98	Sequence 98, Appli
c	39	15.2	66.1	7090	9	US-09-832-292-28	Sequence 28, Appli
c	40	15.2	66.1	8268	9	US-10-074-095-868	Sequence 868, App
c	41	15.2	66.1	8268	10	US-09-764-860-868	Sequence 868, App
c	42	15.2	66.1	8272	9	US-10-074-095-867	Sequence 867, App
c	43	15.2	66.1	8272	10	US-09-764-860-867	Sequence 867, App
	44	15.2	66.1	24768	9	US-10-073-961-602	Sequence 602, App
	45	15.2	66.1	24768	10	US-09-764-887-602	Sequence 602, App

ALIGNMENTS

RESULT 1  
US-10-067-514-1  
; Sequence 1, Application US/10067514  
; Publication No. US20030054531A1  
; GENERAL INFORMATION:  
; APPLICANT: Gretarsdottir, Solveig  
; APPLICANT: Jonsdottir, Sif  
; APPLICANT: Reynisdottir, Sigridur Th.  
; TITLE OF INVENTION: HUMAN STROKE GENE  
; FILE REFERENCE: 2345.2010-003  
; CURRENT APPLICATION NUMBER: US/10/067,514  
; CURRENT FILING DATE: 2002-02-04  
; PRIOR APPLICATION NUMBER: US 09/811/352  
; PRIOR FILING DATE: 2001-03-19  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1691139  
; TYPE: DNA  
; ORGANISM: Human  
US-10-067-514-1

Query Match 74.8%; Score 17.2; DB 9; Length 1691139;  
Best Local Similarity 86.4%; Pred. No. 37;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CGAAGTCGAGCGCTTTCAGCATG 23  
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Db 758783 CGAAGTGATGCTTTCAGCATG 758804  
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RESULT 2  
US-09-864-761-3226/c  
; Sequence 3226, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO  
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

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; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 3226
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL050331.11
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.99
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
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; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.98
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
; US-09-864-761-3226

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Best Local Similarity 90.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 201 AAGTAGAGGCTTCTGCATG 182

RESULT 3
US-09-989-643-155/c
; Sequence 155, Application US/09989643
; Publication No. US20030049636A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Michael D.
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.

; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 3226
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL050331.11
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.99
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.98
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
; US-09-864-761-3226

Query Match 73.0%; Score 16.8; DB 10; Length 454;
Best Local Similarity 90.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 201 AAGTAGAGGCTTCTGCATG 182

RESULT 3
US-09-989-643-155/c
; Sequence 155, Application US/09989643
; Publication No. US20030049636A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Michael D.
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.

```

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(15401)B  
; CURRENT APPLICATION NUMBER: US/09/878,574  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 09/333,535  
; PRIOR FILING DATE: 1999-06-14  
; NUMBER OF SEQ ID NOS: 15775  
; SEQ ID NO 665  
; LENGTH: 310  
; TYPE: DNA  
; ORGANISM: Glycine max  
; OTHER INFORMATION: Clone ID: LIB3028-047-Q1-B1-H11  
US-09-878-574-665

Query Match 68.7%; Score 15.8; DB 10; Length 310;  
Best Local Similarity 78.3%; Pred. No. 1.1e+02;  
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DCGAAGTCGAGGCTTTCAGCATG 23  
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Db 263 TCCAAGTCAAGGTTTAAAGCATG 285

## RESULT 6

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; Sequence 3603, Application US/09878574  
; Patent No. US20020110548A1  
; GENERAL INFORMATION:  
; APPLICANT: BYTUM, Joseph R.  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Thompson, Michael D.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(15401)B  
; CURRENT APPLICATION NUMBER: US/09/878,574  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 09/333,535  
; PRIOR FILING DATE: 1999-06-14  
; NUMBER OF SEQ ID NOS: 15775  
; SEQ ID NO 3603  
; LENGTH: 375  
; TYPE: DNA  
; ORGANISM: Glycine max  
; OTHER INFORMATION: Clone ID: LIB3028-008-Q1-B1-D10  
US-09-878-574-3603

Query Match 68.7%; Score 15.8; DB 10; Length 375;  
Best Local Similarity 78.3%; Pred. No. 1.1e+02;  
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DCGAAGTCGAGGCTTTCAGCATG 23  
: ||||| ||||| ||||| |||||  
Db 180 TCGAAGTCGAGGCTTTCAGATTG 158

## RESULT 7

US-09-867-701-8410  
; Sequence 8410, Application US/09867701  
; Patent No. US20020132237A1  
; GENERAL INFORMATION:  
; APPLICANT: Aglate, Paul A.  
; APPLICANT: Jones, Robert  
; APPLICANT: Harlocker, Susan L.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.497  
; CURRENT APPLICATION NUMBER: US/09/867,701  
; CURRENT FILING DATE: 2001-05-29  
; NUMBER OF SEQ ID NOS: 10912  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8410  
; LENGTH: 397

; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-867-701-8410

Query Match 68.7%; Score 15.8; DB 10; Length 397;  
Best Local Similarity 78.3%; Pred. No. 1.1e+02;  
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DCGAAGTCGAGGCTTTCAGCATG 23  
: ||||| ||||| ||||| |||||  
Db 282 TCAAAGTAGTGGCTTTCGATG 304

## RESULT 8

US-09-991-936-838  
; Sequence 838, Application US/09991936  
; Publication No. US20030073827A1  
; GENERAL INFORMATION:  
; APPLICANT: Brandt, Kevin S.  
; APPLICANT: Gaines, Patrick J.  
; APPLICANT: Stinchcomb, Dan T.  
; APPLICANT: Wisniewski, Nancy  
; TITLE OF INVENTION: FLEA HEAD, NERVE CORD, HINDGUT AND MALPIGHIAN TUBULE  
; FILE OF INVENTION: NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF  
; FILE REFERENCE: FC-6-C1  
; CURRENT APPLICATION NUMBER: US/09/991,936  
; CURRENT FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: US/09/543,668  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: 60/128,704  
; NUMBER OF SEQ ID NOS: 1959  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 838  
; LENGTH: 550  
; TYPE: DNA  
; ORGANISM: Ctencephalides felis  
US-09-991-936-838

Query Match 68.7%; Score 15.8; DB 9; Length 550;  
Best Local Similarity 89.5%; Pred. No. 1.1e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGGCTTTCAGCA 21  
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Db 156 GAAGTCGAGGCTTTCAGCA 174

## RESULT 9

US-09-791-578-5/c  
; Sequence 5, Application US/09791578  
; Patent No. US20020061307A1  
; GENERAL INFORMATION:  
; APPLICANT: WHITLOW, MARC  
; SHORR, ROBERT G.L.  
; FILPULA, DAVID R.  
; LEE, LIHSYNG S.  
; TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 NEW YORK AVENUE, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/791,578  
FILING DATE: 26-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/069,842  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 60/050,472  
FILING DATE: 23-JUN-1997  
APPLICATION NUMBER: US 60/063,074  
FILING DATE: 27-OCT-1997  
APPLICATION NUMBER: US 60/067,341  
FILING DATE: 02-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: JORGE A. GOLDSTEIN  
REGISTRATION/DOCKET NUMBER: 0977.1840002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2540  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 723 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..723  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-791-578-5

Query Match 68.7%; Score 15.8; DB 10; Length 723;  
Best Local Similarity 89.5%; Pred. No. 1.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGGCTTCAGCA 21  
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Db 350 GAAGTAGAGCCTTCAGCA 332

RESULT 10  
US-09-791-540-5/c  
Sequence 5, Application US/09791540  
Patent No. US20020098192A1  
GENERAL INFORMATION:  
APPLICANT: WHITLOW, MARC  
SHORR, ROBERT G.L.  
FILPULA, DAVID R.  
LEE, LIHSYNG S.  
TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN  
POLYPEPTIDES  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVENUE, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/791,540  
FILING DATE: 26-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/069,842  
FILING DATE: 1998-04-30  
APPLICATION NUMBER: US 60/050,472  
FILING DATE: 23-JUN-1997

APPLICATION NUMBER: US 60/063,074  
FILING DATE: 27-OCT-1997  
APPLICATION NUMBER: US 60/067,341  
FILING DATE: 02-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: JORGE A. GOLDSTEIN  
REGISTRATION/DOCKET NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.1840002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 723 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..723  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-791-540-5

Query Match 68.7%; Score 15.8; DB 10; Length 723;  
Best Local Similarity 89.5%; Pred. No. 1.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGGCTTCAGCA 21  
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Db 350 GAAGTAGAGCCTTCAGCA 332

RESULT 11  
US-09-956-086-1/c  
Sequence 1, Application US/09956086  
Patent No. US20020155498A1  
GENERAL INFORMATION:

APPLICANT: FILPULA, DAVID  
WANG, MAOLIANG  
SHORR, ROBERT  
WHITLOW, MARC  
LEE, LIHSYNG S.

TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS  
CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF

NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVE., NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/956,086  
FILING DATE: 20-Sep-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/069,821  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 60/063,074  
FILING DATE: 27-OCT-1997  
APPLICATION NUMBER: US 60/050,472  
FILING DATE: 23-JUN-1997  
APPLICATION NUMBER: US 60/044,449  
FILING DATE: 30-APR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: KIM, JUDITH U.  
REGISTRATION NUMBER: 40,679

REFERENCE/DOCKET NUMBER: 0977.2280003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)371-2600  
TELEFAX: (202)371-2540  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 758 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..747  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-956-086-1

Query Match 68.7%; Score 15.8; DB 9; Length 758;  
Best Local Similarity 89.5%; Pred. No. 1.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGGCTTTCAGCA 21  
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DB 350 GAAGTAGAGCCTTTCAGCA 332

RESULT 12  
US-09-956-087-1/c  
Sequence 1, Application US/09956087  
Patent No. US20020161201A1  
GENERAL INFORMATION:  
APPLICANT: FILPULA, DAVID  
WANG, MAOLIANG  
SHORR, ROBERT  
WHITLOW, MARC  
LEE, LIHSYNG S.  
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS  
CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVE., NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/956,087  
FILING DATE: 20-Sep-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/069,821  
FILING DATE: 1998-04-30  
APPLICATION NUMBER: US 60/063,074  
FILING DATE: 27-OCT-1997  
APPLICATION NUMBER: US 60/050,472  
FILING DATE: 23-JUN-1997  
APPLICATION NUMBER: US 60/044,449  
FILING DATE: 30-APR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: KIM, JUDITH O.  
REGISTRATION NUMBER: 40,679  
REFERENCE/DOCKET NUMBER: 0977.2280003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)371-2600  
TELEFAX: (202)371-2540  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:

LENGTH: 758 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..747  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-956-087-1

Query Match 68.7%; Score 15.8; DB 9; Length 758;  
Best Local Similarity 89.5%; Pred. No. 1.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGGCTTTCAGCA 21  
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DB 350 GAAGTAGAGCCTTTCAGCA 332

RESULT 13  
US-09-985-442-1/c  
Sequence 1, Application US/09985442  
Patent No. US20020156248A1  
GENERAL INFORMATION:  
APPLICANT: FILPULA, DAVID R.  
APPLICANT: Wang, Maoliang  
APPLICANT: Whitlow, Marc D.  
TITLE OF INVENTION: No. US20020156248A1 Method for Targeted Delivery of Nucleic  
FILE REFERENCE: 0977.2300003  
CURRENT APPLICATION NUMBER: US/09/985,442  
CURRENT FILING DATE: 2001-11-02  
PRIOR APPLICATION NUMBER: 09/420,592  
PRIOR FILING DATE: 1999-10-19  
PRIOR APPLICATION NUMBER: 60/104,949  
PRIOR FILING DATE: 1998-10-20  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 782  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: CC49/218 sFV  
NAME/KEY: CDS  
LOCATION: (1)...(771)  
US-09-985-442-1

Query Match 68.7%; Score 15.8; DB 9; Length 782;  
Best Local Similarity 89.5%; Pred. No. 1.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGTCGAGGCTTTCAGCA 21  
||||| ||| ||||| |||||  
DB 350 GAAGTAGAGCCTTTCAGCA 332

RESULT 14  
US-09-791-578-3/c  
Sequence 3, Application US/09791578  
Patent No. US20020061307A1  
GENERAL INFORMATION:  
APPLICANT: WHITLOW, MARC  
SHORR, ROBERT G.L.  
FILPULA, DAVID R.  
LEE, LIHSYNG S.  
TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN  
POLYPEPTIDES  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVENUE, SUITE 600  
CITY: WASHINGTON

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;
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/791.578
; FILING DATE: 26-Feb-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/069,842
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/050,472
; FILING DATE: 23-JUN-1997
; APPLICATION NUMBER: US 60/063,074
; FILING DATE: 27-OCT-1997
; APPLICATION NUMBER: US 60/067,341
; FILING DATE: 02-DEC-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: JORGE A. GOLDSTEIN
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.1840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
;
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 782 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..771
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; Query Match 68.7%; Score 15.8; DB 10; Length 782;
; Best Local Similarity 89.5%; Pred. No. 1.2e+02;
; Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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; DB 350 GAAGTAGAGCCTTTCAGCA 332
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; RESULT 15
; US-09-791-540-3/c
; Sequence 3, Application US/09791540
; Patent No. US20020098192A1
; GENERAL INFORMATION:
; APPLICANT: WHITLOW, MARC
; SHORR, ROBERT G.L.
; FILPULA, DAVID R.
; LEE, LIHSYNG S.
;
; TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN
; POLYPEPTIDES
;
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNER, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/791.540
; FILING DATE: 26-Feb-2001
; CLASSIFICATION: <Unknown>
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/069,842
; FILING DATE: 1998-04-30
; APPLICATION NUMBER: US 60/050,472
; FILING DATE: 23-JUN-1997
; APPLICATION NUMBER: US 60/063,074
; FILING DATE: 27-OCT-1997
; APPLICATION NUMBER: US 60/067,341
; FILING DATE: 02-DEC-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: JORGE A. GOLDSTEIN
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.1840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
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; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 782 base pairs
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; STRANDEDNESS: both
; TOPOLOGY: both
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; DB 350 GAAGTAGAGCCTTTCAGCA 332
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GenCore version 5.1.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 00:35:54 ; Search time 844.228 Seconds  
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Title: US-09-674-195C-17

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: em\_esthum.\*
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- 7: em\_estro.\*
- 8: em\_htc.\*
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- 11: gb\_htc.\*
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- 26: em\_gss\_pro.\*
- 27: em\_gss\_rtd.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 6	18.8	81.7	391	12	BF251561 EST418910

C 7	18.8	81.7	486	10	AW792005
C 8	18.8	81.7	488	12	BF251704
C 9	18.8	81.7	502	12	BF252581
C 10	18.8	81.7	515	10	AW792430
C 11	18.8	81.7	518	12	BF251715
C 12	18.8	81.7	541	12	BF252371
C 13	18.8	81.7	546	12	BF253171
C 14	18.8	81.7	567	12	BF252094
C 15	18.8	81.7	568	12	BF252878
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C 17	18.8	81.7	605	12	BF252135
C 18	18.8	81.7	679	12	BF251385
C 19	18.8	81.7	687	12	BF251001
C 20	18.8	81.7	701	12	BF251666
C 21	18.8	81.7	836	12	BF250962
C 22	18.8	78.3	578	14	W36400
C 23	17.8	77.4	222	10	AW791051
C 24	17.8	77.4	905	17	CNS077PT
C 25	17.8	77.4	914	17	CNS079TL
C 26	17.8	77.4	944	17	CNS07827
C 27	17.8	77.4	957	17	CNS0797C
C 28	17.8	77.4	992	17	CNS0784M
C 29	17.8	77.4	997	17	CNS07A19
C 30	17.8	77.4	1008	17	CNS076RF
C 31	17.8	77.4	1012	17	CNS079X1
C 32	17.8	77.4	1020	17	CNS077XC
C 33	17.8	77.4	1031	17	CNS076VJ
C 34	17.8	77.4	1060	17	CNS078EU
C 35	17.4	75.7	572	17	A2361913
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C 43	17.2	74.8	252	9	AI211979
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ALIGNMENTS

RESULT 1  
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DEFINITION immitis cDNA clone CIAAK37 5' sequence, mRNA sequence.  
ACCESSION BF251708  
VERSION BF251708.1 GI:16931774  
KEYWORDS EST.  
SOURCE Coccidioides immitis.  
ORGANISM Coccidioides immitis.  
REFERENCE 1 (bases 1 to 123)  
AUTHORS Gardner, M.J. and Kirkland, T.  
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library  
JOURNAL Unpublished (2000)  
COMMENT Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org.

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Query Match 81.7%; Score 18.8; DB 12; Length 123;  
Best Local Similarity 90.9%; Pred. No. 50;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CGAAGTCGAGGCTTTCAGCATG 23  
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Db 80 CGAAGTCGAGGCTTTCAGCATG 59

RESULT 2  
BF251693/c  
LOCUS  
DEFINITION EST418877 Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone CIAAK21 5' sequence, mRNA sequence.  
ACCESSION BF251693  
VERSION BF251693.1 GI:16931759  
KEYWORDS EST.  
SOURCE Coccidioides immitis.  
ORGANISM Coccidioides immitis.

REFERENCE  
AUTHORS Gardner, M.J. and Kirkland, T.  
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library  
JOURNAL Unpublished (2000)  
COMMENT Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org.

BASE COUNT 97 a 69 c 81 g 104 t  
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/lab\_host="SOLR"  
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XhoI"

Query Match 81.7%; Score 18.8; DB 12; Length 351;  
Best Local Similarity 90.9%; Pred. No. 94;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CGAAGTCGAGGCTTTCAGCATG 23  
|||||  
Db 176 CGAAGTCGAGGCTTTCAGCATG 155

RESULT 3  
BF251811/c  
LOCUS

DEFINITION EST419073 Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone CIAAM73 5' sequence, mRNA sequence.  
ACCESSION BF251811  
VERSION BF251811.1 GI:16931954  
KEYWORDS EST.  
SOURCE Coccidioides immitis.  
ORGANISM Coccidioides immitis.

REFERENCE  
AUTHORS Gardner, M.J. and Kirkland, T.  
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library  
JOURNAL Unpublished (2000)  
COMMENT Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org.

BASE COUNT 97 a 69 c 81 g 104 t  
ORIGIN  
/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="vector: pbluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI"

Query Match 81.7%; Score 18.8; DB 12; Length 351;  
Best Local Similarity 90.9%; Pred. No. 94;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CGAAGTCGAGGCTTTCAGCATG 23  
|||||  
Db 176 CGAAGTCGAGGCTTTCAGCATG 155

RESULT 3  
BF251811/c  
LOCUS

DEFINITION EST419073 Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone CIAAM73 5' sequence, mRNA sequence.  
ACCESSION BF251811  
VERSION BF251811.1 GI:16931954  
KEYWORDS EST.  
SOURCE Coccidioides immitis.  
ORGANISM Coccidioides immitis.

REFERENCE  
AUTHORS Gardner, M.J. and Kirkland, T.  
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library  
JOURNAL Unpublished (2000)  
COMMENT Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org.

BASE COUNT 98 a 69 c 84 g 111 t  
ORIGIN  
/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="vector: pbluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI"

FEATURES  
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1..362  
Location/Qualifiers

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/organism="Coccidioides immitis"  
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/clone="CIAAM73"  
/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="vector: pbluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI"

Query Match 81.7%; Score 18.8; DB 12; Length 362;  
Best Local Similarity 90.9%; Pred. No. 95;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CGAAGTCGAGGCTTTCAGCATG 23  
|||||  
Db 171 CGAAGTCGAGGCTTTCAGCATG 150

RESULT 4  
BF251964/c  
LOCUS

DEFINITION EST419226 Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone CIAAP15 5' sequence, mRNA sequence.  
ACCESSION BF251964  
VERSION BF251964.1 GI:16932107  
KEYWORDS EST.  
SOURCE Coccidioides immitis.  
ORGANISM Coccidioides immitis.

REFERENCE  
AUTHORS Gardner, M.J. and Kirkland, T.  
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library  
JOURNAL Unpublished (2000)  
COMMENT Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org.

BASE COUNT 103 a 85 c 94 g 95 t  
ORIGIN  
/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="vector: pbluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI"

Query Match 81.7%; Score 18.8; DB 12; Length 377;  
Best Local Similarity 90.9%; Pred. No. 98;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CGAAGTCGAGGCTTTCAGCATG 23  
|||||  
Db 171 CGAAGTCGAGGCTTTCAGCATG 150

RESULT 4  
BF251964/c  
LOCUS

DEFINITION EST419226 Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone CIAAP15 5' sequence, mRNA sequence.  
ACCESSION BF251964  
VERSION BF251964.1 GI:16932107  
KEYWORDS EST.  
SOURCE Coccidioides immitis.  
ORGANISM Coccidioides immitis.

REFERENCE  
AUTHORS Gardner, M.J. and Kirkland, T.  
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library  
JOURNAL Unpublished (2000)  
COMMENT Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org.

BASE COUNT 103 a 85 c 94 g 95 t  
ORIGIN  
/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="vector: pbluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI"

Query Match 81.7%; Score 18.8; DB 12; Length 377;  
Best Local Similarity 90.9%; Pred. No. 98;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CGAAGTCGAGGCTTTCAGCATG 23  
|||||  
Db 171 CGAAGTCGAGGCTTTCAGCATG 150

RESULT 4  
BF251964/c  
LOCUS

DEFINITION EST419226 Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone CIAAP15 5' sequence, mRNA sequence.  
ACCESSION BF251964  
VERSION BF251964.1 GI:16932107  
KEYWORDS EST.  
SOURCE Coccidioides immitis.  
ORGANISM Coccidioides immitis.

REFERENCE  
AUTHORS Gardner, M.J. and Kirkland, T.  
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library  
JOURNAL Unpublished (2000)  
COMMENT Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org.

BASE COUNT 103 a 85 c 94 g 95 t  
ORIGIN  
/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="vector: pbluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI"

Query Match 81.7%; Score 18.8; DB 12; Length 377;  
Best Local Similarity 90.9%; Pred. No. 98;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CGAAGTCGAGGCTTTCAGCATG 23  
|||||  
Db 171 CGAAGTCGAGGCTTTCAGCATG 150

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QY 2 CGAGTCGAGGCTTTCAGCATG 23
    ||||||| ||| |||||
Db 75 CGAGTCGAGGTTTTAGCATG 54

RESULT 5
BF251967/c
LOCUS
DEFINITION
    BF251967 378 bp mRNA linear EST 15-NOV-2001
    immitis cDNA clone CIAAP18 5' sequence, mRNA sequence.
ACCESSION
    BF251967
VERSION
    BF251967.1 GI:16932110
KEYWORDS
    EST.
SOURCE
    Coccidioides immitis.
ORGANISM
    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
    Onygena; mitosporic Onygenales; Coccidioides.
REFERENCE
    1 (bases 1 to 378)
AUTHORS
    Gardner, M.J. and Kirkland, T.
TITLE
    Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL
    Unpublished (2000)
COMMENT
    Contact: Malcolm J. Gardner
    Department of Eukaryotic Genomics
    The Institute for Genomic Research
    9712 Medical Center Drive, Rockville, MD 20850, USA
    Tel: 301 838 3519
    Fax: 301 838 0208
    Email: gardner@tigr.org.

FEATURES
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    1..378
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    /lab_host="SOLR"
    /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
    XhoI"

BASE COUNT 104 a 75 c 94 g 105 t
ORIGIN
    Query Match 81.7%; Score 18.8; DB 12; Length 378;
    Best Local Similarity 90.9%; Pred. No. 98; Indels 0; Gaps 0;
    Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAGTCGAGGCTTTCAGCATG 23
    ||||||| ||| |||||
Db 169 CGAGTCGAGGTTTTAGCATG 148

RESULT 6
BF251561/c
LOCUS
DEFINITION
    BF251561 391 bp mRNA linear EST 15-NOV-2001
    immitis cDNA clone CIAAK57 5' sequence, mRNA sequence.
ACCESSION
    BF251561
VERSION
    BF251561.1 GI:16931792
KEYWORDS
    EST.
SOURCE
    Coccidioides immitis.
ORGANISM
    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
    Onygenales; mitosporic Onygenales; Coccidioides.
REFERENCE
    1 (bases 1 to 391)
AUTHORS
    Gardner, M.J. and Kirkland, T.
TITLE
    Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL
    Unpublished (2000)
COMMENT
    Contact: Malcolm J. Gardner
    Department of Eukaryotic Genomics
    The Institute for Genomic Research
    9712 Medical Center Drive, Rockville, MD 20850, USA
    Tel: 301 838 3519
    Fax: 301 838 0208
    Email: gardner@tigr.org.

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FEATURES
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    /dev_stage="spherule"
    /lab_host="SOLR"
    /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
    XhoI"

BASE COUNT 107 a 76 c 96 g 112 t
ORIGIN
    Query Match 81.7%; Score 18.8; DB 12; Length 391;
    Best Local Similarity 90.9%; Pred. No. 1e+02; Indels 0; Gaps 0;
    Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAGTCGAGGCTTTCAGCATG 23
    ||||||| ||| |||||
Db 176 CGAGTCGAGGTTTTAGCATG 155

RESULT 7
AW792005/c
LOCUS
DEFINITION
    AW792005 486 bp mRNA linear EST 01-MAY-2001
    D00948-R Lambda Zap, Stratagene Blumeria graminis f. sp. hordei
    cDNA clone D00948 similar to non-functional folate binding protein,
    mRNA sequence.
ACCESSION
    AW792005
VERSION
    AW792005.1 GI:13903602
KEYWORDS
    EST.
SOURCE
    Blumeria graminis f. sp. hordei.
ORGANISM
    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomyces;
    Erysiphales; Erysiphaceae; Blumeria.
REFERENCE
    1 (bases 1 to 486)
AUTHORS
    Thomas, S.W., Rasmussen, S.W., Glaring, M.A., Rouster, J.A. and Oliver
    , R.P.
TITLE
    Gene identification in the fungal pathogen Blumeria graminis by
    expressed sequence tag analysis
JOURNAL
    Unpublished (2000)
COMMENT
    Contact: Rasmussen, S.W.
    Department of Yeast Genetics
    Carlsberg Laboratory
    10 Gl. Carlsbergvej, DK-2500, Copenhagen, Denmark
    Tel: 45 3327 5230
    Fax: 45 3327 4766
    Email: sw@erc.dk
    High quality sequence stop: 486
    POLYA-No.

FEATURES
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    Location/Qualifiers
    1..486
    /organism="Blumeria graminis f. sp. hordei"
    /db_xref="taxon:62688"
    /clone_lib="D00948"
    /dev_stage="conidia"
    /cell_type="conidia"
    /lab_host="Hordeum vulgare"
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BASE COUNT 138 a 101 c 115 g 132 t
ORIGIN
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    Best Local Similarity 90.9%; Pred. No. 1.1e+02; Indels 0; Gaps 0;
    Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAGTCGAGGCTTTCAGCATG 23
    ||||||| ||| |||||
Db 176 CGAGTCGAGGTTTTAGCATG 155

RESULT 8
BF251704/c
LOCUS
    BF251704 488 bp mRNA linear EST 15-NOV-2001

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DEFINITION EST418888 Coccidioides immitis spherule cDNA library Coccidioides immitis cDNA clone CIAK33 5' sequence, mRNA sequence.

ACCESSION BF251704  
VERSION BF251704.1 GI:16931770  
KEYWORDS EST.  
SOURCE Coccidioides immitis.

ORGANISM Coccidioides immitis.  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; mitosporic Onygenales; Coccidioides.

REFERENCE 1 (bases 1 to 488)  
AUTHORS Gardner, M.J. and Kirkland, T.  
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library  
JOURNAL Unpublished (2000)  
COMMENT Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org.

FEATURES  
source Location/Qualifiers

1..488  
/organism="Coccidioides immitis"  
/db\_xref="taxon:5501"  
/clone="CIAK33"  
/clone\_lib="Coccidioides immitis spherule cDNA library"  
/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT 129 a 97 c 126 g 136 t

Query Match 81.7%; Score 18.8; DB 12; Length 488;  
Best Local Similarity 90.9%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTCAGCATG 23  
||||| ||||| ||||| ||||| |||||  
Db 176 CGAAGTCGAGGCTTTTAGCATG 155

RESULT 9  
BF252581/c

LOCUS BF252581 502 bp mRNA linear EST 15-NOV-2001  
DEFINITION EST419843 Coccidioides immitis spherule cDNA library Coccidioides immitis cDNA clone CIAAY35 5' sequence, mRNA sequence.

ACCESSION BF252581  
VERSION BF252581.1 GI:16932724  
KEYWORDS EST.  
SOURCE Coccidioides immitis.

ORGANISM Coccidioides immitis.  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; mitosporic Onygenales; Coccidioides.

REFERENCE 1 (bases 1 to 502)  
AUTHORS Gardner, M.J. and Kirkland, T.  
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library  
JOURNAL Unpublished (2000)  
COMMENT Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org.

FEATURES  
source Location/Qualifiers

1..502  
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/db\_xref="taxon:5501"  
/clone="CIAAY35"  
/clone\_lib="Coccidioides immitis spherule cDNA library"  
/dev\_stage="spherule"  
/lab\_host="SOLR"

/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT 142 a 101 c 126 g 133 t

Query Match 81.7%; Score 18.8; DB 12; Length 502;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTCAGCATG 23  
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Db 179 CGAAGTCGAGGCTTTTAGCATG 158

RESULT 10  
AW792430/c

LOCUS AW792430 515 bp mRNA linear EST 01-MAY-2001  
DEFINITION D01189-R Lambda Zap, Stratagene Blumeria graminis f. sp. hordei cDNA clone D01189 similar to non-functional folate binding protein, mRNA sequence.

ACCESSION AW792430  
VERSION AW792430.1 GI:13904027  
KEYWORDS EST.  
SOURCE Blumeria graminis f. sp. hordei.

ORGANISM Blumeria graminis f. sp. hordei.  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes; Erysiphales; Erysiphaceae; Blumeria.

REFERENCE 1 (bases 1 to 515)  
AUTHORS Thomas, S.W., Rasmussen, S.W., Glaring, M.A., Rouster, J.A. and Oliver, R.P.

TITLE Gene identification in the fungal pathogen Blumeria graminis by expressed sequence tag analysis  
JOURNAL Unpublished (2000)  
COMMENT Contact: Rasmussen, S.W.  
Department of Yeast Genetics  
Carlsberg Laboratory  
10 GI. Carlsbergvej, DK-2500, Copenhagen, Denmark  
Tel: 45 3327 5230  
Fax: 45 3327 4766  
Email: swr@crc.dk  
High quality sequence stop: 515  
POLYA-No.

FEATURES  
source Location/Qualifiers

1..515  
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/db\_xref="taxon:62688"  
/clone="D01189"  
/clone\_lib="Lambda zap, Stratagene"  
/cell\_type="conidia"  
/lab\_host="Hordeum vulgare"

BASE COUNT 150 a 104 c 119 g 142 t

Query Match 81.7%; Score 18.8; DB 10; Length 515;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTCAGCATG 23  
||||| ||||| ||||| ||||| |||||  
Db 169 CGAAGTCGAGGCTTTTAGCATG 148

RESULT 11  
BF251715/c

LOCUS BF251715 518 bp mRNA linear EST 15-NOV-2001  
DEFINITION EST418899 Coccidioides immitis spherule cDNA library Coccidioides immitis cDNA clone CIAAK45 5' sequence, mRNA sequence.

ACCESSION BF251715  
VERSION BF251715.1 GI:16931781  
KEYWORDS EST.  
SOURCE Coccidioides immitis.

ORGANISM Coccidioides immitis.  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Onygenales; mitosporic Onygenales; Coccidioides.  
1 (bases 1 to 518)  
Gardner M.J. and Kirkland, T.  
Generation of ESTs from Coccidioides immitis spherule cDNA library  
Unpublished (2000)  
Contact: Malcolm J. Gardner  
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The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org.

FEATURES  
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1..518  
/organism="Coccidioides immitis"  
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/clone="CIAA45"  
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/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI"

BASE COUNT 141 a 104 c 133 g 140 t  
ORIGIN  
Query Match 81.7%; Score 18.8; DB 12; Length 518;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTCAGCATG 23  
|||||  
Db 176 CGAAGTCGAGGCTTCAGCATG 155

RESULT 12  
BF252371/c  
LOCUS  
DEFINITION  
EST419633 Coccidioides immitis spherule cDNA library EST 15-NOV-2001  
Immitis cDNA clone CIAA41 5' sequence, mRNA sequence.  
BF252371  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Coccidioides immitis.  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; Mitosporic Onygenales; Coccidioides.  
1 (bases 1 to 541)  
Gardner M.J. and Kirkland, T.  
Generation of ESTs from Coccidioides immitis spherule cDNA library  
Unpublished (2000)  
Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org.

FEATURES  
source  
1..541  
/organism="Coccidioides immitis"  
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/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI"

BASE COUNT 157 a 109 c 133 g 142 t  
ORIGIN  
Query Match 81.7%; Score 18.8; DB 12; Length 541;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTCAGCATG 23  
|||||  
Db 176 CGAAGTCGAGGCTTCAGCATG 155

RESULT 13  
BF253171/c  
LOCUS  
DEFINITION  
EST445666 Coccidioides immitis spherule cDNA library EST 15-NOV-2001  
Immitis cDNA clone CIGAB68 5' sequence, mRNA sequence.  
BF253171  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Coccidioides immitis.  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; Mitosporic Onygenales; Coccidioides.  
1 (bases 1 to 546)  
Gardner M.J. and Kirkland, T.  
Generation of ESTs from Coccidioides immitis spherule cDNA library  
Unpublished (2000)  
Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org.

FEATURES  
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1..546  
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/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI"

BASE COUNT 157 a 109 c 135 g 145 t  
ORIGIN  
Query Match 81.7%; Score 18.8; DB 12; Length 546;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTCAGCATG 23  
|||||  
Db 179 CGAAGTCGAGGCTTCAGCATG 158

RESULT 14  
BF252094/c  
LOCUS  
DEFINITION  
EST419356 Coccidioides immitis spherule cDNA library EST 15-NOV-2001  
Immitis cDNA clone CIAAQ80 5' sequence, mRNA sequence.  
BF252094  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Coccidioides immitis.  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; Mitosporic Onygenales; Coccidioides.  
1 (bases 1 to 567)  
Gardner M.J. and Kirkland, T.  
Generation of ESTs from Coccidioides immitis spherule cDNA library  
Unpublished (2000)  
Contact: Malcolm J. Gardner  
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The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519

Fax: 301 838 0208  
 Email: gardner@tigr.org.  
 Location/Qualifiers  
 1. .567  
 /organism="Coccidioides immitis"  
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 /clone\_lib="Coccidioides immitis spherule cDNA library"  
 /dev\_stage="spherule"  
 /lab\_host="SOLR"  
 /note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
 XhoI"  
 BASE COUNT 161 a 118 c 142 g 146 t  
 ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 567;  
 Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAAGTCGAGGCTTTCAGCATG 23  
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 Db 182 CGAAGTCGAGGCTTTCAGCATG 161

RESULT 15  
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 DEFINITION ES7420141 Coccidioides immitis spherule cDNA library Coccidioides  
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 ACCESSION BF252878  
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 KEYWORDS EST.  
 SOURCE Coccidioides immitis.  
 ORGANISM Coccidioides immitis.  
 REFERENCE 1 (bases 1 to 568)  
 AUTHORS Onygenales; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 Title Generation of ESTs from Coccidioides immitis spherule cDNA library  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Malcolm J. Gardner  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301 838 3519  
 Fax: 301 838 0208  
 Email: gardner@tigr.org.

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 /lab\_host="SOLR"  
 /note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
 XhoI"  
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 ORIGIN

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QY 2 CGAAGTCGAGGCTTTCAGCATG 23  
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 Db 182 CGAAGTCGAGGCTTTCAGCATG 161

Search completed: June 12, 2003, 04:35:06  
 Job time : 845.943 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 22:21:06 ; Search time 348.269 Seconds  
(without alignments)  
1921.975 Million cell updates/sec

Title: US-09-674-195c-18  
Perfect score: 23  
Sequence: 1 dcatgctgaagcctgcacttcg 23

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_hgt.\*  
3: gb\_in.\*  
4: gb\_om.\*  
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6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*  
15: em\_ba.\*  
16: em\_fun.\*  
17: em\_hum.\*  
18: em\_in.\*  
19: em\_mu.\*  
20: em\_om.\*  
21: em\_or.\*  
22: em\_ov.\*  
23: em\_pat.\*  
24: em\_ph.\*  
25: em\_pl.\*  
26: em\_to.\*  
27: em\_sts.\*  
28: em\_un.\*  
29: em\_vi.\*  
30: em\_hgt\_hum.\*  
31: em\_hgt\_inv.\*  
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33: em\_hgt\_mus.\*  
34: em\_hgt\_pln.\*  
35: em\_hgt\_rod.\*  
36: em\_hgt\_mam.\*  
37: em\_hgt\_vrt.\*  
38: em\_sy.\*  
39: em\_hgt\_hum.\*  
40: em\_hgt\_mus.\*  
41: em\_hgt\_other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	22.2	96.5	1704	8	HCC18SRRN	Z75306 H.capsulatu
2	22.2	96.5	1704	8	HCC18SRRN	Z75307 H.capsulatu
3	22.2	96.5	1713	8	HCC18SR	X58572 H.capsulatu
4	22.2	96.5	1726	8	AF320009	AF320009 Ajellomyces
5	20.6	89.6	494	8	AF030916	AF030916 Aspergill
6	20.6	89.6	786	8	AF088252	AF088252 Teloschis
7	20.6	89.6	969	8	AF113712	AF113712 Dibaeis b
8	20.6	89.6	990	8	AF107345	AF107345 Dibaeis b
9	20.6	89.6	1031	8	AF203458	AF203458 Cycloaneus
10	20.6	89.6	1054	8	AB030917	AB030917 Aspergill
11	20.6	89.6	1479	8	AE045438	U45438 Amylocarpus
12	20.6	89.6	1673	8	SCU72712	U72712 Siphula cer
13	20.6	89.6	1678	8	AN18SR	X78538 A.niger (is
14	20.6	89.6	1686	8	PVY13996	Y13996 Paecilomyces
15	20.6	89.6	1687	8	AF113713	AF113713 Dibaeis b
16	20.6	89.6	1687	8	AF184749	AF184749 Bunodopho
17	20.6	89.6	1692	8	AF113710	AF113710 Siphula p
18	20.6	89.6	1896	8	AF113711	AF113711 Siphula p
19	20.6	89.6	1701	8	AF085473	AF085473 Dibaeis b
20	20.6	89.6	1721	8	AF242259	AF242259 Acrosparm
21	20.6	89.6	1732	8	AB008408	AB008408 Aspergill
22	20.6	89.6	1733	8	AB008397	AB008397 Aspergill
23	20.6	89.6	1733	8	AB008413	AB008413 Aspergill
24	20.6	89.6	1733	8	D63695	D63695 Aspergillus
25	20.6	89.6	1733	8	D63697	D63697 Aspergillus
26	20.6	89.6	1734	8	AB006716	AB006716 Talaromyc
27	20.6	89.6	1737	8	AB033479	AB033479 Leveillul
28	20.6	89.6	1746	8	AF053726	AF053726 Kirschste
29	20.6	89.6	1770	8	AB002079	AB002079 Aspergill
30	20.6	89.6	1771	8	AB002066	AB002066 Aspergill
31	20.6	89.6	1772	8	AF053729	AF053729 Helicascu
32	20.6	89.6	1774	8	AB003947	AB003947 Talaromyc
33	20.6	89.6	1776	8	AB003946	AB003946 Penicilli
34	20.6	89.6	1777	8	AB003808	AB003808 Aspergill
35	20.6	89.6	1989	8	CSP301706	AJ301706 Capnobotr
36	20.6	89.6	2150	8	AB003945	AB003945 Penicilli
37	20.6	89.6	2734	8	AFU421692	AJ421692 Anaptychi
38	20.6	89.6	3717	8	PPE421689	AJ421689 Physconia
39	19.6	85.2	1759	8	AB005561	AB005561 Kockovael
40	19	82.6	144	8	AB046947	AB046947 Endophyte
41	19	82.6	144	8	AB046948	AB046948 Endophyte
42	19	82.6	144	8	AB046949	AB046949 Endophyte
43	19	82.6	192	8	AF062662	AF062662 Endophyte
44	19	82.6	192	8	AF062664	AF062664 Endophyte
45	19	82.6	192	8	AF062675	AF062675 Endophyte

# ALIGNMENTS

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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE

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H.capsulatum ssp. duboisii 18S rRNA gene.  
Z75306  
Z75306.1 GI:1419549  
18S ribosomal RNA; 18S rRNA gene; small subunit ribosomal RNA.  
Ajellomyces capsulatus.  
Ajellomyces capsulatus.  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; Onygenaceae; Ajellomyces.  
1 (bases 1 to 1704)  
Okeke,C.N., Kappe,R., Zakikhani,S., Nolte,O. and Sonntag,H.G.  
Ribosomal genes of Histoplasma capsulatum var. duboisii and var.  
farciminosum

Pred. No. is the number of results predicted by chance to have a

JOURNAL Mycoses 41 (9-10), 355-362 (1998)  
MEDLINE 99114487  
PUBMED 9916456  
REFERENCE 2 (bases 1 to 1704)  
AUTHORS Kappe,R.  
TITLE Direct Submission  
JOURNAL Submitted (06-JUL-1996) Reinhard Kappe, Hygiene & Med.  
Microbiology, University of Heidelberg, Hygiene Institute, Im  
Neuenheimer Feld 324, Heidelberg, D-69120, Germany  
FEATURES Location/Qualifiers  
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Db 111 ACATGCTGAAGCCTCGACTTCG 133  
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RESULT 2  
HC18SRN 1704 bp DNA linear PLN 10-DEC-1999  
LOCUS H.capsulatum ssp. farciminosum 18S rRNA gene.  
DEFINITION 275307  
VERSION 18S ribosomal RNA; 18S rRNA gene; small subunit ribosomal RNA.  
KEYWORDS Ajellomyces capsulatus.  
SOURCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; Onygenaceae; Ajellomyces.  
ORGANISM Okeke,C.N., Kappe,R., Zakikhani,S., Nolte,O. and Sonntag,H.G.  
TITLE Ribosomal genes of Histoplasma capsulatum var. duboisii and var.  
farciminosum  
JOURNAL Mycoses 41 (9-10), 355-362 (1998)  
MEDLINE 99114487  
PUBMED 9916456  
REFERENCE 2 (bases 1 to 1704)  
AUTHORS Kappe,R.  
TITLE Direct Submission  
JOURNAL Submitted (06-JUL-1996) Reinhard Kappe, Hygiene & Med.  
Microbiology, University of Heidelberg, Hygiene Institute, Im  
Neuenheimer Feld 324, Heidelberg, D-69120, Germany  
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Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
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Db 111 ACATGCTGAAGCCTCGACTTCG 133  
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LOCUS H.capsulatum DNA for 18S ribosomal RNA, partial.  
DEFINITION X58572.1 GI:2759  
VERSION 18S ribosomal RNA.  
KEYWORDS Ajellomyces capsulatus.  
SOURCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; Onygenaceae; Ajellomyces.  
ORGANISM Bowman,B.H.  
TITLE Direct Submission  
JOURNAL Submitted (19-MAR-1991) B.H. Bowman, Roche Molecular Systems, 1145  
Atlantic Avenue, Alameda CA 94501, USA  
REFERENCE 2 (bases 1 to 1713)  
AUTHORS Bowman,B.H., Taylor,J.W. and White,T.J.  
TITLE Molecular evolution of the fungi: human pathogens  
JOURNAL Mol. Biol. Evol. 9 (5), 893-904 (1992)  
MEDLINE 92408455  
PUBMED 1528111  
REFERENCE 3 (bases 1 to 1713)  
AUTHORS Barbee,M.L. and Taylor,J.W.  
TITLE Convergence in ascospore discharge mechanism among pyrenomycete  
fungi based on 18S ribosomal RNA gene sequence  
JOURNAL Mol. Phylogenet. Evol. 1 (1), 59-71 (1992)  
MEDLINE 1342925  
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REMARK Annotation  
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Db 131 ACATGCTGAAGCCTCGACTTCG 153  
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LOCUS Ajellomyces capsulatus ATCC26032 18S ribosomal RNA gene, partial  
DEFINITION sequence.  
VERSION AF320009  
KEYWORDS AF320009.1 GI:12751371  
SOURCE Ajellomyces capsulatus.  
ORGANISM Ajellomyces capsulatus  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; Onygenaceae; Ajellomyces.  
REFERENCE 1 (bases 1 to 1726)  
AUTHORS Kasuga,T., White,T.J. and Taylor,J.W.  
TITLE The Molecular Clock in Fungi in the Class Plectomycetes  
JOURNAL Unpublished

JOURNAL Mycoses 41 (9-10), 355-362 (1998)  
MEDLINE 99114487  
PUBMED 9916456  
REFERENCE 2 (bases 1 to 1704)  
AUTHORS Kappe,R.  
TITLE Direct Submission  
JOURNAL Submitted (06-JUL-1996) Reinhard Kappe, Hygiene & Med.  
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Neuenheimer Feld 324, Heidelberg, D-69120, Germany  
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Db 111 ACATGCTGAAGCCTCGACTTCG 133  
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LOCUS H.capsulatum ssp. farciminosum 18S rRNA gene.  
DEFINITION 275307  
VERSION 18S ribosomal RNA; 18S rRNA gene; small subunit ribosomal RNA.  
KEYWORDS Ajellomyces capsulatus.  
SOURCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; Onygenaceae; Ajellomyces.  
ORGANISM Okeke,C.N., Kappe,R., Zakikhani,S., Nolte,O. and Sonntag,H.G.  
TITLE Ribosomal genes of Histoplasma capsulatum var. duboisii and var.  
farciminosum  
JOURNAL Mycoses 41 (9-10), 355-362 (1998)  
MEDLINE 99114487  
PUBMED 9916456  
REFERENCE 2 (bases 1 to 1704)  
AUTHORS Kappe,R.  
TITLE Direct Submission  
JOURNAL Submitted (06-JUL-1996) Reinhard Kappe, Hygiene & Med.  
Microbiology, University of Heidelberg, Hygiene Institute, Im  
Neuenheimer Feld 324, Heidelberg, D-69120, Germany  
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Db 111 ACATGCTGAAGCCTCGACTTCG 133  
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DEFINITION X58572.1 GI:2759  
VERSION 18S ribosomal RNA.  
KEYWORDS Ajellomyces capsulatus.  
SOURCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; Onygenaceae; Ajellomyces.  
ORGANISM Bowman,B.H.  
TITLE Direct Submission  
JOURNAL Submitted (19-MAR-1991) B.H. Bowman, Roche Molecular Systems, 1145  
Atlantic Avenue, Alameda CA 94501, USA  
REFERENCE 2 (bases 1 to 1713)  
AUTHORS Bowman,B.H., Taylor,J.W. and White,T.J.  
TITLE Molecular evolution of the fungi: human pathogens  
JOURNAL Mol. Biol. Evol. 9 (5), 893-904 (1992)  
MEDLINE 92408455  
PUBMED 1528111  
REFERENCE 3 (bases 1 to 1713)  
AUTHORS Barbee,M.L. and Taylor,J.W.  
TITLE Convergence in ascospore discharge mechanism among pyrenomycete  
fungi based on 18S ribosomal RNA gene sequence  
JOURNAL Mol. Phylogenet. Evol. 1 (1), 59-71 (1992)  
MEDLINE 1342925  
PUBMED  
REMARK Annotation  
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end of coding region"  
BASE COUNT 434 a 368 c 473 g 438 t  
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Query Match 96.5%; Score 22.2; DB 8; Length 1713;  
Best Local Similarity 95.7%; Pred. No. 1.1;  
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
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Db 131 ACATGCTGAAGCCTCGACTTCG 153  
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RESULT 4  
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LOCUS Ajellomyces capsulatus ATCC26032 18S ribosomal RNA gene, partial  
DEFINITION sequence.  
VERSION AF320009  
KEYWORDS AF320009.1 GI:12751371  
SOURCE Ajellomyces capsulatus.  
ORGANISM Ajellomyces capsulatus  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; Onygenaceae; Ajellomyces.  
REFERENCE 1 (bases 1 to 1726)  
AUTHORS Kasuga,T., White,T.J. and Taylor,J.W.  
TITLE The Molecular Clock in Fungi in the Class Plectomycetes  
JOURNAL Unpublished

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REFERENCE 2 (bases 1 to 1726)
AUTHORS Kasuga,T., White,T.J. and Taylor,J.W.
TITLE Direct Submission
JOURNAL Submitted (07-NOV-2000) Roche Molecular Systems, 1145 Atlantic
Ave., Alameda, CA 94501, USA
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Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
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DEFINITION Aspergillus niger gene for 18S rRNA, partial sequence.
ACCESSION AB030916
VERSION 1 GI:5738920
KEYWORDS 18S rRNA; 18S ribosomal RNA.
SOURCE Aspergillus niger (strain:IEF1) DNA.
ORGANISM
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
Shintani,T. and Matsumoto,Y.
TITLE Aspergillus niger gene for 18S rRNA, partial sequence
JOURNAL Published Only in Database (1999)
REFERENCE 2 (bases 1 to 494)
AUTHORS Shintani,T. and Matsumoto,Y.
TITLE Direct Submission
JOURNAL Submitted (10-AUG-1999) Tomoyoshi Shintani, Industrial Research
Center of Ehime Prefecture, Laboratory of Food Process; 487-2
Kumekubota, Matsuyama, Ehime 791-1101, Japan
(E-mail:shintani@iri.pref.ehime.jp, URL:www.iri.pref.ehime.jp,
Tel:81-89-976-7612, Fax:81-89-976-7313)
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Best Local Similarity 91.3%; Pred. No. 7.2;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23
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Db 149 ACATGCTGAAGCCTCGACTTCG 171

RESULT 6
LOCUS AF088252 786 bp DNA linear PLN 17-JUN-1999
DEFINITION Teloschistes cf. chrysophthalmus Feige and Mies ESS-6640 18S
ribosomal RNA, partial sequence.

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ACCESSION AF088252.1 GI:4731142
VERSION AF088252.1
KEYWORDS Teloschistes cf. chrysophthalmus Feige and Mies ESS-6640.
SOURCE Teloschistes cf. chrysophthalmus Feige and Mies ESS-6640
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;
Lecanorales; Teloschistaceae; Teloschistaceae; Teloschistes.
REFERENCE 1 (bases 1 to 786)
AUTHORS Steenroos,S.K. and DePriest,P.T.
TITLE SSU rDNA phylogeny of cladoniiform lichens
JOURNAL Am. J. Bot. 85, 1548-1559 (1998)
REFERENCE 2 (bases 1 to 786)
AUTHORS DePriest,P.T., Ivanova,N. and Gargas,A.
TITLE Direct Submission
JOURNAL Submitted (31-AUG-1998) Department of Botany, NHB-166, Smithsonian
Institution, National Museum of Natural History, 10th &
Constitution Avenue NW, Washington, DC 20560-0166, USA
FEATURES
source Location/Qualifiers
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/organism="Teloschistes cf. chrysophthalmus Feige and Mies
ESS-6640"
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Best Local Similarity 91.3%; Pred. No. 7.5;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23
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Db 112 ACATGCTGAAGCCTCGACTTCG 134

RESULT 7
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sequence.
ACCESSION AF113712
VERSION AF113712.1 GI:6502558
KEYWORDS Dibaeis baeomyces.
SOURCE Dibaeis baeomyces.
ORGANISM Dibaeis baeomyces
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;
Lecanoromycetes incertae sedis; Icmadophilaceae; Dibaeis.
Platt,J.L. and Spatafora,J.W.
REFERENCE 1 (bases 1 to 969)
AUTHORS Platt,J.L. and Spatafora,J.W.
TITLE Evolutionary relationships of nonsexual lichenized fungi: molecular
phylogenetic hypotheses for the genera Siphula and Thamnolia from
SSU and LSU rDNA analyses
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 969)
AUTHORS Platt,J.L. and Spatafora,J.W.
TITLE Direct Submission
JOURNAL Submitted (16-DEC-1998) Department of Botany & Plant Pathology,
Oregon State University, 2082 Cordley Hall, Corvallis, OR
97331-2902, USA
FEATURES
source Location/Qualifiers
1..969
/organism="Dibaeis baeomyces"
/db_xref="taxon:83478"
<1..>969
/product="small subunit ribosomal RNA"
BASE COUNT 268 a 189 c 243 g 268 t 1 others
ORIGIN
Query Match 89.6%; Score 20.6; DB 8; Length 969;

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KEYWORDS  
SOURCE  
ORGANISM

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;  
 Helotiales; Helotiales incertae sedis; Amylocarpus.  
 1 (bases 1 to 1479)  
 REFERENCE  
 AUTHORS Landvik,S., Shailer,N.F.J. and Eriksson,O.E.  
 TITLE SSU rDNA sequences support for a close relationship between the  
 Elaphomycetales and the Eurotiales and Onygenales  
 JOURNAL Mycoscience 37, 237-241 (1996)  
 REFERENCE  
 2 (bases 1 to 1479)  
 AUTHORS Landvik,S., Shailer,N.F.J. and Eriksson,O.E.  
 TITLE Direct Submission.  
 JOURNAL Submitted (11-JAN-1996) Sara Landvik, Ecological Botany, Umea,  
 S-90187, Sweden  
 FEATURES  
 source Location/Qualifiers  
 1. .1479  
 /organism="Amylocarpus encephaloides"  
 /strain="UME 23765"  
 /db\_xref="taxon:45428"  
 1. .1479  
 /product="small subunit ribosomal RNA"  
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 Best Local Similarity 91.3%; Pred. No. 7.9;  
 Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DCATGCTGAAGCCTCGACTTCG 23  
 :||||| |||||||||  
 Db 86 ACATGCTAAAGCCTCGACTTCG 108  
 RESULT 12  
 SCU72712 1648 bp DNA linear PLN 30-JUL-1997.  
 LOCUS Siphula ceratites 18S small subunit ribosomal RNA gene, complete  
 DEFINITION  
 sequence.  
 ACCESSION U72712  
 VERSION U72712.1 GI:2286071  
 SOURCE Siphula ceratites.  
 ORGANISM Siphula ceratites.  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;  
 Lecanoromycetes incertae sedis; Imadophyllaceae; Siphula.  
 1 (bases 1 to 1648)  
 REFERENCE  
 AUTHORS Steenroos,S., Lohlander,K. and Tehler,A.  
 TITLE Direct Submission  
 JOURNAL Submitted (27-SEP-1996) Botany, National Museum of Natural History,  
 Smithsonian Institution, NHB-166, 10th St. & Constitution Ave.,  
 Washington, DC 20560, USA  
 FEATURES  
 source Location/Qualifiers  
 1. .1648  
 /organism="Siphula ceratites"  
 /db\_xref="taxon:53373"  
 1. .1648  
 /product="18S small subunit ribosomal RNA"  
 BASE COUNT 424 a 343 c 442 g 439 t  
 ORIGIN  
 Query Match 89.6%; Score 20.6; DB 8; Length 1648;  
 Best Local Similarity 91.3%; Pred. No. 8;  
 Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DCATGCTGAAGCCTCGACTTCG 23  
 :||||| |||||||||  
 Db 88 ACATGCTGAAGCCTCGACTTCG 110  
 RESULT 13  
 AN18SRR  
 LOCUS A.niger (isolate CBS102.12) 18S rRNA gene.  
 DEFINITION  
 X78538  
 ACCESSION X78538  
 VERSION X78538.1 GI:469079

18S ribosomal RNA.  
 Aspergillus niger.  
 ORGANISM Aspergillus niger  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
 1 (bases 1 to 1673)  
 REFERENCE  
 AUTHORS Melchers,W.J., Verweij,P.E., van den Hurk,P., van Belkum,A., De  
 Pauw,B.E., Hoogkamp-Korstanje,J.A. and Meis,J.F.  
 TITLE General primer-mediated PCR for detection of Aspergillus species  
 JOURNAL J. Clin. Microbiol. 32 (7), 1710-1717 (1994)  
 MEDLINE 95014936  
 PUBMED 7929762  
 REFERENCE  
 2 (bases 1 to 1673)  
 AUTHORS Melchers,W.J.G.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-MAR-1994) W.J.G. Melchers, Department of Medical  
 Microbiology, University of Nijmegen, P O Box 9101, 6500 HB  
 Nijmegen, NETHERLANDS  
 FEATURES  
 source Location/Qualifiers  
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 /isolate="CBS102.12"  
 /db\_xref="taxon:5061"  
 <1. >1673  
 /product="18S ribosomal RNA"  
 /evidence="experimental"  
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 ORIGIN  
 Query Match 89.6%; Score 20.6; DB 8; Length 1673;  
 Best Local Similarity 91.3%; Pred. No. 8;  
 Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DCATGCTGAAGCCTCGACTTCG 23  
 :||||| |||||||||  
 Db 109 ACATGCTGAAGCCTCGACTTCG 131  
 RESULT 14  
 PVY13996 1678 bp DNA linear PLN 23-JUL-1997  
 LOCUS Paecilomyces variotii 18S rRNA gene.  
 DEFINITION  
 Paecilomyces variotii  
 ACCESSION Y13996  
 VERSION Y13996.1 GI:2224834  
 KEYWORDS 18S ribosomal RNA; 18S rRNA gene.  
 SOURCE Paecilomyces variotii.  
 ORGANISM Paecilomyces variotii.  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 Eurotiales; Trichocomaceae; mitosporic Trichocomaceae;  
 Paecilomyces.  
 1 (bases 1 to 1678)  
 REFERENCE  
 AUTHORS Zakikhani,S., Okeke,C.N. and Kappe,R.  
 TITLE 18S rDNA sequence of Paecilomyces variotii CBS339.51  
 JOURNAL Unpublished  
 REFERENCE  
 2 (bases 1 to 1678)  
 AUTHORS Kappe,R.  
 TITLE Direct Submission  
 JOURNAL Submitted (24-JUN-1997) Kappe R., Hygiene Institute, University of  
 Heidelberg, Im Neuenheimer Feld 324 D-69120 GERMANY  
 FEATURES  
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 1. .1678  
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 /strain="CBS339.51"  
 /isolate="Man, sputum"  
 /db\_xref="taxon:45996"  
 1. .1678  
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 /product="18S ribosomal RNA"  
 /evidence="experimental"  
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Query Match 89.6%; Score 20.6; DB 8; Length 1678;  
 Best Local Similarity 91.3%; Pred. No. 8;  
 Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23  
 :|||||  
 Db 83 ACATGCTGAAGCCTCGACTTCG 105

RESULT 15  
 AF113713  
 LOCUS 1686 bp DNA linear PLN 06-DEC-1999  
 DEFINITION Dibaeis baemyces isolate OSC53939 small subunit ribosomal RNA  
 gene, partial sequence.  
 ACCESSION AF113713  
 VERSION AF113713.1 GI:6502559  
 KEYWORDS  
 SOURCE Dibaeis baemyces.  
 ORGANISM Dibaeis baemyces  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;  
 Lecanoromycetes incertae sedis; Icmadophilaceae; Dibaeis.  
 REFERENCE 1 (bases 1 to 1686)  
 AUTHORS Platt,J.L. and Spatafora,J.W.  
 TITLE Evolutionary relationships of nonsexual lichenized fungi: molecular  
 phylogenetic hypotheses for the genera Siphula and Thamnolia from  
 SSU and LSU rDNA analyses  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1686)  
 AUTHORS Platt,J.L. and Spatafora,J.W.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-DEC-1998) Department of Botany & Plant Pathology,  
 Oregon State University, 2082 Cordley Hall, Corvallis, OR  
 97331-2902, USA

FEATURES  
 source  
 1..1686  
 Location/Qualifiers  
 /organism="Dibaeis baemyces"  
 /isolate="OSC53939"  
 /db\_xref="taxon:83478"  
 <1..>1686  
 rRNA  
 /product="small subunit ribosomal RNA"  
 BASE COUNT 441 a 346 c 438 g 460 t 1 others  
 ORIGIN

Query Match 89.6%; Score 20.6; DB 8; Length 1686;  
 Best Local Similarity 91.3%; Pred. No. 8;  
 Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23  
 :|||||  
 Db 106 ACATGCTGAAGCCTCGACTTCG 128

Search completed: June 12, 2003, 02:33:54  
 Job time : 349.269 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 22:17:41 ; Search time 117.802 seconds  
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439.686 Million cell updates/sec

Title: US-09-674-195c-18  
Perfect score: 23  
Sequence: 1 dcatgctgaagctcacttcg 23

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues  
Total number of hits satisfying chosen parameters: 4370478

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Maximum Match 100%  
Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*  
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	22	95.7	22	15	AAQ73433 Histoplasma capsul
C 2	22	95.7	22	15	AAQ73436 Histoplasma capsul
C 3	22	95.7	22	15	AAQ73437 Histoplasma capsul
C 4	22	95.7	22	15	AAQ86436 Histoplasma capsul
C 5	20.6	89.6	568	21	AAF11545 Aspergillus niger
C 6	19	82.6	1733	20	AZ00859 A. fumigatus 18S r
C 7	17.4	75.7	1745	24	AAZ01152 Deuteromycetes pol
C 8	17.4	75.7	4403765	22	AAI99683 Mycobacterium tube
C 9	17.4	75.7	4411529	22	AAI99682 Mycobacterium tube

10	17	73.9	492	23	AA565314	DNA encoding novel
11	16.8	73.0	454	22	ABA44550	Human breast cell
12	16.8	73.0	454	22	ABA54997	Human foetal liver
13	16.8	73.0	454	22	ABA24760	Probe #3226 for ge
14	16.8	73.0	454	22	AAK03286	Human brain expres
15	16.8	73.0	454	22	AAK28719	Human bone marrow
16	16.8	73.0	454	22	AAI13296	Probe #3229 for ge
17	16.8	73.0	454	22	AAI34650	Probe #3336 used t
18	16.8	73.0	454	22	AAI03197	Probe #3188 used t
19	16.8	73.0	454	24	ABS03233	Human genome-deriv
20	16.4	71.3	1932	23	AA567693	DNA encoding novel
C 21	16.2	70.4	351	21	AAK04990	Human secreted pro
22	16.2	70.4	891	19	AAH01747	DNA sequence used
23	16.2	70.4	891	22	AAH01747	Fibrobacter succin
C 24	16.2	70.4	1097	24	ABK72888	Bacillus lichenifo
C 25	16.2	70.4	9228	23	ABL11660	Drosophila melanog
26	15.8	68.7	51	22	AAI75640	Human silent SNP c
27	15.8	68.7	51	22	AAI75641	Human silent SNP c
C 28	15.8	68.7	550	21	AAK94343	Cat flea head and
C 29	15.8	68.7	570	21	AAF08498	Fusarium venenatu
30	15.8	68.7	586	24	ABN61440	Human cancer relat
31	15.8	68.7	617	21	AAF10913	Fusarium venenatu
C 32	15.8	68.7	654	21	AAZ53824	Neisseria gonorrhe
33	15.8	68.7	695	22	AAK91828	Human cDNA 5'-end
34	15.8	68.7	695	22	AAK93228	Human cDNA clone r
35	15.8	68.7	738	14	AAQ43293	Sequence encoding
36	15.8	68.7	738	15	AAQ66841	CC49 VL / 217 / 4-
37	15.8	68.7	738	20	AAK04747	DNA encoding a pro
38	15.8	68.7	738	20	AAK99764	Fusion polypeptide
39	15.8	68.7	738	21	AAK95090	DNA encoding bival
40	15.8	68.7	738	21	AAK59622	DNA encoding a sin
41	15.8	68.7	738	21	AAZ57095	DNA (SEQ ID NO:22)
42	15.8	68.7	738	21	AAZ90344	Antibody CC49/anti
43	15.8	68.7	738	21	AAZ37393	Sequence encoding
44	15.8	68.7	744	14	AAQ43288	DNA encoding a pro
45	15.8	68.7	744	20	AAK04742	

ALIGNMENTS

RESULT 1  
AAQ73433/C  
ID AAQ73433 standard; DNA; 22 BP.

XX AC AAQ73433;

XX DT 18-MAY-1995 (first entry)

XX DE Histoplasma capsulatum-specific DNA hybridisation probe.

XX KW Probe; detection; Histoplasma capsulatum; 18S; rRNA; rDNA; hybridisation;  
KW Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;  
KW water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.

XX OS Synthetic.

XX PN US5352579-A.

XX PD 04-OCT-1994.

XX PF 28-JUN-1991; 91US-0720587.

XX PR 28-JUN-1991; 91US-0720587.

XX PA (GENP-) GEN-PROBE INC.

XX PI Millman CL;

XX DR WPI; 1994-316178/39.

XX PT Hybridisation probe specific for Histoplasma capsulatum -  
allowing differentiation from all other fungi for detection or



AAQ86436/c  
 ID AAQ86436 standard; RNA; 22 BP.  
 XX AC AAQ86436;  
 XX DT 18-MAY-1995 (first entry)  
 XX DE Histoplasma capsulatum-specific complementary RNA hybridisation probe.  
 XX KW Probe; detection: Histoplasma capsulatum; 18S: rRNA; rDNA; hybridisation;  
 KW Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;  
 KW water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.  
 XX OS Synthetic.  
 XX PN US5352579-A.  
 XX PD 04-OCT-1994.  
 XX PF 28-JUN-1991; 91US-0720587.  
 XX PR 28-JUN-1991; 91US-0720587.  
 XX PA (GENP-) GEN-PROBE INC.  
 XX PI Millman CL;  
 XX DR WPI; 1994-316178/39.  
 XX PT Hybridisation probe specific for Histoplasma capsulatum -  
 PT allowing differentiation from all other fungi for detection or  
 PT quantitation in body fluids, etc.  
 XX PS Claim 9; Column 13; 8pp; English.  
 XX CC A probe (AAQ73433) or its complement (AAQ73436) and corresponding RNA  
 CC sequences (AAQ73437 and AAQ86436) used for the specific detection of all  
 CC strains of Histoplasma capsulatum (H.c.). The probes are manufactured  
 CC complementary to the H.c. 18S rRNA or rDNA gene. This region also  
 CC corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.  
 CC The probe is specific for H.c. and can be used to distinguish the fungus  
 CC from all others, even its nearest phylogenetic neighbour Blastomyces  
 CC dermatitidis. Nucleic acid hybridisation of the specific probe is  
 CC enhanced by the use of helper probes (AAQ73434-5). This method allows  
 CC the detection and/or the quantitation of H.c. from samples e.g. body  
 CC fluids, tissue samples, soil and water.  
 XX SQ Sequence 22 BP; 5 A; 5 C; 7 G; 5 U; 0 other;  
 Query Match 95.7%; Score 22; DB 15; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.13;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 CATGCTGAAGCCTCGACTTCG 23  
 |||||  
 Db 22 CATGCTGAAGCCTCGACTTCG 1  
 RESULT 5  
 AAF11545  
 ID AAF11545 standard; cDNA; 568 BP.  
 XX AC AAF11545;  
 XX DT 13-MAR-2001 (first entry)  
 XX DE Aspergillus niger EST SEQ ID NO:4068.  
 XX KW Multiple gene expression: filamentous fungal cell; EST;  
 KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;  
 KW Aspergillus oryzae; Trichoderma reesei; identification; recombination;  
 KW culture condition; environmental stress; spore morphogenesis;  
 KW metabolic pathway engineering; catabolic pathway engineering; ss.

XX OS Aspergillus niger.  
 XX PN WO200056762-A2.  
 XX PD 28-SEP-2000.  
 XX PF 22-MAR-2000; 2000WO-US07781.  
 XX PR 22-MAR-1999; 99US-0273623.  
 XX PA (NOVO ) NOVO NORDISK BIOTECH INC.  
 XX PA (NOVO ) NOVO NORDISK AS.  
 XX PI Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;  
 XX WPI; 2000-594572/56.  
 XX DR Monitoring differential expression of genes in filamentous fungal cells  
 XX PT uses fluorescence-labeled nucleic acids isolated from the cells and a  
 XX PT substrate of expressed sequence tags -  
 XX PS Claim 87; Page 1791-1792; 3161pp; English.  
 XX CC The present invention describes a method for monitoring differential  
 CC expression of genes in a first filamentous fungal (FF) cell relative to  
 CC expression of the same genes in one or more second filamentous fungal  
 CC cells. The method uses fluorescence-labeled nucleic acids isolated from  
 CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs  
 CC are used in the methods for monitoring differential expression of genes  
 CC in a first filamentous fungal (FF) cell relative to expression of the  
 CC same genes in one or more second filamentous fungal cells. Monitoring  
 CC the global expression of genes from FF cells allows the production  
 CC potential of the microorganisms to be improved. New genes may be  
 CC discovered, possible functions of unknown open reading frames can be  
 CC identified and gene copy number variation and stability can be  
 CC monitored. The expression of genes can be used to study how FF cells  
 CC adapt to changes in culture conditions, environmental stress, spore  
 CC morphogenesis, recombination, metabolic or catabolic pathway  
 CC engineering. Using ESTs provides several advantages over genomic or  
 CC random CDNA clones including elimination of redundancy as one spot on an  
 CC array equals one gene or open reading frame, and organisation of the  
 CC microarrays based on function of the gene products to facilitate  
 CC analysis of the results. AAF07478 to AAF11247 represents ESTs from  
 CC Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus  
 CC niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and  
 CC AAF14879 to AAF1537 represents ESTs from Trichoderma reesei, which are  
 CC all specifically claimed in the present invention.  
 XX SQ Sequence 568 BP; 155 A; 116 C; 141 G; 150 T; 6 other;  
 Query Match 89.6%; Score 20.6; DB 21; Length 568;  
 Best Local Similarity 91.3%; Pred. No. 0.98;  
 Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DCATGCTGAAGCCTCGACTTCG 23  
 :|||||  
 Db 156 ACATGCTGAAGCCTCGACTTCG 178  
 RESULT 6  
 AAZ00859  
 ID AAZ00859 standard; DNA; 1733 BP.  
 XX AC AAZ00859;  
 XX DT 11-OCT-1999 (first entry)  
 XX DE A. fumigatus 18S rRNA DNA.  
 XX KW Detection; diagnosis; 18S rRNA; aspergillosis; oncology;  
 KW invasive infection; haematology; immune system suppression; ss.

OS Aspergillus fumigatus.  
 PN DE19806274-A1.  
 XX  
 PD 19-AUG-1999.  
 XX  
 PF 16-FEB-1998; 98DE-1006274.  
 XX  
 PF 16-FEB-1998; 98DE-1006274.  
 XX  
 PR (BUCH/) BUCHHEIDT D.  
 XX (HEHL/) HEHLMANN R.  
 PA (SKLA/) SKLADNY H.  
 XX  
 PI Buchheidt D, Hehlmann R, Skladny H;  
 XX WPI: 1999-470047/40.  
 DR  
 XX  
 XX Detecting Aspergillus nucleic acid in body samples by two-step  
 PT polymerase chain reaction, for diagnosing aspergillosis  
 XX  
 XX Claim 2; Fig 1; 16pp; German.  
 PS  
 XX This invention describes a novel method for detecting Aspergillus nucleic  
 CC acid (1) in a body sample which comprises the isolation of (1) followed  
 CC by a two-step polymerase chain reaction (PCR) amplification of any  
 CC nucleic acid having a sequence essentially homologous to part of the  
 CC 3'-end of the Aspergillus 18S rRNA gene using primers used in the first  
 CC step that do not overlap with those in the second step. The method is  
 CC used for early diagnosis, and monitoring, of aspergillosis, particularly  
 CC invasive infections in hematological-oncological patients with long-term  
 CC suppression of the immune system. Unlike the known method using  
 CC overlapping primers, this process provides efficient and reliable  
 CC detection of Aspergillus in clinical situations. It is specific for  
 CC Aspergillus (it detects the species terreus, niger, versicolor, clavatus,  
 CC flavus, and fumigatus, but not oryzae, nor bacteria or fungi from any  
 CC other genera). This sequence represents the DNA sequence of Aspergillus  
 CC fumigatus 18S rRNA.  
 XX  
 XX Sequence 1733 BP; 446 A; 374 C; 475 G; 438 T; 0 other;  
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 Query Match 82.6%; Score 19; DB 20; Length 1733;  
 Best Local Similarity 87.0%; Pred. No. 7.4;  
 Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 OY 1 DCATGCTGAAGCCTCGACTTCG 23  
 :||||| ||| |||||||||  
 DB 131 ACATGCTAANAACCTCGACTTCG 153  
 RESULT 7  
 ABA01152  
 ID ABA01152 standard; DNA; 1745 BP.  
 XX  
 AC ABA01152;  
 XX  
 XX 24-JAN-2002 (first entry)  
 DT  
 DE Deuteromycetes polynucleotide SEQ ID 1.  
 DE  
 XX Aldonic acid; ds.  
 KW  
 XX Deuteromycetes sp.  
 OS  
 XX JP2001245657-A.  
 PN  
 XX 11-SEP-2001.  
 PD  
 XX 26-DEC-2000; 2000JP-0394766.  
 PF  
 XX 27-DEC-1999; 99JP-0369714.  
 PR  
 XX (TAKE-) TAKEHARA KAGAKU KOGYO KK.  
 PA

PA (OSAKA ) OSAKA CITY.  
 XX  
 XX WPI: 2002-002933/01.  
 XX  
 PT A new microbe for producing aldonic acid, comprises a new strain of  
 PT Acinetobacter or Burkholderis -  
 XX  
 XX Disclosure; Page 17; 22pp; Japanese.  
 XX  
 CC The present invention relates to a new microbe of Acinetobacter or  
 CC Burkholderis genus producing aldonic acid and oxidising specifically the  
 CC hemiacetal hydroxy group of a saccharide having said hydroxy group.  
 CC Aldonic acid is used as a mineral reinforcing agent. The present sequence  
 CC was used to illustrate the present invention.  
 XX  
 XX Sequence 1745 BP; 448 A; 382 C; 465 G; 450 T; 0 other;  
 SQ  
 Query Match 75.7%; Score 17.4; DB 24; Length 1745;  
 Best Local Similarity 82.6%; Pred. No. 49;  
 Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 OY 1 DCATGCTGAAGCCTCGACTTCG 23  
 :||||| ||| |||||||||  
 DB 145 ACATGCTAANAACCTCGACTTCG 167  
 RESULT 8  
 AAI99683/C  
 ID AAI99683 standard; DNA; 4403765 BP.  
 XX  
 AC AAI99683;  
 XX  
 XX 15-JAN-2002 (first entry)  
 DT  
 DE Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 2.  
 DE  
 XX Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome;  
 KW variation; epidemiology; patient treatment; epidemic monitoring; ds.  
 KW  
 XX Mycobacterium tuberculosis.  
 OS  
 XX US6294328-B1.  
 PN  
 XX 25-SEP-2001.  
 PD  
 XX 24-JUN-1998; 98US-0103840.  
 PF  
 XX 24-JUN-1998; 98US-0103840.  
 PR  
 XX (GENO-) INST GENOMIC RES.  
 PA  
 XX Fleischmann RD, White OR, Fraser CM, Venter JC;  
 PI  
 XX WPI: 2001-647261/74.  
 DR  
 XX Evaluating strain variation of Mycobacterium tuberculosis, comprises  
 PT determining the nucleotide sequence of the strain at positions in the  
 PT genome corresponding to positions where M. tuberculosis strains CDC  
 PT 1551 and H37Rv differ -  
 XX  
 XX Claim 4; SEQ ID NO 2; 3pp + Sequence Listing; English.  
 PS  
 XX The invention relates to evaluating strain variation within and between  
 CC different populations of the tuberculosis bacterial pathogen,  
 CC Mycobacterium tuberculosis or related Mycobacterium by determining the  
 CC nucleotide sequence of the first strain at positions in the complete  
 CC sequence of the genome that correspond to positions that differ in the  
 CC nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and  
 CC H37Rv (AAI99682). The method is useful for evaluating strain variation of  
 CC M. tuberculosis and has valuable application in the fields of  
 CC tuberculosis genetics, epidemiology, patient treatment and epidemic  
 CC monitoring.  
 CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from USPTO  
CC at seqdata.uspto.gov/sequence.html?DocID=6294328B1.

XX Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189 other;

Query Match 75.7%; Score 17.4; DB 22; Length 4403765;  
Best Local Similarity 82.6%; Pred. No. 1.2e+02;  
Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23

:||||| ||||| ||||| ||||| ||

Db 172072 TCATGCTGAAGCCTCGACGCG 172050

## RESULT 9

AAI99682/C

ID AAI99682 standard; DNA; 4411529 BP.

XX

AC AAI99682;

XX

DT 15-JAN-2002 (first entry)

XX

DE Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 1.

XX

KW Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome;  
variation; epidemiology; patient treatment; epidemic monitoring; ds.

XX

OS Mycobacterium tuberculosis.

XX

PN US6294328-B1.

XX

PD 25-SEP-2001.

XX

PF 24-JUN-1998; 98US-0103840.

XX

PR 24-JUN-1998; 98US-0103840.

XX

PA (GENO-) INST GENOMIC RES.

XX

PI Fleischmann RD, White OR, Fraser CM, Venter JC;

XX

WPI; 2001-647261/74.

XX

PT Evaluating strain variation of Mycobacterium tuberculosis, comprises  
determining the nucleotide sequence of the strain at positions in the  
genome corresponding to positions where M. tuberculosis strains CDC  
1551 and H37Rv differ

XX

PS Claim 3; SEQ ID NO 1; 3pp + Sequence Listing; English.

XX

CC The invention relates to evaluating strain variation within and between  
different populations of the tuberculosis bacterial pathogen,  
Mycobacterium tuberculosis or related Mycobacterium by determining the  
nucleotide sequence of the first strain at positions in the complete  
sequence of the genome that correspond to positions that differ in the  
nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and  
H37Rv (AAI99682). The method is useful for evaluating strain variation of  
M. tuberculosis and has valuable application in the fields of  
tuberculosis genetics, epidemiology, patient treatment and epidemic  
monitoring.

CC Note: The sequence data for this patent did not form part of the printed  
specification, but was obtained in electronic format directly from USPTO  
CC at seqdata.uspto.gov/sequence.html?DocID=6294328B1.

XX

SQ Sequence 4411529 BP; 758565 A; 1449983 C; 1444602 G; 758379 T; 0 other;

Query Match 75.7%; Score 17.4; DB 22; Length 4411529;

Best Local Similarity 82.6%; Pred. No. 1.2e+02;  
Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23

:||||| ||||| ||||| ||||| ||

Db 171903 TCATGCTGAAGCCTCGACGCG 171881

## RESULT 10

AAS65314

ID AAS65314 standard; cDNA; 492 BP.

XX

AC AAS65314;

XX

DT 13-FEB-2002 (first entry)

XX

DE DNA encoding novel human diagnostic protein #1118.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX

OS Homo sapiens.

XX

PN WO200175067-A2.

XX

PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US08631.

XX

PR 31-MAR-2000; 2000US-0540217.

XX

PR 23-AUG-2000; 2000US-0649167.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Drmanac RT, Liu C, Tang YT;

XX

WPI; 2001-639362/73.

XX

P-PSDB; ABG01127.

DR

XX

PT New isolated polynucleotide and encoded polypeptides, useful in  
diagnostics, forensics, gene mapping, identification of mutations  
responsible for genetic disorders or other traits and to assess  
biodiversity

XX

PS Claim 1; SEQ ID No 1118; 103pp; English.

XX

CC The invention relates to isolated polynucleotide (I) and  
polypeptide (II) sequences. (I) is useful as hybridisation probes,  
polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
and gene mapping, and in recombinant production of (II). The  
polynucleotides are also used in diagnostics as expressed sequence tags  
for identifying expressed genes. (I) is useful in gene therapy techniques  
to restore normal activity of (II) or to treat disease states involving  
(II). (II) is useful for generating antibodies against it, detecting or  
quantitating a polypeptide in tissue, as molecular weight markers and as  
a food supplement. (II) and its binding partners are useful in medical  
imaging of sites expressing (II). (I) and (II) are useful for treating  
disorders involving aberrant protein expression or biological activity.  
The polypeptide and polynucleotide sequences have applications in  
diagnostics, forensics, gene mapping, identification of mutations  
responsible for genetic disorders or other traits to assess biodiversity  
and to produce other types of data and products dependent on DNA and  
amino acid coding sequences. AAS64197-AAS94564 represent novel human  
diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed  
specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX

SQ Sequence 492 BP; 134 A; 115 C; 142 G; 101 T; 0 other;

Query Match 73.9%; Score 17; DB 23; Length 492;

Best Local Similarity 85.7%; Pred. No. 67;  
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTT 21

:||||| ||||| ||||| ||||| ||

Db 378 ACATGCTGAAGCCTAGAGTT 398



```

XX PN WO200157274-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000666.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PF WI; 2001-488899/53.
XX PT Single exon nucleic acid probes for analyzing gene expression in human
XX hearts
XX PS Claim 1; SEQ ID NO 3226; 530pp; English.
XX CC The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart. The
XX present sequence is one such probe. The probes may be used for
XX predicting, measuring and displaying gene expression in samples derived
XX from the human heart via microarrays. By measuring gene expression, the
XX probes are useful for predicting, diagnosing, grading, staging,
XX monitoring and prognosing diseases of the human heart and vascular system
XX e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX congenital heart disease.
XX CC Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;

Query Match 73.0%; Score 16.8; DB 22; Length 454;
Best Local Similarity 90.0%; Pred. No. 84;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATGCTGAAGCCTCGACTT 21
Db 182 CATGCAGAAAGCCTCTACTT 201

RESULT 14
AAK03266
ID AAK03266 standard; DNA; 454 BP.
XX AC AAK03266;
XX DT 05-NOV-2001 (first entry)
XX DE Human brain expressed single exon probe SEQ ID NO: 3257.
XX KW Human; brain expressed exon; gene expression analysis; probe;
XX KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
XX KW epilepsy; cancer; ss.
XX OS Homo sapiens.
XX PN WO200157275-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000667.
XX PR 04-FEB-2000; 2000US-0180312.

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PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PF WI; 2001-483446/52.
XX PT Single exon nucleic acid probes for analyzing gene expression in human
XX brains
XX PS Example 4; SEQ ID NO: 3257; 650pp + Sequence Listing; English.
XX CC The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is one of the probes of the
XX invention.
XX SQ Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;

Query Match 73.0%; Score 16.8; DB 22; Length 454;
Best Local Similarity 90.0%; Pred. No. 84;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATGCTGAAGCCTCGACTT 21
Db 182 CATGCAGAAAGCCTCTACTT 201

RESULT 15
AAK28719
ID AAK28719 standard; DNA; 454 BP.
XX AC AAK28719;
XX DT 06-NOV-2001 (first entry)
XX DE Human bone marrow expressed single exon probe SEQ ID NO: 3276.
XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
XX KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX OS Homo sapiens.
XX PN WO200157276-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000668.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PF WI; 2001-488900/53.
XX PT Human genome-derived single exon nucleic acid probes useful for

```

PT analyzing gene expression in human bone marrow -  
 XX  
 PS Example 4; SEQ ID NO: 3276; 658pp + Sequence Listing; English.  
 XX  
 CC The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC bone marrow. They can be used to measure gene expression in bone marrow  
 CC samples, which may enable the improved diagnosis and treatment of cancers  
 CC such as lymphoma, leukaemia and myeloma. The present sequence is one of  
 CC the probes of the invention.  
 XX  
 SQ Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;  
 Query Match 73.0%; Score 16.8; DB 22; Length 454;  
 Best Local Similarity 90.0%; Pred. No. 84;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Oy 2 CATGCTGAAAGCCTCGACTT 21  
 Db 182 CATGCTGAAAGCCTCGACTT 201

Search completed: June 12, 2003, 01:44:42  
 Job time : 133.802 secs

GenCore version 5.1.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 01:18:34 ; Search time 22.066 Seconds  
(without alignments)  
319.658 Million cell updates/sec

Title: US-09-674-195C-18  
Perfect score: 23  
Sequence: 1 dcatgtgaagcctcgactctg 23  
Scoring table: IDENTITY\_NUC  
Gapop 10.0 ; Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:  
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3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:  
5: /cgn2\_6/ptodata/1/ina/PTCUS\_COMB.seq:  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	22	95.7	22	1	US-07-720-587A-1
C 2	17.4	75.7	4403765	4	US-09-103-840A-2
C 3	17.4	75.7	4411529	4	US-09-103-840A-1
C 4	15.8	68.7	738	2	US-08-224-591-13
5	15.8	68.7	738	2	US-08-392-338A-22
6	15.8	68.7	738	2	US-08-926-789-13
7	15.8	68.7	738	3	US-09-166-750-22
8	15.8	68.7	738	3	US-09-166-093-22
9	15.8	68.7	738	3	US-09-172-019-22
10	15.8	68.7	738	3	US-09-166-094-22
11	15.8	68.7	738	5	PTC-US93-11138-13
12	15.8	68.7	744	2	US-08-392-338A-12
13	15.8	68.7	744	3	US-09-166-750-12
14	15.8	68.7	744	3	US-09-166-093-12
15	15.8	68.7	744	3	US-09-172-019-12
16	15.8	68.7	744	3	US-09-166-094-12
17	15.8	68.7	758	4	US-09-069-821-1
18	15.8	68.7	797	1	US-08-420-592A-1
19	15.8	68.7	797	1	US-08-323-445A-3
20	15.8	68.7	797	1	US-08-515-903A-3
21	15.8	68.7	797	5	PTC-US95-12840-3
22	15.8	68.7	803	1	US-08-323-445A-7
23	15.8	68.7	803	5	PTC-US95-12840-7
24	15.8	68.7	818	4	US-09-420-592A-3
25	15.8	68.7	1460	2	US-08-392-338A-18
26	15.8	68.7	1460	3	US-09-166-750-18
27	15.8	68.7	1460	3	US-09-166-750-18

28	15.8	68.7	1460	3	US-09-166-093-18	Sequence 18, Appl
29	15.8	68.7	1460	3	US-09-172-019-18	Sequence 18, Appl
30	15.8	68.7	1460	3	US-09-166-094-18	Sequence 18, Appl
C 31	15.8	68.7	1722	1	US-08-055-945-1	Sequence 1, Appl
32	15.8	68.7	2033	1	US-08-148-910-14	Sequence 14, Appl
33	15.8	68.7	2033	1	US-08-448-937A-14	Sequence 14, Appl
34	15.8	68.7	2293	4	US-09-645-073-1	Sequence 1, Appl
35	15.4	67.0	522	4	US-09-221-017B-1065	Sequence 1065, Ap
C 36	15.4	67.0	709	4	US-08-998-416-281	Sequence 281, Appl
37	15.4	67.0	9515	1	US-08-920-812-13	Sequence 13, Appl
38	15.4	67.0	9515	1	US-08-920-827-13	Sequence 13, Appl
39	15.4	67.0	9515	1	US-08-921-177-13	Sequence 13, Appl
40	15.4	67.0	9515	1	US-08-362-577C-13	Sequence 13, Appl
41	15.4	67.0	9515	2	US-08-920-828-13	Sequence 13, Appl
42	15.2	66.1	870	1	US-08-411-706-1	Sequence 1, Appl
43	15.2	66.1	12412	1	US-08-390-878-18	Sequence 18, Appl
44	15.2	66.1	4403765	4	US-09-103-840A-2	Sequence 2, Appl
45	14.8	64.3	444	1	US-08-093-144-5	Sequence 5, Appl

## ALIGNMENTS

RESULT 1  
US-07-720-587A-1/c  
; Sequence 1, Application US/07720587A  
; Patent No. 5352579  
; GENERAL INFORMATION:  
; APPLICANT: Curt L. Millman  
; TITLE OF INVENTION: NUCLEIC ACIDS PROBES  
; TITLE OF INVENTION: TO HISTOPLASMA CAPSULATUM  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM PS/2 Model 502 or 55SX  
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
; SOFTWARE: WordPerfect (Version 5.0)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07720,587A  
; FILING DATE: 19910628  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION DATA: including application  
; PRIOR APPLICATION DATA: described below:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 193/121  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 22  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-07-720-587A-1

none

Query Match 95.7%; Score 22; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CATGCTGAAAGCCTCGACTTCG 23  
|||||  
Db 22 CATGCTGAAAGCCTCGACTTCG 1

RESULT 2  
US-09-103-840A-2/c  
; Sequence 2, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; TITLE OF INVENTION: TUBERCULOSIS  
; FILE REFERENCE: 24366-20007.00  
; CURRENT APPLICATION NUMBER: US/09/103.840A  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 4403765  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; FEATURE:  
; OTHER INFORMATION: CDC 1551  
; OTHER INFORMATION: "n" bases at various positions throughout the sequence  
; OTHER INFORMATION: represent a, t, c or g  
US-09-103-840A-2

Query Match 75.7%; Score 17.4; DB 4; Length 4403765;  
Best Local Similarity 82.6%; Pred. No. 21;  
Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DCATGCTGAAAGCCTCGACTTCG 23  
:|||||  
Db 172072 TCATGGTGAAGCCTCGACACGC 172050

RESULT 3  
US-09-103-840A-1/c  
; Sequence 1, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; TITLE OF INVENTION: TUBERCULOSIS  
; FILE REFERENCE: 24366-20007.00  
; CURRENT APPLICATION NUMBER: US/09/103.840A  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 4411529  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; OTHER INFORMATION: H37Rv  
US-09-103-840A-1

Query Match 75.7%; Score 17.4; DB 4; Length 4411529;  
Best Local Similarity 82.6%; Pred. No. 21;  
Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DCATGCTGAAAGCCTCGACTTCG 23  
:|||||  
Db 171903 TCATGGTGAAGCCTCGACACGC 171881

RESULT 4

US-08-224-591-13  
; Sequence 13, Application US/08224591  
; Patent No. 5856456  
; GENERAL INFORMATION:  
; APPLICANT: Whitlow, Marc  
; APPLICANT: Filpula, David  
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/224,591  
; FILING DATE: Herewith  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/002,845  
; FILING DATE: 15-JAN-1993  
; APPLICATION NUMBER: US 07/980,529  
; FILING DATE: 20-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0977.1920002/JAG  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 738 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: join(1..726)  
US-08-224-591-13

Query Match 68.7%; Score 15.8; DB 2; Length 738;  
Best Local Similarity 89.5%; Pred. No. 45;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TGCTGAAAGCCTCGACTTC 22  
|||||  
Db 332 TGCTGAAAGCCTCTACTTC 350

RESULT 5  
US-08-392-338A-22  
; Sequence 22, Application US/08392338A  
; Patent No. 5869620  
; GENERAL INFORMATION:  
; APPLICANT: Whitlow, Marc  
; APPLICANT: Wood, James F.  
; APPLICANT: Hardman, Karl  
; APPLICANT: Bird, Robert  
; APPLICANT: Filpula, David  
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, NW  
; CITY: Washington  
; STATE: D.C.

COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/392,338A  
FILING DATE: 22-FEB-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/989,846  
FILING DATE: 20-NOV-1992  
APPLICATION DATA:  
APPLICATION NUMBER: US 07/796,936  
FILING DATE: 25-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.0030007  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 738 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..726  
US-08-392-338A-22

Query Match 68.7%; Score 15.8; DB 2; Length 738;  
Best Local Similarity 89.5%; Pred. No. 45;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGCTGAAGCGCTCGACTTC 22  
||||| ||| |||||  
DB 332 TGCTGAAGCGCTCTACTTC 350

RESULT 6  
US-08-926-789-13  
Sequence 13, Application US/08926789  
Patent No. 5990275  
GENERAL INFORMATION:  
APPLICANT: Whitlow, Marc  
TITLE OF INVENTION: Linker For Linked Fusion Polypeptides  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/926,789  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/224,591  
FILING DATE:  
APPLICATION NUMBER: US 08/002,845

FILING DATE: 15-JAN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/980,529  
FILING DATE: 20-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.1920002/JAG  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 738 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(1..726)  
US-08-926-789-13

Query Match 68.7%; Score 15.8; DB 2; Length 738;  
Best Local Similarity 89.5%; Pred. No. 45;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGCTGAAGCGCTCGACTTC 22  
||||| ||| |||||  
DB 332 TGCTGAAGCGCTCTACTTC 350

RESULT 7  
US-09-166-750-22  
Sequence 22, Application US/09166750  
Patent No. 6025165  
GENERAL INFORMATION:  
APPLICANT: Whitlow, Marc  
APPLICANT: Wood, James F.  
APPLICANT: Hardman, Karl  
APPLICANT: Bird, Robert  
APPLICANT: Filpula, David  
APPLICANT: Rollence, Michelle  
TITLE OF INVENTION: Methods for Producing Multivalent Antigen-Binding  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, NW  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/166,750  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/392,338  
FILING DATE: 22-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/989,846  
FILING DATE: 20-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/796,936  
FILING DATE: 25-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021

; REFERENCE/DOCKET NUMBER: 0977.003000C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 738 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..726  
US-09-166-750-22

Query Match 68.7%; Score 15.8; DB 3; Length 738;  
Best Local Similarity 89.5%; Pred. No. 45;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGCTGAAGGCTCGACTTC 22  
DB 332 TGCTGAAGGCTCTACTTC 350

## RESULT 8

US-09-166-093-22  
; Sequence 22, Application US/09166093  
; Patent No. 6027725

## GENERAL INFORMATION:

; APPLICANT: Whitlow, Marc  
; APPLICANT: Wood, James F.  
; APPLICANT: Hardman, Karl  
; APPLICANT: Bird, Robert  
; APPLICANT: Filpula, David  
; APPLICANT: Rollence, Michelle  
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, NW  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/166,093  
; FILING DATE: Herewith

## CLASSIFICATION:

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/392,338  
; FILING DATE: 22-FEB-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/989,846  
; FILING DATE: 20-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/796,936  
; FILING DATE: 25-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021

; REFERENCE/DOCKET NUMBER: 0977.003000B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 738 base pairs  
; TYPE: nucleic acid

; STRANDEDNESS: both  
; TOPOLOGY: both  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..726  
US-09-166-093-22

Query Match 68.7%; Score 15.8; DB 3; Length 738;  
Best Local Similarity 89.5%; Pred. No. 45;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGCTGAAGGCTCGACTTC 22  
DB 332 TGCTGAAGGCTCTACTTC 350

## RESULT 9

US-09-172-019-22  
; Sequence 22, Application US/09172019  
; Patent No. 6103889

## GENERAL INFORMATION:

; APPLICANT: Whitlow, Marc  
; APPLICANT: Hardman, Karl  
; APPLICANT: Bird, Robert  
; APPLICANT: Filpula, David  
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Single-Chain  
; TITLE OF INVENTION: Antigen-Binding Proteins (As Amended)  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, NW  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/172,019  
; FILING DATE: Herewith

## CLASSIFICATION:

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/392,338  
; FILING DATE: 22-FEB-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/989,846  
; FILING DATE: 20-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/796,936  
; FILING DATE: 25-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0977.003000D  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 738 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..726  
US-09-172-019-22

Query Match 68.7%; Score 15.8; DB 3; Length 738;  
Best Local Similarity 89.5%; Pred. No. 45;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGCTGAAAGCCTCGACTTC 22  
||||||| ||| |||||  
Db 332 TGCTGAAAGCCTCTACTTC 350

## RESULT 10

US-09-166-094-22  
; Sequence 22, Application US/09166094  
; Patent No. 6121424  
; GENERAL INFORMATION:  
; APPLICANT: Whitlow, Marc  
; APPLICANT: Wood, James F.  
; APPLICANT: Hardman, Karl  
; APPLICANT: Bird, Robert  
; APPLICANT: Filpula, David  
; APPLICANT: Rollence, Michelle  
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, NW  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/166,094  
; FILING DATE: Herewith

CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/392,338  
; FILING DATE: 22-FEB-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/989,846  
; FILING DATE: 20-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/796,936  
; FILING DATE: 25-NOV-1991

ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0977.003000A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2540  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 738 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..726

## US-09-166-094-22

Query Match 68.7%; Score 15.8; DB 3; Length 738;  
Best Local Similarity 89.5%; Pred. No. 45;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGCTGAAAGCCTCGACTTC 22  
||||||| ||| |||||  
Db 332 TGCTGAAAGCCTCTACTTC 350

## RESULT 11

PCT-US93-11138-13  
; Sequence 13, Application PC/TUS9311138  
; GENERAL INFORMATION:  
; APPLICANT: Enzon, Inc.

; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-3934

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/11138  
; FILING DATE: Herewith

CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/980,529  
; FILING DATE: 20-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/002,845  
; FILING DATE: 15-JAN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0977.2006604/JAG  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 738 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..738

## PCT-US93-11138-13

Query Match 68.7%; Score 15.8; DB 5; Length 738;  
Best Local Similarity 89.5%; Pred. No. 45;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGCTGAAAGCCTCGACTTC 22  
||||||| ||| |||||  
Db 332 TGCTGAAAGCCTCTACTTC 350

## RESULT 12

US-08-392-338A-12  
; Sequence 12, Application US/08392338A  
; Patent No. 5869620

GENERAL INFORMATION:  
; APPLICANT: Whitlow, Marc  
; APPLICANT: Wood, James F.  
; APPLICANT: Hardman, Karl  
; APPLICANT: Bird, Robert  
; APPLICANT: Filpula, David  
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

; STREET: 1100 New York Avenue, NW  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.

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; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/392,338A
; FILING DATE: 22-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/989,846
; FILING DATE: 20-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,936
; FILING DATE: 25-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.0030007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 744 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..732
; US-08-392-338A-12

Query Match 68.7%; Score 15.8; DB 2; Length 744;
Best Local Similarity 89.5%; Pred. No. 45;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGCTGAAGCCTCGACTTC 22
Db 332 TGCTGAAGCCTCTACTTC 350

RESULT 13
; Sequence 12, Application US/09166750
; Patent No. 6025165
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Wood, James F.
; APPLICANT: Hardman, Karl
; APPLICANT: Bird, Robert
; APPLICANT: Filpula, David
; APPLICANT: Rollence, Michelle
; TITLE OF INVENTION: Methods for Producing Multivalent Antigen-Binding
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/166,750
; FILING DATE: Herewith
; CLASSIFICATION:
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; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/392,338
; FILING DATE: 22-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/989,846
; FILING DATE: 20-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,936
; FILING DATE: 25-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.003000C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 744 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..732
; US-09-166-750-12

Query Match 68.7%; Score 15.8; DB 3; Length 744;
Best Local Similarity 89.5%; Pred. No. 45;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGCTGAAGCCTCGACTTC 22
Db 332 TGCTGAAGCCTCTACTTC 350

RESULT 14
; Sequence 12, Application US/09166093
; Patent No. 6027725
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Wood, James F.
; APPLICANT: Hardman, Karl
; APPLICANT: Bird, Robert
; APPLICANT: Filpula, David
; APPLICANT: Rollence, Michelle
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/166,093
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/392,338
; FILING DATE: 22-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/989,846
; FILING DATE: 20-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,936
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SEQUENCE CHARACTERISTICS:  
LENGTH: 744 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..732  
US-09-172-019-12  
Query Match 68.7%; Score 15.8; DB 3; Length 744;  
Best Local Similarity 89.5%; Pred. No. 45;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 4 TGCTGAAAGGCTCGACTTC 22  
DB 332 TGCTGAAAGGCTCGACTTC 350  
Search completed: June 12, 2003, 04:40:00  
Job time : 56.066 secs

FILING DATE: 25-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.003000B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 744 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..732  
US-09-166-093-12  
Query Match 68.7%; Score 15.8; DB 3; Length 744;  
Best Local Similarity 89.5%; Pred. No. 45;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 4 TGCTGAAAGGCTCGACTTC 22  
DB 332 TGCTGAAAGGCTCGACTTC 350

RESULT 15  
US-09-172-019-12  
Sequence 12, Application US/09172019  
Patent No. 6103889  
GENERAL INFORMATION:  
APPLICANT: Whitlow, Marc  
APPLICANT: Hardman, Karl  
APPLICANT: Bird, Robert  
APPLICANT: Filpula, David  
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Single-Chain  
Antigen-Binding Proteins (As Amended)  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, NW  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/172,019  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/392,338  
FILING DATE: 22-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/989,846  
FILING DATE: 20-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/796,936  
FILING DATE: 25-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.003000D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 12:



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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 01:27:04 ; Search time 134.381 seconds  
(without alignments)  
239.539 Million cell updates/sec

Title: US-09-674-195C-18  
Perfect score: 23  
Sequence: 1 dcatgctgaaagcctcgacttcg 23

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_NA.\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
C 1	17.2	74.8	1691139	9	US-10-067-514-1
C 2	16.8	73.0	454	10	US-09-864-761-3226
C 3	16.2	70.4	891	9	US-09-989-643-155
C 4	16.2	70.4	1097	10	US-09-974-300-179
C 5	15.8	68.7	310	10	US-09-878-574-665
C 6	15.8	68.7	550	9	US-09-991-936-838
C 7	15.8	68.7	723	10	US-09-791-578-5
C 8	15.8	68.7	723	10	US-09-791-540-5
C 9	15.8	68.7	758	9	US-09-956-086-1
C 10	15.8	68.7	758	9	US-09-956-087-1
C 11	15.8	68.7	782	9	US-09-985-442-1
C 12	15.8	68.7	782	10	US-09-791-578-3
C 13	15.8	68.7	782	10	US-09-791-540-3
C 14	15.8	68.7	782	10	US-09-983-580-1
C 15	15.8	68.7	818	9	US-09-983-580-3
C 16	15.8	68.7	818	10	US-09-983-580-3
C 17	15.8	68.7	933	9	US-09-938-842A-536
C 18	15.8	68.7	981	10	US-09-770-445-271
C 19	15.8	68.7	1279	9	US-10-165-603-19

20	15.8	68.7	2036	10	US-09-954-456-552
21	15.8	68.7	2036	10	US-09-880-107-1612
22	15.8	68.7	20556	10	US-09-880-107-3945
C 23	15.8	68.7	177556	9	US-09-952-2130-6
24	15.6	67.8	375	10	US-09-878-574-3603
C 25	15.6	67.8	397	10	US-09-867-701-8410
C 26	15.4	67.0	365	10	US-09-783-590-10265
27	15.4	67.0	8268	9	US-10-074-095-868
28	15.4	67.0	8268	10	US-09-764-860-868
29	15.4	67.0	8272	9	US-10-074-095-867
30	15.4	67.0	8272	10	US-09-764-860-867
C 31	15.2	66.1	768	10	US-09-910-943-408
32	15.2	66.1	843	9	US-10-164-433-1
33	15.2	66.1	1186	9	US-09-925-299-98
34	15.2	66.1	1186	10	US-09-925-299-98
35	15.2	66.1	1413	9	US-09-894-844-25
36	15.2	66.1	1579	10	US-09-822-849A-139
37	15.2	66.1	3119	10	US-09-867-701-10873
38	15.2	66.1	7090	9	US-09-832-292-28
C 39	15.2	66.1	24768	9	US-10-073-961-602
C 40	15.2	66.1	24768	10	US-09-764-887-602
C 41	15.2	66.1	34094	9	US-10-199-550-1
C 42	15.2	66.1	1503841	9	US-09-946-807-1
C 43	15.2	66.1	1503841	10	US-09-795-668-1
C 44	15.2	66.1	1503841	10	US-09-795-686-1
C 45	15	65.2	1014	10	US-09-815-242-7828

## ALIGNMENTS

RESULT 1  
US-10-067-514-1/c  
; Sequence 1, Application US/10067514  
; Publication No. US20030054531A1  
; GENERAL INFORMATION:  
; APPLICANT: Gretarsdottir, Solveig  
; APPLICANT: Jonsdottir, Sif  
; APPLICANT: Reynisdottir, Sigridur Th.  
; TITLE OF INVENTION: HUMAN STROKE GENE  
; FILE REFERENCE: 2345 2010-003  
; CURRENT APPLICATION NUMBER: US/10/067,514  
; PRIOR FILING DATE: 2002-02-04  
; PRIOR APPLICATION NUMBER: US 09/811/352  
; PRIOR FILING DATE: 2001-03-19  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1691139  
; TYPE: DNA  
; ORGANISM: Human  
US-10-067-514-1

Query Match 74.8%; Score 17.2; DB 9; Length 1691139;  
Best Local Similarity 86.4%; Pred. No. 38;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 CATGCTGAAAGCTCGACTTCG 23  
DB 758804 CATGCTGAAAGCATACACTTCG 758783

RESULT 2  
US-09-864-761-3226  
; Sequence 3226, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY



;; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
;; FILE OF INVENTION: Plants  
;; FILE REFERENCE: 38-21(15401)B  
;; CURRENT APPLICATION NUMBER: US/09/878,574  
;; CURRENT FILING DATE: 2001-12-21  
;; PRIOR APPLICATION NUMBER: 09/333,535  
;; PRIOR FILING DATE: 1999-06-14  
;; NUMBER OF SEQ ID NOS: 15775  
;; SEQ ID NO 665  
;; LENGTH: 310  
;; TYPE: DNA  
;; ORGANISM: Glycine max  
;; OTHER INFORMATION: Clone ID: LIB3028-047-Q1-B1-H11  
US-09-878-574-665

Query Match 68.7%; Score 15.8; DB 10; Length 310;  
Best Local Similarity 78.3%; Pred. No. 1.1e+02;  
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23  
Db 286 TCATGCTTAAACCTTGACTGG 264

## RESULT 6

US-09-991-936-838/c  
;; Sequence 838, Application US/09991936  
;; Publication No. US20030073827A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Brandt, Kevin S.  
;; APPLICANT: Gaines, Patrick J.  
;; APPLICANT: Stinchcomb, Dan T.  
;; APPLICANT: Wisniewski, Nancy  
;; TITLE OF INVENTION: FLEA HEAD, NERVE CORD, HINDGUT AND MALPIGHIAN TUBULE  
;; FILE OF INVENTION: NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF  
;; FILE REFERENCE: FC-6-C1  
;; CURRENT APPLICATION NUMBER: US/09/991,936  
;; CURRENT FILING DATE: 2001-11-21  
;; PRIOR APPLICATION NUMBER: US/09/543,668  
;; PRIOR FILING DATE: 2000-04-07  
;; PRIOR APPLICATION NUMBER: 60/128,704  
;; PRIOR FILING DATE: 1999-04-09  
;; NUMBER OF SEQ ID NOS: 1959  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 838  
;; LENGTH: 550  
;; TYPE: DNA  
;; ORGANISM: Ctencephalides felis  
US-09-991-936-838

Query Match 68.7%; Score 15.8; DB 9; Length 550;  
Best Local Similarity 89.5%; Pred. No. 1.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGCTGAAGCCTCGACTTC 22  
Db 174 TGCTGAAGCCTCACTTC 156

## RESULT 7

US-09-791-578-5  
;; Sequence 5, Application US/09791578  
;; Patent No. US20020061307A1  
;; GENERAL INFORMATION:  
;; APPLICANT: WHITLOW, MARC  
;; SHORR, ROBERT G.L.  
;; FILPULA, DAVID R.  
;; LEE, LIHSYNG S.  
;; TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN  
;; NUMBER OF SEQUENCES: 6  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

;; STREET: 1100 NEW YORK AVENUE, SUITE 600  
;; CITY: WASHINGTON  
;; STATE: DC  
;; COUNTRY: USA  
;; ZIP: 20005  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/791,578  
;; FILING DATE: 26-Feb-2001  
;; CLASSIFICATION: <Unknown>  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 09/069,842  
;; FILING DATE: <Unknown>  
;; APPLICATION NUMBER: US 60/050,472  
;; FILING DATE: 23-JUN-1997  
;; APPLICATION NUMBER: US 60/063,074  
;; FILING DATE: 27-OCT-1997  
;; APPLICATION NUMBER: US 60/067,341  
;; FILING DATE: 02-DEC-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: JORGE A. GOLDSTEIN  
;; REGISTRATION NUMBER: 29,021  
;; REFERENCE/DOCKET NUMBER: 0977.1840002  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-371-2600  
;; TELEFAX: 202-371-2540  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 723 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: both  
;; TOPOLOGY: both  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: 1..723  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-791-578-5

Query Match 68.7%; Score 15.8; DB 10; Length 723;  
Best Local Similarity 89.5%; Pred. No. 1.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGCTGAAGCCTCGACTTC 22  
Db 332 TGCTGAAGGCTCTACTTC 350

## RESULT 8

US-09-791-540-5  
;; Sequence 5, Application US/09791540  
;; Patent No. US20020098192A1  
;; GENERAL INFORMATION:  
;; APPLICANT: WHITLOW, MARC  
;; SHORR, ROBERT G.L.  
;; FILPULA, DAVID R.  
;; LEE, LIHSYNG S.  
;; TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN  
;; NUMBER OF SEQUENCES: 6  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
;; STREET: 1100 NEW YORK AVENUE, SUITE 600  
;; CITY: WASHINGTON  
;; STATE: DC  
;; COUNTRY: USA  
;; ZIP: 20005  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/791,540
; FILING DATE: 26-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/069,842
; FILING DATE: 1998-04-30
; APPLICATION NUMBER: US 60/050,472
; FILING DATE: 23-JUN-1997
; APPLICATION NUMBER: US 60/063,074
; FILING DATE: 27-OCT-1997
; APPLICATION NUMBER: US 60/067,341
; FILING DATE: 02-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: JORGE A. GOLDSTEIN
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.1840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 723 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..723
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-791-540-5

Query Match 68.7%; Score 15.8; DB 10; Length 723;
Best Local Similarity 89.5%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TGCTGAAAGCCTCGACTTC 22
Db 332 TGCTGAAAGGCTCTACTTC 350

RESULT 9
US-09-956-086-1
; Sequence 1, Application US/09956086
; Patent No. US20020155498A1
; GENERAL INFORMATION:
; APPLICANT: FILPULA, DAVID
; WANG, MAOLIANG
; SHORR, ROBERT
; WHITLOW, MARC
; LEE, LIHSYNG S.
; TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
; CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/956,086
; FILING DATE: 20-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: 09/069,821
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/063,074
; FILING DATE: 27-OCT-1997
; APPLICATION NUMBER: US 60/050,472
; FILING DATE: 23-JUN-1997
; APPLICATION NUMBER: US 60/044,449
; FILING DATE: 30-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KIM, JUDITH U.
; REGISTRATION NUMBER: 40,679
; REFERENCE/DOCKET NUMBER: 0977.2280003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 758 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..747
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-956-086-1

Query Match 68.7%; Score 15.8; DB 9; Length 758;
Best Local Similarity 89.5%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TGCTGAAAGCCTCGACTTC 22
Db 332 TGCTGAAAGGCTCTACTTC 350

RESULT 10
US-09-956-087-1
; Sequence 1, Application US/09956087
; Patent No. US20020161201A1
; GENERAL INFORMATION:
; APPLICANT: FILPULA, DAVID
; WANG, MAOLIANG
; SHORR, ROBERT
; WHITLOW, MARC
; LEE, LIHSYNG S.
; TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
; CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/956,087
; FILING DATE: 20-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/069,821
; FILING DATE: 1998-04-30
; APPLICATION NUMBER: US 60/063,074
; FILING DATE: 27-OCT-1997
; APPLICATION NUMBER: US 60/050,472
; FILING DATE: 23-JUN-1997
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APPLICATION NUMBER: US 60/044,449  
FILING DATE: 30-APR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: KIM, JUDITH U.  
REGISTRATION NUMBER: 40,679  
REFERENCE/DOCKET NUMBER: 0977.2280003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)371-2600  
TELEFAX: (202)371-2540  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 758 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..747  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-956-087-1

Query Match 68.7%; Score 15.8; DB 9; Length 758;  
Best Local Similarity 89.5%; Pred. No. 1.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGCTGAAAGCCTCGACTTC 22  
||||||| ||| |||||  
Db 332 TGCTGAAAGGCTCTACTTC 350

RESULT 11  
US-09-985-442-1  
; Sequence 1, Application US/09985442  
; Patent No. US20020156248A1  
; GENERAL INFORMATION:  
; APPLICANT: Filpula, David R.  
; APPLICANT: Wang, Maoliang  
; APPLICANT: Whitlow, Marc D.  
; TITLE OF INVENTION: No. US20020156248A1 Method for Targeted Delivery of Nucleic Acid  
; FILE REFERENCE: 0977.2300003  
; CURRENT APPLICATION NUMBER: US/09/985,442  
; CURRENT FILING DATE: 2001-11-02  
; PRIOR APPLICATION NUMBER: 09/420,592  
; PRIOR FILING DATE: 1999-10-19  
; PRIOR APPLICATION NUMBER: 60/104,949  
; PRIOR FILING DATE: 1998-10-20  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 782  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: CC49/218 sfv  
; NAME/KEY: CDS  
; LOCATION: (1)..(771)  
US-09-985-442-1

Query Match 68.7%; Score 15.8; DB 9; Length 782;  
Best Local Similarity 89.5%; Pred. No. 1.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGCTGAAAGCCTCGACTTC 22  
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Db 332 TGCTGAAAGGCTCTACTTC 350

RESULT 12  
US-09-791-578-3  
; Sequence 3, Application US/09791578  
; Patent No. US20020061307A1  
; GENERAL INFORMATION:

APPLICANT: WHITLOW, MARC  
SHORR, ROBERT G.L.  
FILPULA, DAVID R.  
LEE, LIHSYNG S.  
TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN  
POLYPEPTIDES  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVENUE, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/09/791,578  
FILING DATE: 26-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/069,842  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 60/050,472  
FILING DATE: 23-JUN-1997  
APPLICATION NUMBER: US 60/063,074  
FILING DATE: 27-OCT-1997  
APPLICATION NUMBER: US 60/067,341  
FILING DATE: 02-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: JORGE A. GOLDSTEIN  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.1840002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 782 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..771  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-791-578-3

Query Match 68.7%; Score 15.8; DB 10; Length 782;  
Best Local Similarity 89.5%; Pred. No. 1.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGCTGAAAGCCTCGACTTC 22  
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Db 332 TGCTGAAAGGCTCTACTTC 350

RESULT 13  
US-09-791-540-3  
; Sequence 3, Application US/09791540  
; Patent No. US20020098192A1  
; GENERAL INFORMATION:  
; APPLICANT: WHITLOW, MARC  
; SHORR, ROBERT G.L.  
; FILPULA, DAVID R.  
; LEE, LIHSYNG S.  
; TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN  
POLYPEPTIDES  
; NUMBER OF SEQUENCES: 6

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
;; STREET: 1100 NEW YORK AVENUE, SUITE 600  
;; CITY: WASHINGTON  
;; STATE: DC  
;; COUNTRY: USA  
;; ZIP: 20005  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/791,540  
;; FILING DATE: 26-Feb-2001  
;; CLASSIFICATION: <Unknown>  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 09/069,842  
;; FILING DATE: 1998-04-30  
;; APPLICATION NUMBER: US 60/050,472  
;; FILING DATE: 23-JUN-1997  
;; APPLICATION NUMBER: US 60/063,074  
;; FILING DATE: 27-OCT-1997  
;; APPLICATION NUMBER: US 60/067,341  
;; FILING DATE: 02-DEC-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: JORGE A. GOLDSTEIN  
;; REGISTRATION NUMBER: 29,021  
;; REFERENCE/DOCKET NUMBER: 0977.1840002  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-371-2600  
;; TELEFAX: 202-371-2540  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 782 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: both  
;; TOPOLOGY: both  
;; MOLECULE TYPE: cDNA  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: 1..771  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
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Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 4 TGCTGAAAGCCTCGACTTC 22  
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Db 332 TGCTGAAAGCCTCTACTTC 350  
  
RESULT 14  
US-09-983-580-1  
; Sequence 1, Application US/09983580  
; Patent No. US20020151061A1  
; GENERAL INFORMATION:  
; APPLICANT: Filpula, David R.  
; APPLICANT: Wang, Maoliang  
; APPLICANT: Whitlow, Marc D.  
; TITLE OF INVENTION: No. US20020151061A1 Method for Targeted Delivery of Nucleic Ac  
; FILE REFERENCE: 0977.2300002  
; CURRENT APPLICATION NUMBER: US/09/983,580  
; CURRENT FILING DATE: 2001-10-25  
; PRIOR APPLICATION NUMBER: 09/420,592  
; PRIOR FILING DATE: 1999-10-19  
; PRIOR APPLICATION NUMBER: 60/104,949  
; PRIOR FILING DATE: 1998-10-20  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
  
Query Match 68.7%; Score 15.8; DB 10; Length 782;  
Best Local Similarity 89.5%; Pred. No. 1.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 4 TGCTGAAAGCCTCGACTTC 22  
||||| ||| |||||  
Db 332 TGCTGAAAGCCTCTACTTC 350  
  
RESULT 15  
US-09-985-442-3  
; Sequence 3, Application US/09985442  
; Patent No. US20020156248A1  
; GENERAL INFORMATION:  
; APPLICANT: Filpula, David R.  
; APPLICANT: Wang, Maoliang  
; APPLICANT: Whitlow, Marc D.  
; TITLE OF INVENTION: No. US20020156248A1 Method for Targeted Delivery of Nucleic  
; FILE REFERENCE: 0977.2300003  
; CURRENT APPLICATION NUMBER: US/09/985,442  
; CURRENT FILING DATE: 2001-11-02  
; PRIOR APPLICATION NUMBER: 09/420,592  
; PRIOR FILING DATE: 1999-10-19  
; PRIOR APPLICATION NUMBER: 60/104,949  
; PRIOR FILING DATE: 1998-10-20  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 818  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: CC49/218 sFV  
; NAME/KEY: CDS  
; LOCATION: (1)..(807)  
US-09-985-442-3  
  
Query Match 68.7%; Score 15.8; DB 9; Length 818;  
Best Local Similarity 89.5%; Pred. No. 1.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
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||||| ||| |||||  
Db 332 TGCTGAAAGCCTCTACTTC 350  
  
Search completed: June 12, 2003, 04:58:47  
Job time : 143.666 secs

;; LENGTH: 782  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
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; Sequence 3, Application US/09985442  
; Patent No. US20020156248A1  
; GENERAL INFORMATION:  
; APPLICANT: Filpula, David R.  
; APPLICANT: Wang, Maoliang  
; APPLICANT: Whitlow, Marc D.  
; TITLE OF INVENTION: No. US20020156248A1 Method for Targeted Delivery of Nucleic  
; FILE REFERENCE: 0977.2300003  
; CURRENT APPLICATION NUMBER: US/09/985,442  
; CURRENT FILING DATE: 2001-11-02  
; PRIOR APPLICATION NUMBER: 09/420,592  
; PRIOR FILING DATE: 1999-10-19  
; PRIOR APPLICATION NUMBER: 60/104,949  
; PRIOR FILING DATE: 1998-10-20  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 818  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: CC49/218 sFV  
; NAME/KEY: CDS  
; LOCATION: (1)..(807)  
US-09-985-442-3  
  
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Best Local Similarity 89.5%; Pred. No. 1.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 4 TGCTGAAAGCCTCGACTTC 22  
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Db 332 TGCTGAAAGCCTCTACTTC 350  
  
Search completed: June 12, 2003, 04:58:47  
Job time : 143.666 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run On: June 12, 2003, 00:35:54 ; Search time 844.228 Seconds  
(without alignments)  
441.227 Million cell updates/sec

Title: US-09-674-195C-18  
Perfect score: 23  
Sequence: 1 dcatgctgaagcctgacttcg 23

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: EST.\*

- 1: em\_estba.\*
- 2: em\_esthum.\*
- 3: em\_estin.\*
- 4: em\_estnu.\*
- 5: em\_estov.\*
- 6: em\_estpl.\*
- 7: em\_estro.\*
- 8: em\_htc.\*
- 9: gb\_est1.\*
- 10: gb\_est2.\*
- 11: gb\_htc.\*
- 12: gb\_est3.\*
- 13: gb\_est4.\*
- 14: gb\_est5.\*
- 15: em\_estfun.\*
- 16: em\_estom.\*
- 17: gb\_gss.\*
- 18: em\_gss\_hum.\*
- 19: em\_gss\_inv.\*
- 20: em\_gss\_pln.\*
- 21: em\_gss\_vrt.\*
- 22: em\_gss\_fun.\*
- 23: em\_gss\_mam.\*
- 24: em\_gss\_mus.\*
- 25: em\_gss\_other.\*
- 26: em\_gss\_pro.\*
- 27: em\_gss\_rod.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	82.6	123	12	BF251708
2	19	82.6	351	12	BF251693
3	19	82.6	362	12	BF251811
4	19	82.6	377	12	BF251964
5	19	82.6	378	12	BF251967
6	19	82.6	391	12	BF251561

7	19	82.6	486	10	AW792005
8	19	82.6	488	12	BF251704
9	19	82.6	502	12	BF252581
10	19	82.6	515	10	AW792430
11	19	82.6	518	12	BF251715
12	19	82.6	541	12	BF252371
13	19	82.6	546	12	BF252371
14	19	82.6	567	12	BF252094
15	19	82.6	568	12	BF252878
16	19	82.6	572	12	BF252095
17	19	82.6	605	12	BF252135
18	19	82.6	679	12	BF251385
19	19	82.6	687	12	BF251001
20	19	82.6	701	12	BF251666
21	19	82.6	836	12	BF250962
22	18	78.3	222	10	AW791051
23	18	78.3	905	17	CNS077PT
24	18	78.3	914	17	CNS079TL
25	18	78.3	944	17	CNS07877
26	18	78.3	957	17	CNS0797C
27	18	78.3	992	17	CNS0784M
28	18	78.3	997	17	CNS07A19
29	18	78.3	1008	17	CNS076RF
30	18	78.3	1012	17	CNS079X1
31	18	78.3	1020	17	CNS077XC
32	18	78.3	1031	17	CNS076VJ
33	18	78.3	1060	17	CNS078EU
34	17.8	77.4	578	14	W36400
35	17.4	75.7	85	17	AQ025794
36	17.4	75.7	176	9	A1213893
37	17.4	75.7	244	9	A1212196
38	17.4	75.7	250	9	AA784878
39	17.4	75.7	252	9	A1211979
40	17.4	75.7	260	9	A1329914
41	17.4	75.7	269	9	AA966666
42	17.4	75.7	273	9	AA966294
43	17.4	75.7	280	9	AA965352
44	17.4	75.7	293	9	AA783904
45	17.4	75.7	295	9	AA788074

# ALIGNMENTS

RESULT 1	BF251708	BF251708	123 bp	mRNA	linear	EST 15-NOV-2001
LOCUS	EST418892	Coccidioides immitis	spherule	CDNA	library	Coccidioides
DEFINITION	immitis CDNA clone CIAAK37	5' sequence,	mrna	sequence.		
ACCESSION	BF251708					
VERSION	EST.					
KEYWORDS	EST.					
SOURCE	BF251708.1	GI:16931774				
ORGANISM	Coccidioides immitis.					
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;					
AUTHORS	Ongenaes; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;					
TITLE	1 (bases 1 to 123)					
JOURNAL	Gardner,M.J. and Kirkland,T.					
COMMENT	Generation of ESTs from Coccidioides immitis spherule CDNA library					
	Unpublished (2000)					
	Contact: Malcolm J. Gardner					
	Department of Eukaryotic Genomics					
	The Institute for Genomic Research					
	9712 Medical Center Drive, Rockville, MD 20850, USA					
	Tel: 301 838 3519					
	Fax: 301 838 0208					
	Email: gardner@tigr.org					
FEATURES	Location/Qualifiers					
source	1..123					
	/organism="Coccidioides immitis"					
	/db_xref="taxon:5501"					
	/clone="CIAAK37"					
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Thu Jun 12 08:47:55 2003

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REFERENCE
AUTHORS      Gardner,M.J. and Kirkland,T.
TITLE        Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL      Unpublished (2000)
COMMENT      Contact: Malcolm J. Gardner
              Department of Eukaryotic Genomics
              The Institute for Genomic Research
              9712 Medical Center Drive, Rockville, MD 20850, USA
              Tel: 301 838 3519
              Fax: 301 838 0208
              Email: gardner@tigr.org.

FEATURES
source
1..362
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIAAM73"
/clone_lib="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

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ORIGIN
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Best Local Similarity 87.0%; Pred. No. 79;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 DCATGCTGAAGCCTCGACTTCG 23
          :||||| ||| |||||||||
Db      149 ACATGCTAAAAACCTCGACTTCG 171

RESULT 4
BF251964
LOCUS
DEFINITION      BF251964 377 bp mRNA linear EST 15-NOV-2001
                  Coccidioides immitis spherule cDNA library Coccidioides
                  immitis cDNA clone CIAAP15 5' sequence, mRNA sequence.
ACCESSION      BF251964
VERSION
KEYWORDS
SOURCE
ORGANISM
Coccidioides immitis.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Nygenales; mitosporic Nygenales; Coccidioides.
REFERENCE
AUTHORS      Gardner,M.J. and Kirkland,T.
JOURNAL      Unpublished (2000)
COMMENT      Contact: Malcolm J. Gardner
              Department of Eukaryotic Genomics
              The Institute for Genomic Research
              9712 Medical Center Drive, Rockville, MD 20850, USA
              Tel: 301 838 3519
              Fax: 301 838 0208
              Email: gardner@tigr.org.

FEATURES
source
1..351
/organism="Coccidioides immitis"
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XhoI"

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Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db      154 ACATGCTAAAAACCTCGACTTCG 176

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ACCESSION      BF251811
VERSION
KEYWORDS
SOURCE
ORGANISM
Coccidioides immitis.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Nygenales; mitosporic Nygenales; Coccidioides.

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QY 1 DCATGCTGAAGCCTCGACTTCG 23
Db 53 ACATGCTAAACCTCGACTTCG 75

RESULT 5
BF251967
LOCUS
DEFINITION
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immitis cDNA clone CIAAP18 5' sequence, mRNA sequence.
ACCESSION
BF251967
VERSION
BF251967.1 GI:16932110
KEYWORDS
EST.
SOURCE
Coccidioides immitis.
ORGANISM
Coccidioides immitis.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Mitosporic Onygenales; Coccidioides.
REFERENCE
1 (bases 1 to 378)
Gardner, M.J. and Kirkland, T.
Generation of ESTs from Coccidioides immitis spherule cDNA library
Unpublished (2000)
Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org.

FEATURES
Location/Qualifiers
1..378
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/db_xref="taxon:5501"
/clone="CIAAP18"
/clone_lib="Coccidioides immitis spherule cDNA library"
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XhoI"

BASE COUNT 104 a 75 c 94 g 105 t
ORIGIN

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Best Local Similarity 87.0%; Pred. No. 81;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23
Db 147 ACATGCTAAACCTCGACTTCG 169

RESULT 6
BF251561
LOCUS
DEFINITION
EST18910 Coccidioides immitis spherule cDNA library Coccidioides
immitis cDNA clone CIAAK57 5' sequence, mRNA sequence.
ACCESSION
BF251561
VERSION
BF251561.1 GI:16931792
KEYWORDS
EST.
SOURCE
Coccidioides immitis.
ORGANISM
Coccidioides immitis.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Mitosporic Onygenales; Coccidioides.
REFERENCE
1 (bases 1 to 391)
Gardner, M.J. and Kirkland, T.
Generation of ESTs from Coccidioides immitis spherule cDNA library
Unpublished (2000)
Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org.

QY 1 DCATGCTGAAGCCTCGACTTCG 23
Db 53 ACATGCTAAACCTCGACTTCG 75

RESULT 7
BF252005
LOCUS
DEFINITION
AW792005
486 bp mRNA linear EST 01-MAY-2001
D00948-R Lambda Zap, Stratagene Blumeria graminis f. sp. hordei
cDNA clone D00948 similar to non-functional folate binding protein,
mRNA sequence.
ACCESSION
AW792005
VERSION
AW792005.1 GI:13903602
KEYWORDS
EST.
SOURCE
Blumeria graminis f. sp. hordei.
ORGANISM
Blumeria graminis f. sp. hordei.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Erysiphales; Erysiphaceae; Blumeria.
REFERENCE
1 (bases 1 to 486)
Thomas, S.W., Rasmussen, S.W., Glaring, M.A., Rouster, J.A. and Oliver
, R.P.
Gene identification in the fungal pathogen Blumeria graminis by
expressed sequence tag analysis
Unpublished (2000)
Contact: Rasmussen, S.W.
Department of Yeast Genetics
Carlsberg Laboratory
10 Gl. Carlsbergvej, DK-2500, Copenhagen, Denmark
Tel: 45 3327 5230
Fax: 45 3327 4766
Email: sw@erc.dk
High quality sequence stop: 486
POLYA-No.

FEATURES
Location/Qualifiers
1..486
/organism="Blumeria graminis f. sp. hordei"
/db_xref="taxon:62688"
/clone="D00948"
/clone_lib="Lambda Zap, Stratagene"
/cell_type="conidia"
/lab_host="Hordeum vulgare"

BASE COUNT 138 a 101 c 115 g 132 t
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Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23
Db 154 ACATGCTAAACCTCGACTTCG 176

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/lab_host="SOLR"
/notes="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 107 a 76 c 96 g 112 t
ORIGIN

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Best Local Similarity 87.0%; Pred. No. 82;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23
Db 154 ACATGCTAAACCTCGACTTCG 176

RESULT 7
BF252005
LOCUS
DEFINITION
AW792005
486 bp mRNA linear EST 01-MAY-2001
D00948-R Lambda Zap, Stratagene Blumeria graminis f. sp. hordei
cDNA clone D00948 similar to non-functional folate binding protein,
mRNA sequence.
ACCESSION
AW792005
VERSION
AW792005.1 GI:13903602
KEYWORDS
EST.
SOURCE
Blumeria graminis f. sp. hordei.
ORGANISM
Blumeria graminis f. sp. hordei.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Erysiphales; Erysiphaceae; Blumeria.
REFERENCE
1 (bases 1 to 486)
Thomas, S.W., Rasmussen, S.W., Glaring, M.A., Rouster, J.A. and Oliver
, R.P.
Gene identification in the fungal pathogen Blumeria graminis by
expressed sequence tag analysis
Unpublished (2000)
Contact: Rasmussen, S.W.
Department of Yeast Genetics
Carlsberg Laboratory
10 Gl. Carlsbergvej, DK-2500, Copenhagen, Denmark
Tel: 45 3327 5230
Fax: 45 3327 4766
Email: sw@erc.dk
High quality sequence stop: 486
POLYA-No.

FEATURES
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Location/Qualifiers
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/db_xref="taxon:62688"
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/cell_type="conidia"
/lab_host="Hordeum vulgare"

BASE COUNT 138 a 101 c 115 g 132 t
ORIGIN

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Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db 154 ACATGCTAAACCTCGACTTCG 176

RESULT 8
BF251704
LOCUS

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BF251704
488 bp mRNA linear EST 15-NOV-2001

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Thu Jun 12 08:47:55 2003

/note="vector: pbluescript SK(-); Site\_1: EcoRI; Site\_2: XhoI"

EST418888 Coccidioides immitis spherule cDNA library Coccidioides immitis cDNA clone CIAAK33 5' sequence, mRNA sequence.

BASE COUNT 142 a 101 c 126 g 133 t  
ORIGIN

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Best Local Similarity 87.0%; Pred. No. 96;  
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23  
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Db 157 ACATGCTAAAACCTCGACTTCG 179

RESULT 10  
AW792430 515 bp mRNA linear EST 01-MAY-2001  
LOCUS D01189-R Lambda zap, Stratagene Blumeria graminis f. sp. hordei  
DEFINITION cDNA clone D01189 similar to non-functional folate binding protein, mRNA sequence.

ACCESSION AW792430 GI:13904027  
VERSION EST.  
KEYWORDS Blumeria graminis f. sp. hordei.  
SOURCE Blumeria graminis f. sp. hordei  
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;  
REFERENCE 1 (bases 1 to 515)  
AUTHORS Thomas, S.W., Rasmussen, S.W., Glaring, M.A., Rouster, J.A. and Oliver, R.P.

TITLE Gene identification in the fungal pathogen Blumeria graminis by expressed sequence tag analysis  
JOURNAL Unpublished (2000)  
COMMENT Contact: Rasmussen, S.W.  
Department of Yeast Genetics  
Carlsberg Laboratory  
10 Gl. Carlsbergvej, DK-2500, Copenhagen, Denmark  
Tel: 45 3327 5230  
Fax: 45 3327 4766  
Email: swre@rc.dk  
High quality sequence stop: 515  
POLYA-No.

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/lab\_host="Hordeum vulgare"  
BASE COUNT 150 a 104 c 119 g 142 t  
ORIGIN

Query Match 82.6%; Score 19; DB 10; Length 515;  
Best Local Similarity 87.0%; Pred. No. 97;  
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23  
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Db 147 ACATGCTAAAACCTCGACTTCG 169

RESULT 11  
BF251715 518 bp mRNA linear EST 15-NOV-2001  
LOCUS EST418899 Coccidioides immitis spherule cDNA library Coccidioides immitis cDNA clone CIAAK45 5' sequence, mRNA sequence.  
DEFINITION

ACCESSION BF251715 GI:16931781  
VERSION EST.  
KEYWORDS Coccidioides immitis.  
SOURCE Coccidioides immitis  
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

EST418888 Coccidioides immitis spherule cDNA library Coccidioides immitis cDNA clone CIAAK33 5' sequence, mRNA sequence.  
BF251704  
DEFINITION BF251704.1 GI:16931770  
EST.  
Coccidioides immitis.  
Coccidioides immitis  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Orygenales; mitosporic Onygenales; Coccidioides.  
1 (bases 1 to 488)  
Gardner, M.J. and Kirkland, T.  
Generation of ESTs from Coccidioides immitis spherule cDNA library  
Unpublished (2000)  
Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org.

Location/Qualifiers  
1..488  
/organism="Coccidioides immitis"  
/db\_xref="taxon:5501"  
/clone="CIAAK33"  
/clone\_lib="Coccidioides immitis spherule cDNA library"  
/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="vector: pbluescript SK(-); Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT 129 a 97 c 126 g 136 t  
ORIGIN

Query Match 82.6%; Score 19; DB 12; Length 488;  
Best Local Similarity 87.0%; Pred. No. 94;  
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23  
:||||| ||| |||||||||  
Db 154 ACATGCTAAAACCTCGACTTCG 176

RESULT 9  
BF252581 502 bp mRNA linear EST 15-NOV-2001  
LOCUS EST419843 Coccidioides immitis spherule cDNA library Coccidioides immitis cDNA clone CIAAK35 5' sequence, mRNA sequence.  
DEFINITION

ACCESSION BF252581 GI:16932724  
VERSION EST.  
KEYWORDS Coccidioides immitis.  
Coccidioides immitis  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Orygenales; mitosporic Onygenales; Coccidioides.  
1 (bases 1 to 502)  
Gardner, M.J. and Kirkland, T.  
Generation of ESTs from Coccidioides immitis spherule cDNA library  
Unpublished (2000)  
Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org.

Location/Qualifiers  
1..502  
/organism="Coccidioides immitis"  
/db\_xref="taxon:5501"  
/clone="CIAAK35"  
/clone\_lib="Coccidioides immitis spherule cDNA library"  
/dev\_stage="spherule"  
/lab\_host="SOLR"

FEATURES source

Onygenales; mitosporic Onygenales; Coccidioides.

REFERENCE  
1 (bases 1 to 518)  
AUTHORS  
Gardner, M.J. and Kirkland, T.  
TITLE  
Generation of ESTs from Coccidioides immitis spherule cDNA library  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org.

FEATURES  
source

1..518  
Location/Qualifiers  
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/db\_xref="taxon:5501"  
/clone="CIAK45"  
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/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI"

BASE COUNT 141 a 104 c 133 g 140 t

ORIGIN

Query Match 82.6%; Score 19; DB 12; Length 518;  
Best Local Similarity 87.0%; Pred. No. 98;  
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23

Db 154 ACATGCTAAAACCTCGACTTCG 176

RESULT 12

BF252371

LOCUS  
DEFINITION  
EST419633 Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone CIAA41 5' sequence, mRNA sequence.

ACCESSION  
BF252371

VERSION  
BF252371.1 GI:16932514

KEYWORDS  
EST.

SOURCE  
Coccidioides immitis.

ORGANISM  
Coccidioides immitis  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; mitosporic Onygenales; Coccidioides.

REFERENCE  
1 (bases 1 to 541)

AUTHORS  
Gardner, M.J. and Kirkland, T.  
TITLE  
Generation of ESTs from Coccidioides immitis spherule cDNA library  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org.

FEATURES  
source

1..541  
Location/Qualifiers  
/organism="Coccidioides immitis"  
/db\_xref="taxon:5501"  
/clone="CIAA41"  
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/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI"

BASE COUNT 157 a 109 c 133 g 142 t

ORIGIN

Query Match 82.6%; Score 19; DB 12; Length 541;  
Best Local Similarity 87.0%; Pred. No. 1e+02;  
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23

Db 153 ACATGCTAAAACCTCGACTTCG 175

RESULT 13

BF253171

LOCUS

DEFINITION

EST445666 Coccidioides immitis spherule cDNA library Coccidioides

immitis cDNA clone CIGAB68 5' sequence, mRNA sequence.

ACCESSION  
BF253171

VERSION  
BF253171.1 GI:16933314

KEYWORDS  
EST.

SOURCE  
Coccidioides immitis.

ORGANISM  
Coccidioides immitis

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Onygenales; mitosporic Onygenales; Coccidioides.

REFERENCE  
1 (bases 1 to 546)

AUTHORS  
Gardner, M.J. and Kirkland, T.

TITLE  
Generation of ESTs from Coccidioides immitis spherule cDNA library

JOURNAL  
Unpublished (2000)

COMMENT  
Other ESTs: EST445665

Contact: Malcolm J. Gardner

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Email: gardner@tigr.org.

FEATURES  
source

1..546

Location/Qualifiers

/organism="Coccidioides immitis"

/db\_xref="taxon:5501"

/clone="CIGAB68"

/clone\_lib="Coccidioides immitis spherule cDNA library"

/dev\_stage="spherule"

/lab\_host="SOLR"

/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI"

BASE COUNT 157 a 109 c 135 g 145 t

ORIGIN

Query Match 82.6%; Score 19; DB 12; Length 546;

Best Local Similarity 87.0%; Pred. No. 1e+02;

Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

TITLE

QY 1 DCATGCTGAAGCCTCGACTTCG 23

Db 157 ACATGCTAAAACCTCGACTTCG 179

RESULT 14

BF252094

LOCUS

DEFINITION

EST419356 Coccidioides immitis spherule cDNA library Coccidioides

immitis cDNA clone CIAA080 5' sequence, mRNA sequence.

ACCESSION  
BF252094

VERSION  
BF252094.1 GI:16932237

KEYWORDS  
EST.

SOURCE  
Coccidioides immitis.

ORGANISM  
Coccidioides immitis

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Onygenales; mitosporic Onygenales; Coccidioides.

REFERENCE  
1 (bases 1 to 567)

AUTHORS  
Gardner, M.J. and Kirkland, T.

TITLE  
Generation of ESTs from Coccidioides immitis spherule cDNA library

JOURNAL  
Unpublished (2000)

COMMENT  
Contact: Malcolm J. Gardner

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Tel: 301 838 3519

Fax: 301 838 0208  
Email: gardner@tigr.org.  
Location/Qualifiers  
1. .567  
/organism="Coccidioides immitis"  
/db\_xref="taxon:5501"  
/clone="CIAQ80"  
/clone\_lib="Coccidioides immitis spherule cDNA library"  
/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI"

BASE COUNT 161 a 118 c 142 g 146 t  
ORIGIN

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Best Local Similarity 87.0%; Pred. No. 1e+02;  
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23  
Db 160 ACATGCTAAACCTCGACTTCG 182

RESULT 15  
BF252878  
LOCUS 568 bp mRNA linear EST 15-NOV-2001  
DEFINITION Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone CIAB92 5' sequence, mRNA sequence.  
ACCESSION BF252878  
VERSION BF252878.1 GI:16933021  
KEYWORDS EST.  
SOURCE Coccidioides immitis.  
ORGANISM Coccidioides immitis  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; mitosporic Onygenales; Coccidioides.  
1 (bases 1 to 568)  
AUTHORS Gardner M.J. and Kirkland T.  
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library  
JOURNAL Unpublished (2000)  
COMMENT Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org.  
Location/Qualifiers  
1. .568  
/organism="Coccidioides immitis"  
/db\_xref="taxon:5501"  
/clone="CIAB92"  
/clone\_lib="Coccidioides immitis spherule cDNA library"  
/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI"

BASE COUNT 162 a 117 c 143 g 146 t  
ORIGIN

Query Match 82.6%; Score 19; DB 12; Length 568;  
Best Local Similarity 87.0%; Pred. No. 1e+02;  
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCATGCTGAAGCCTCGACTTCG 23  
Db 160 ACATGCTAAACCTCGACTTCG 182

Search completed: June 12, 2003, 04:35:07  
Job time : 845.943 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 22:21:06 ; Search time 348.269 Seconds  
(without alignments)  
1921.975 Million cell updates/sec

Title: US-09-674-195c-19  
Perfect score: 23  
Sequence: 1 rcaugcugaagccucgacuuucy 23

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues.

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_btg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_rod.\*
- 36: em\_htg\_mam.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	22.6	98.3	1704	8	HCC18SRRN	275306 H.capsulatu
2	22.6	98.3	1704	8	HCC18SRRN	275307 H.capsulatu
3	22.6	98.3	1713	8	HCC18SR	X58572 H.capsulatu
4	22.6	98.3	1726	8	AF320009	AF320009 Ajellomyces
5	21	91.3	494	8	AB030916	AB030916 Ajellomyces
6	21	91.3	786	8	AF088252	AF088252 Teloschis
7	21	91.3	969	8	AF113712	AF113712 Dibaeis b
8	21	91.3	990	8	AF107345	AF107345 Dibaeis b
9	21	91.3	1031	8	AF203458	AF203458 Cycloaneus
10	21	91.3	1054	8	AB030917	AB030917 Aspergill
11	21	91.3	1479	8	AEU45438	U45438 Amylocarpus
12	21	91.3	1648	8	SCU72712	U72712 Siphula cer
13	21	91.3	1673	8	AN18SR	X78538 A.niger (is
14	21	91.3	1678	8	PV113996	Y13996 Paecilomyces
15	21	91.3	1686	8	AF113713	AF113713 Dibaeis b
16	21	91.3	1687	8	AF184749	AF184749 Bunodopho
17	21	91.3	1892	8	AF113710	AF113710 Siphula p
18	21	91.3	1896	8	AF113711	AF113711 Siphula p
19	21	91.3	1701	8	AF085473	AF085473 Dibaeis b
20	21	91.3	1721	8	AF242259	AF242259 Acrospem
21	21	91.3	1732	8	AB008408	AB008408 Aspergill
22	21	91.3	1733	8	AB008397	AB008397 Aspergill
23	21	91.3	1733	8	AB008413	AB008413 Aspergill
24	21	91.3	1733	8	D63695	D63695 Aspergillus
25	21	91.3	1733	8	D63697	D63697 Aspergillus
26	21	91.3	1734	8	AB006716	AB006716 Talaromyces
27	21	91.3	1737	8	AB033479	AB033479 Leveilul
28	21	91.3	1746	8	AF053726	AF053726 Kirschste
29	21	91.3	1776	8	AB003947	AB003947 Talaromyces
30	21	91.3	1777	8	AB003946	AB003946 Penicilli
31	21	91.3	1989	8	AB003808	AB003808 Aspergill
32	21	91.3	2150	8	CSP301706	AJ301706 Capnobotr
33	21	91.3	2734	8	AB003945	AB003945 Penicilli
34	21	91.3	2734	8	AR0421692	AJ421692 Anaptychi
35	21	91.3	2734	8	PPE421689	AJ421689 Physconia
36	21	91.3	2734	8	AB005561	AB005561 Kockovael
37	21	91.3	2734	8	AB005561	AB005561 Kockovael
38	21	91.3	2734	8	AB005561	AB005561 Kockovael
39	20	87.0	1759	8	AB005561	AB005561 Kockovael
40	19.4	84.3	144	8	AB046947	AB046947 Endophyte
41	19.4	84.3	144	8	AB046948	AB046948 Endophyte
42	19.4	84.3	144	8	AB046949	AB046949 Endophyte
43	19.4	84.3	192	8	AF062662	AF062662 Endophyte
44	19.4	84.3	192	8	AF062664	AF062664 Endophyte
45	19.4	84.3	192	8	AF062675	AF062675 Endophyte

ALIGNMENTS

RESULT 1  
HCC18SRRN  
LOCUS HCC18SRRN  
DEFINITION H.capsulatum ssp. duboisii 18S rRNA gene.  
ACCESSION 275306  
VERSION 275306.1 GI:1419549  
KEYWORDS 18S ribosomal RNA; 18S rRNA gene; small subunit ribosomal RNA.  
SOURCE Ajellomyces capsulatus.  
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; Onygenaceae; Ajellomyces.  
REFERENCE 1 (bases 1 to 1704)  
AUTHORS Okeke,C.N., Kappe,R., Zakikhani,S., Nolte,O. and Sonntag,H.G.  
TITLE Ribosomal genes of Histoplasma capsulatum var. duboisii and var. farciminosum

JOURNAL Mycoses 41 (9-10), 355-362 (1998)  
 MEDLINE 99114487  
 PUBMED 9916456  
 REFERENCE 2 (bases 1 to 1704)  
 AUTHORS Kappe,R.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-JUL-1996) Reinhard Kappe, Hygiene & Med. Microbiology, University of Heidelberg, Hygiene Institute, Im Neuenheimer Feld 324, Heidelberg, D-69120, Germany

FEATURES  
 Location/Qualifiers  
 1..1704  
 /organism="Ajellomyces capsulatus"  
 /strain="CBS75.57"  
 /sub\_species="duboisii"  
 /db\_xref="taxon:5037"  
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 /gene="18S rRNA"  
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 /gene="18S rRNA"  
 /product="18S ribosomal RNA"  
 432 a 365 c 470 g 437 t

BASE COUNT 432 a 365 c 470 g 437 t  
 ORIGIN

Query Match 98.3%; Score 22.6; DB 8; Length 1704;  
 Best Local Similarity 73.9%; Pred. No. 0.74;  
 Matches 17; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 1 RCAUGCUGAAGCCUCCGACUUCG 23  
 :||:||||:||||:||||:||||:|  
 Db 111 ACATGCTGAAGCCCTCGACTTCG 133

RESULT 2  
 HCF18SRN 1704 bp DNA linear PLN 10-DEC-1999  
 LOCUS H.capsulatum ssp. farciniosum 18S rRNA gene.  
 DEFINITION 275307  
 VERSION 18S ribosomal RNA: 18S rRNA gene; small subunit ribosomal RNA.  
 KEYWORDS Ajellomyces capsulatus.  
 SOURCE Ajellomyces capsulatus  
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 Onygenales; Onygenaceae; Ajellomyces.  
 REFERENCE 1 (bases 1 to 1704)  
 AUTHORS Okeke,C.N., Kappe,R., Zakikhani,S., Nolte,O. and Sonntag,H.G.  
 TITLE Ribosomal genes of Histoplasma capsulatum var. duboisii and var. farciniosum  
 JOURNAL Mycoses 41 (9-10), 355-362 (1998)  
 MEDLINE 99114487  
 PUBMED 9916456  
 REFERENCE 2 (bases 1 to 1704)  
 AUTHORS Kappe,R.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-JUL-1996) Reinhard Kappe, Hygiene & Med. Microbiology, University of Heidelberg, Hygiene Institute, Im Neuenheimer Feld 324, Heidelberg, D-69120, Germany

FEATURES  
 Location/Qualifiers  
 1..1704  
 /organism="Ajellomyces capsulatus"  
 /strain="CBS205.35, CBS478.64"  
 /sub\_species="farciniosum"  
 /db\_xref="taxon:5037"  
 1..1704  
 /gene="18S rRNA"  
 1..1704  
 /gene="18S rRNA"  
 /product="18S ribosomal RNA"  
 432 a 364 c 471 g 437 t

BASE COUNT 432 a 364 c 471 g 437 t  
 ORIGIN

Query Match 98.3%; Score 22.6; DB 8; Length 1704;  
 Best Local Similarity 73.9%; Pred. No. 0.74;  
 Matches 17; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 1 RCAUGCUGAAGCCUCCGACUUCG 23  
 :||:||||:||||:||||:||||:|  
 Db 111 ACATGCTGAAGCCCTCGACTTCG 133

RESULT 3  
 HCF18SR 1713 bp DNA linear PLN 30-JUN-1993  
 LOCUS H.capsulatum DNA for 18S ribosomal RNA, partial.  
 DEFINITION X58572 S45469  
 ACCESSION X58572.1 GI:2759  
 VERSION 18S ribosomal RNA.  
 KEYWORDS Ajellomyces capsulatus.  
 SOURCE Ajellomyces capsulatus  
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 Onygenales; Onygenaceae; Ajellomyces.  
 REFERENCE 1 (bases 1 to 1713)  
 AUTHORS Bowman,B.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (19-MAR-1991) B.H. Bowman, Roche Molecular Systems, 1145 Atlantic Avenue, Alameda CA 94501, USA

REFERENCE 2 (bases 1 to 1713)  
 AUTHORS Bowman,B.H., Taylor,J.W. and White,T.J.  
 TITLE Molecular evolution of the fungi: human pathogens  
 JOURNAL Mol. Biol. Evol. 9 (5), 893-904 (1992)  
 MEDLINE 92408455  
 PUBMED 1528111

REFERENCE 3 (bases 1 to 1713)  
 AUTHORS Berbee,M.L. and Taylor,J.W.  
 TITLE Convergence in ascospore discharge mechanism among pyrenomycete fungi based on 18S ribosomal RNA gene sequence  
 JOURNAL Mol. Phylogenet. Evol. 1 (1), 59-71 (1992)  
 MEDLINE 94115689  
 PUBMED 1342925

REMARK Annotation  
 FEATURES Location/Qualifiers  
 source 1..1713  
 /organism="Ajellomyces capsulatus"  
 /strain="ATCC 11408"  
 /db\_xref="taxon:5037"  
 <1..>1713  
 /product="18S ribosomal RNA"  
 /note="missing approx. 38 bases from 5' and 49 from 3' end of coding region"  
 434 a 368 c 473 g 438 t

BASE COUNT 434 a 368 c 473 g 438 t  
 ORIGIN

Query Match 98.3%; Score 22.6; DB 8; Length 1713;  
 Best Local Similarity 73.9%; Pred. No. 0.74;  
 Matches 17; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 1 RCAUGCUGAAGCCUCCGACUUCG 23  
 :||:||||:||||:||||:||||:|  
 Db 131 ACATGCTGAAGCCCTCGACTTCG 153

RESULT 4  
 AF320009 1726 bp DNA linear PLN 13-FEB-2001  
 LOCUS Ajellomyces capsulatus ATCC26032 18S ribosomal RNA gene, partial sequence.  
 DEFINITION AF320009  
 ACCESSION AF320009.1 GI:12751371  
 VERSION AF320009  
 KEYWORDS Ajellomyces capsulatus.  
 SOURCE Ajellomyces capsulatus  
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 Onygenales; Onygenaceae; Ajellomyces.  
 REFERENCE 1 (bases 1 to 1726)  
 AUTHORS Kasuga,T., White,T.J. and Taylor,J.W.  
 TITLE The Molecular Clock in Fungi in the Class Plectomycetes  
 JOURNAL Unpublished

```

REFERENCE
AUTHORS      2 (bases 1 to 1726)
TITLE        Kasuga,T., White,T.J. and Taylor,J.W.
JOURNAL      Direct Submission
SUBMITTED    Submitted (07-NOV-2000) Roche Molecular Systems, 1145 Atlantic
              Ave., Alameda, CA 94501, USA
FEATURES
SOURCE       Location/Qualifiers
              1..1726
              /organism="Ajellomyces capsulatus"
              /strain="ATCC26032; G2178"
              /db_xref="ATCC:26032"
              /db_xref="taxon:5037"
              /note="class 2 North American population"
              <1..>1726
              /product="18S ribosomal RNA"
BASE COUNT   440 a 371 c 475 g 440 t
ORIGIN
Query Match 98.3%; Score 22.6; DB 8; Length 1726;
Best Local Similarity 73.9%; Pred. No. 0.75;
Matches 17; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCAUGCUGAAAGCCUGACUUCG 23
    :||:|||||:|||||:|||||:
Db 131 ACATGCTGAAGCCTCGACTTCG 153

RESULT 5
LOCUS      AB030916
DEFINITION Aspergillus niger gene for 18S rRNA, partial sequence.
ACCESSION AB030916
VERSION    AB030916.1 GI:5738920
KEYWORDS   18S rRNA; 18S ribosomal RNA.
SOURCE     Aspergillus niger (strain:IEF1) DNA.
ORGANISM   Aspergillus niger
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
            Shintani,T. and Matsumoto,Y.
            Aspergillus niger gene for 18S rRNA, partial sequence
            Published Only in DataBase (1999)
REFERENCE  2 (bases 1 to 494)
AUTHORS    Shintani,T. and Matsumoto,Y.
TITLE      Direct Submission
JOURNAL    Submitted (10-AUG-1999) Tomoyoshi Shintani, Industrial Research
            Center of Ehime Prefecture, Laboratory of Food Process; 487-2
            Kume Kubota, Matsuyama, Ehime 791-1101, Japan
            (E-mail:shintani@eri.pref.ehime.jp, URL:www.iri.pref.ehime.jp,
            Tel:81-89-976-7612, Fax:81-89-976-7313)
            Location/Qualifiers
FEATURES
SOURCE     1..494
            /organism="Aspergillus niger"
            /strain="IEF1"
            /db_xref="taxon:5061"
            <1..>494
            /product="18S ribosomal RNA"
BASE COUNT 141 a 100 c 121 g 131 t
ORIGIN
Query Match 91.3%; Score 21; DB 8; Length 494;
Best Local Similarity 69.8%; Pred. No. 4.9;
Matches 16; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCAUGCUGAAAGCCUGACUUCG 23
    :||:|||||:|||||:|||||:
Db 149 ACATGCTGAAGCCTCGACTTCG 171

RESULT 6
LOCUS      AF088252
DEFINITION Teloschistes cf. chrysophthalmus Feige and Mies ESS-6640
            ribosomal RNA, partial sequence.
REFERENCE  1 (bases 1 to 786)
AUTHORS    Stenroos,S.K. and DePriest,P.T.
TITLE      SSU rDNA phylogeny of cladoniiform lichens
JOURNAL    Am. J. Bot. 85, 1548-1559 (1998)
AUTHORS    Depriest,P.T., Ivanova,N. and Gargas,A.
TITLE      Direct Submission
JOURNAL    Submitted (31-AUG-1998) Department of Botany, NHB-166, Smithsonian
            Institution, National Museum of Natural History, 10th &
            Constitution Avenue NW, Washington, DC 20560-0166, USA
            Location/Qualifiers
FEATURES
SOURCE     1..786
            /organism="Teloschistes cf. chrysophthalmus Feige and Mies
            ESS-6640"
            /specimen_voucher="Feige & Mies Ess-6640 (US)"
            /db_xref="taxon:88650"
            /country="Cape Verde:Santo Antao, 1988"
            <1..>786
            /product="18S ribosomal RNA"
            /note="small subunit ribosomal RNA"
BASE COUNT 208 a 161 c 198 g 219 t
ORIGIN
Query Match 91.3%; Score 21; DB 8; Length 786;
Best Local Similarity 69.8%; Pred. No. 5.1;
Matches 16; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCAUGCUGAAAGCCUGACUUCG 23
    :||:|||||:|||||:|||||:
Db 112 ACATGCTGAAGCCTCGACTTCG 134

RESULT 7
LOCUS      AF113712
DEFINITION Dibaeis baeomyces small subunit ribosomal RNA gene, partial
            sequence.
ACCESSION  AF113712
VERSION     AF113712
KEYWORDS    AF113712.1 GI:6502558
SOURCE      Dibaeis baeomyces.
            Dibaeis baeomyces
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;
            Lecanoromycetes incertae sedis; Imadophilaceae; Dibaeis.
            Platt,J.L. and Spatafora,J.W.
            Evolutionary relationships of nonsexual lichenized fungi: molecular
            phylogenetic hypotheses for the genera Siphula and Thamnolia from
            SSU and LSU rDNA analyses
            Unpublished
            2 (bases 1 to 969)
            Platt,J.L. and Spatafora,J.W.
            Direct Submission
            Submitted (16-DEC-1998) Department of Botany & Plant Pathology,
            Oregon State University, 2082 Cordley Hall, Corvallis, OR
            97331-2902, USA
            Location/Qualifiers
FEATURES
SOURCE     1..969
            /organism="Dibaeis baeomyces"
            /db_xref="taxon:83478"
            <1..>969
            /product="small subunit ribosomal RNA"
BASE COUNT 268 a 189 c 243 g 268 t
ORIGIN
Query Match 91.3%; Score 21; DB 8; Length 969;

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ACCESSION  AF088252.1 GI:4731142
VERSION     AF088252
KEYWORDS    Teloschistes cf. chrysophthalmus Feige and Mies ESS-6640.
            Teloschistes cf. chrysophthalmus Feige and Mies ESS-6640.
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;
            Lecanorales; Teloschistaceae; Teloschistaceae; Teloschistes.
            Stenroos,S.K. and DePriest,P.T.
            SSU rDNA phylogeny of cladoniiform lichens
            1 (bases 1 to 786)
            Am. J. Bot. 85, 1548-1559 (1998)
            2 (bases 1 to 786)
            Depriest,P.T., Ivanova,N. and Gargas,A.
            Direct Submission
            Submitted (31-AUG-1998) Department of Botany, NHB-166, Smithsonian
            Institution, National Museum of Natural History, 10th &
            Constitution Avenue NW, Washington, DC 20560-0166, USA
            Location/Qualifiers
FEATURES
SOURCE     1..786
            /organism="Teloschistes cf. chrysophthalmus Feige and Mies
            ESS-6640"
            /specimen_voucher="Feige & Mies Ess-6640 (US)"
            /db_xref="taxon:88650"
            /country="Cape Verde:Santo Antao, 1988"
            <1..>786
            /product="18S ribosomal RNA"
            /note="small subunit ribosomal RNA"
BASE COUNT 208 a 161 c 198 g 219 t
ORIGIN
Query Match 91.3%; Score 21; DB 8; Length 786;
Best Local Similarity 69.8%; Pred. No. 5.1;
Matches 16; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCAUGCUGAAAGCCUGACUUCG 23
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Db 112 ACATGCTGAAGCCTCGACTTCG 134

RESULT 7
LOCUS      AF113712
DEFINITION Dibaeis baeomyces small subunit ribosomal RNA gene, partial
            sequence.
ACCESSION  AF113712
VERSION     AF113712
KEYWORDS    AF113712.1 GI:6502558
SOURCE      Dibaeis baeomyces.
            Dibaeis baeomyces
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;
            Lecanoromycetes incertae sedis; Imadophilaceae; Dibaeis.
            Platt,J.L. and Spatafora,J.W.
            Evolutionary relationships of nonsexual lichenized fungi: molecular
            phylogenetic hypotheses for the genera Siphula and Thamnolia from
            SSU and LSU rDNA analyses
            Unpublished
            2 (bases 1 to 969)
            Platt,J.L. and Spatafora,J.W.
            Direct Submission
            Submitted (16-DEC-1998) Department of Botany & Plant Pathology,
            Oregon State University, 2082 Cordley Hall, Corvallis, OR
            97331-2902, USA
            Location/Qualifiers
FEATURES
SOURCE     1..969
            /organism="Dibaeis baeomyces"
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BASE COUNT 268 a 189 c 243 g 268 t
ORIGIN
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Best Local Similarity 69.6%; Pred. No. 5.1;  
Matches 16; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCAUGCUGAAGCCUGACUUCG 23  
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Db 106 ACATGCTGAAACCTCGACTTCG 128

RESULT 8  
AF107345 990 bp DNA linear PLN 10-NOV-1999  
LOCUS  
DEFINITION Dibaels baecomyces small subunit ribosomal RNA gene, partial  
sequence.

ACCESSION AF107345  
VERSION AF107345.1 GI:6318520

KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS Dibaels baecomyces.  
TITLE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;  
Lecanoromycetes incertae sedis; Icmadophilaceae; Dibaels.

JOURNAL  
REFERENCE Platt, J.L., Camacho, F.J. and Spatafora, J.W.  
AUTHORS Evolution of the lichen symbiosis within the Leotiales; molecular  
TITLE phylogenetic hypotheses for Dibaels and Baecomyces  
JOURNAL Unpublished

REFERENCE  
AUTHORS Platt, J.L. and Spatafora, J.W.  
TITLE Direct Submission  
JOURNAL Submitted (18-NOV-1998) Botany & Plant Pathology, Oregon State  
University, 2082 Cordley Hall, Corvallis, OR 97331, USA

FEATURES  
source  
Location/Qualifiers  
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/organism="Dibaels baecomyces"  
/isolate="OSC56400"  
/db\_xref="taxon:83478"

BASE COUNT 269 a 189 c 248 g 284 t  
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Matches 16; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCAUGCUGAAGCCUGACUUCG 23  
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Db 95 ACATGCTGAAACCTCGACTTCG 117

RESULT 9  
AF203458 1031 bp DNA linear PLN 02-NOV-2001  
LOCUS  
DEFINITION Cyclaneusma minus small subunit ribosomal RNA gene, partial  
sequence.

ACCESSION AF203458  
VERSION AF203458.1 GI:9622908

KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS Cyclaneusma minus.  
TITLE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;  
Rhytismatales; Rhytismataceae; Cyclaneusma.

JOURNAL  
REFERENCE Gerandt, D.S., Platt, J.L., Stone, J.K., Spatafora, J.W.,  
AUTHORS Holst-Jensen, A., Hamelin, R.C. and Kohn, L.M.  
TITLE Phylogenetics of Helotiales and Rhytismatales based on partial  
small subunit nuclear ribosomal DNA sequences

MYCOLOGIA 93 (5), 915-933 (2001)  
REFERENCE  
AUTHORS Gerandt, D.S., Platt, J.L., Stone, J.K., Spatafora, J.W.,  
TITLE Direct Submission  
JOURNAL Submitted (12-NOV-1999) Department of Botany and Plant Pathology,  
Oregon State University, 2082 Cordley Hall, Corvallis, OR

97331-2902, USA

FEATURES  
source  
Location/Qualifiers  
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/organism="Cyclaneusma minus"  
/strain="93197"  
/specific\_host="Pinus sylvestris"  
/db\_xref="taxon:64355"

BASE COUNT 275 a 203 c 264 g 289 t  
ORIGIN  
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Best Local Similarity 69.6%; Pred. No. 5.2;  
Matches 16; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCAUGCUGAAGCCUGACUUCG 23  
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Db 95 ACATGCTGAAACCTCGACTTCG 117

RESULT 10  
AB030917 1054 bp DNA linear PLN 14-OCT-1999  
LOCUS  
DEFINITION Aspergillus niger var. awamori gene for 18S rRNA, partial sequence.

ACCESSION AB030917  
VERSION AB030917.1 GI:5738921

KEYWORDS 18S rRNA; 18S ribosomal RNA.  
SOURCE Aspergillus niger var. awamori (strain:IEF2) DNA.  
ORGANISM Aspergillus awamori

REFERENCE  
AUTHORS Shintani, T. and Matsumoto, Y.  
TITLE Aspergillus awamori gene for 18S rRNA, partial sequence  
JOURNAL Published Only in DataBase (1999)

REFERENCE  
AUTHORS Shintani, T. and Matsumoto, Y.  
TITLE Direct Submission  
JOURNAL Submitted (10-AUG-1999) Tomoyoshi Shintani, Industrial Research  
Center of Ehime Prefecture, Laboratory of Food Process; 487-2  
Kumekubota, Matsuyama, Ehime 791-1101, Japan  
(E-mail:shintani@iri.pref.ehime.jp, URL:www.iri.pref.ehime.jp,  
Tel:81-89-976-7612, Fax:81-89-976-7313)

FEATURES  
source  
Location/Qualifiers  
1..1054

/organism="Aspergillus awamori"  
/strain="IEF2"  
/db\_xref="taxon:105351"  
/note="synonym:Aspergillus awamori"

BASE COUNT 288 a 215 c 274 g 277 t  
ORIGIN  
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Best Local Similarity 69.6%; Pred. No. 5.2;  
Matches 16; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCAUGCUGAAGCCUGACUUCG 23  
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Db 133 ACATGCTGAAACCTCGACTTCG 155

RESULT 11  
AEU45438  
LOCUS  
DEFINITION Amylocarpus encephaloides small subunit rRNA gene.

ACCESSION AEU45438  
VERSION U45438.1 GI:1736923

KEYWORDS  
SOURCE Amylocarpus encephaloides.  
ORGANISM Amylocarpus encephaloides

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes; Helotiales; Helotiales incertae sedis; Amylocarpus.

REFERENCE  
AUTHORS Landvik,S., Shaller,N.F.J. and Eriksson,O.E.  
TITLE SSU rDNA sequences support for a close relationship between the Elaphomycetales and the Eurotiales and Onygenales  
JOURNAL Mycoscience 37, 237-241 (1996)  
REFERENCE  
AUTHORS Landvik,S., Shaller,N.F.J. and Eriksson,O.E.  
TITLE Direct Submission  
JOURNAL Submitted (11-JAN-1996) Sara Landvik, Ecological Botany, Umea, S-90187, Sweden

FEATURES  
source Location/Qualifiers  
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/strain="UME 29765"  
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1. .1479  
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BASE COUNT 382 a 300 c 399 g 398 t

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Matches 16; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCAUGCUGAAGCCGACUUCG 23  
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DB 86 ACATGCTAAGGCTCGACTTCG 108

RESULT 12  
SCU72712  
LOCUS Siphula ceratites 1648 bp DNA linear PLN 30-JUL-1997  
DEFINITION Siphula ceratites 18S small subunit ribosomal RNA gene, complete sequence.  
ACCESSION U72712  
VERSION U72712.1 GI:2286071  
KEYWORDS  
SOURCE Siphula ceratites.  
ORGANISM Siphula ceratites.  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes; Lecanoromycetes incertae sedis; Icmadophiliaceae; Siphula.

REFERENCE  
AUTHORS Stenroos,S., Lohtander,K. and Tehler,A.  
TITLE Direct Submission  
JOURNAL Submitted (27-SEP-1996) Botany, National Museum of Natural History, Smithsonian Institution, NHB-166, 10th St. & Constitution Ave., Washington, DC 20560, USA

FEATURES  
source Location/Qualifiers  
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BASE COUNT 424 a 343 c 442 g 439 t

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Best Local Similarity 69.6%; Pred. No. 5.4;  
Matches 16; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCAUGCUGAAGCCGACUUCG 23  
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DB 88 ACATGCTAAGGCTCGACTTCG 110

RESULT 13  
AN18SRR  
LOCUS A.niger (isolate CBS102.12) 18S rRNA gene. PLN 13-MAR-1995  
DEFINITION  
ACCESSION X78538  
VERSION X78538.1 GI:469079

18S ribosomal RNA.  
Aspergillus niger.  
Aspergillus niger  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
1 (bases 1 to 1673)  
Melchers,W.J., Verweij,P.E., van den Hurk,P., van Belkum,A., De Pauw,B.E., Hoogkamp-Korstanje,J.A. and Meis,J.F.  
General primer-mediated PCR for detection of Aspergillus species  
J. Clin. Microbiol. 32 (7), 1710-1717 (1994)  
95014936  
7929762  
2 (bases 1 to 1673)  
Melchers,W.J.G.  
Direct Submission  
Submitted (25-NAR-1994) W.J.G. Melchers, Department of Medical Microbiology, University of Nijmegen, P O Box 9101, 6500 HB Nijmegen, NETHERLANDS

FEATURES  
source Location/Qualifiers  
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/isolate="CBS102.12"  
/db\_xref="taxon:5061"  
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/product="18S ribosomal RNA"  
/evidence="experimental"

BASE COUNT 423 a 365 c 458 g 426 t

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Matches 16; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

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DB 109 ACATGCTAAGGCTCGACTTCG 131

RESULT 14  
PVY13996  
LOCUS Paecilomyces variotii 1678 bp DNA linear PLN 23-JUL-1997  
DEFINITION Paecilomyces variotii 18S rRNA gene.  
ACCESSION Y13996  
VERSION Y13996.1 GI:2224834  
KEYWORDS 18S ribosomal RNA; 18S rRNA gene.  
SOURCE Paecilomyces variotii.  
ORGANISM Paecilomyces variotii.  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Paecilomyces.

REFERENCE  
AUTHORS Zakikhani,S., Okeke,C.N. and Kappe,R.  
TITLE 18S rDNA sequence of Paecilomyces variotii CBS339.51  
JOURNAL Unpublished  
REFERENCE  
AUTHORS Kappe,R.  
TITLE Direct Submission  
JOURNAL Submitted (24-JUN-1997) Kappe R., Hygiene Institute, University of Heidelberg, Im Neuenheimer Feld 324 D-69120 GERMANY

FEATURES  
source Location/Qualifiers  
1. .1678  
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/strain="CBS339.51"  
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/db\_xref="taxon:45996"  
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/product="18S ribosomal RNA"  
/evidence="experimental"

BASE COUNT 422 a 363 c 467 g 426 t

ORIGIN

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 Matches 16; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCAUGCUGAAGCCGACUUCG 23  
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 Db 83 ACATGCTGAAAACCTCGACTTCG 105

RESULT 15  
 AF113713  
 LOCUS 1686 bp DNA linear PLN 06-DEC-1999  
 DEFINITION Dibaeis baemyces isolate OSC53939 small subunit ribosomal RNA  
 gene, partial sequence.  
 ACCESSION AF113713  
 VERSION AF113713.1 GI:6502559  
 KEYWORDS  
 SOURCE Dibaeis baemyces.  
 ORGANISM Dibaeis baemyces  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;  
 Lecanoromycetes incertae sedis; Icmadophilaceae; Dibaeis.  
 REFERENCE 1 (bases 1 to 1686)  
 AUTHORS Platt,J.L. and Spatafora,J.W.  
 TITLE Evolutionary relationships of nonsexual lichenized fungi: molecular  
 phylogenetic hypotheses for the genera siphula and Thamnolia from  
 SSU and LSU rDNA analyses  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1686)  
 AUTHORS Platt,J.L. and Spatafora,J.W.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-DEC-1998) Department of Botany & Plant Pathology,  
 Oregon State University, 2082 Cordley Hall, Corvallis, OR  
 97331-2902, USA

FEATURES  
 source 1. 1686  
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 /product="small subunit ribosomal RNA"  
 BASE COUNT 441 a 346 c 438 g 460 t 1 others  
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 Best Local Similarity 69.6%; Pred. NO. 5.4;  
 Matches 16; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCAUGCUGAAGCCGACUUCG 23  
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 Db 106 ACATGCTGAAAACCTCGACTTCG 128

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 22:17:41 ; Search time 117.802 Seconds  
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439.686 Million cell updates/sec

Title: US-09-674-195C-19

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Sequence: 1 rcaugcugaagccgacuuyc 23

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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C 1	22	95.7	22	15	AAQ73433 Histoplasma capsul
2	22	95.7	22	15	AAQ73436 Histoplasma capsul
3	22	95.7	22	15	AAQ73437 Histoplasma capsul
C 4	22	95.7	22	15	AAQ86436 Histoplasma capsul
5	21	91.3	568	21	AAF11545 Aspergillus niger
6	19.4	84.3	1733	20	AZ00859 A. fumigatus 18S r
7	17.8	77.4	1745	24	ABR01152 Deuteromycetes pol
8	17.4	75.7	492	23	AA565314 DNA encoding novel
C 9	17.2	74.8	4403765	22	AAI99683 Mycobacterium tube

C	10	17.2	74.8	4411529	22	AAI93682	Mycobacterium tube
	11	16.8	73.0	454	22	ABA44550	Human breast cell
	12	16.8	73.0	454	22	ABA54997	Human foetal liver
	13	16.8	73.0	454	22	ABA24760	Probe #3226 for ge
	14	16.8	73.0	454	22	AAK03266	Human brain expres
	15	16.8	73.0	454	22	AAK28719	Human bone marrow
	16	16.8	73.0	454	22	AAI13296	Probe #3229 for ge
	17	16.8	73.0	454	22	AAI34850	Probe #3336 used t
	18	16.8	73.0	454	22	AAI03197	Probe #3188 used t
	19	16.8	73.0	454	24	ABS03233	Human genome-deriv
	20	16.2	70.4	51	22	AAI75640	Human silent SNP c
	21	16.2	70.4	51	22	AAI75641	Human silent SNP c
C	22	16.2	70.4	351	21	AA04990	Human secreted pro
C	23	16.2	70.4	570	21	AAF08498	Fusarium venenatum
	24	16.2	70.4	586	24	ABN61440	Human cancer relat
	25	16.2	70.4	617	21	AAF10913	Fusarium venenatum
	26	16.2	70.4	891	19	AAV37154	DNA sequence used
	27	16.2	70.4	891	22	AAH01747	Fibrobacter succin
C	28	16.2	70.4	1097	24	ABK72888	Bacillus lichenifo
	29	16.2	70.4	1731	24	ABAO1154	Deuteromycetes pol
	30	16.2	70.4	1771	19	ABV61668	Fusarium oxysporum
	31	16.2	70.4	1858	22	AAI60405	Human polynucleoti
	32	16.2	70.4	1861	22	AAI58619	Human polynucleoti
	33	16.2	70.4	1932	23	AA067693	DNA encoding novel
	34	16.2	70.4	2033	15	AAQ63951	Hepatocyte growth
	35	16.2	70.4	2036	24	ABN95114	Gene #1612 used to
	36	16.2	70.4	2036	24	ABN95114	Lung cancer relate
	37	16.2	70.4	2293	23	AA016211	Fungus genomic DNA
C	38	16.2	70.4	2825	23	ABL20098	Drosophila melanog
	39	16.2	70.4	3002	23	ABL29849	Polynucleotide seq
C	40	16.2	70.4	4448	20	AAK20564	Drosophila melanog
	41	16.2	70.4	7264	23	ABL29848	Drosophila melanog
C	42	16.2	70.4	8336	23	ABL23958	Drosophila melanog
	43	16.2	70.4	9228	23	ABL11660	Gene #3948 used to
C	44	16.2	70.4	20556	24	ABN97450	Streptococcus poly
	45	15.8	68.7	375	24	ABN71041	

#### ALIGNMENTS

RESULT 1  
AAQ73433/c  
ID AAQ73433 standard; DNA; 22 BP.

XX AC AAQ73433;

XX DT 18-MAY-1995 (first entry)

XX DE Histoplasma capsulatum-specific DNA hybridisation probe.

XX KW Probe; detection; Histoplasma capsulatum; 18S; rRNA; hybridisation;  
KW Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;  
KW water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.

XX OS Synthetic.

XX PN US5352579-A.

XX PD 04-OCT-1994.

XX PF 28-JUN-1991; 91US-0720587.

XX PR 28-JUN-1991; 91US-0720587.

XX PA (GENP-) GEN-PROBE INC.

XX PI Milliman CL;

XX XX WPI; 1994-316178/39.

XX DR Hybridisation probe specific for Histoplasma capsulatum -  
XX PT allowing differentiation from all other fungi for detection or

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PT quantitation in body fluids, etc.
XX
PS Claim 4; Column 11; 8pp; English.
XX
CC A probe (AAQ73433) or its complement (AAQ73436) and corresponding RNA
CC sequences (AAQ73437 and AAQ86436) used for the specific detection of all
CC strains of Histoplasma capsulatum (H.c.). The probes are manufactured
CC complementary to the H.c. 18S rRNA or rDNA gene. This region also
CC corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.
CC The probe is specific for H.c. and can be used to distinguish the fungus
CC from all others, even its nearest phylogenetic neighbour Blastomyces
CC dermatitidis. Nucleic acid hybridisation of the specific probe is
CC enhanced by the use of helper probes (AAQ73434-5). This method allows
CC the detection and/or the quantitation of H.c. from samples e.g. body
CC fluids, tissue samples, soil and water.
XX
SQ Sequence 22 BP; 5 A; 5 C; 7 G; 5 T; 0 other;

Query Match 95.7%; Score 22; DB 15; Length 22;
Best Local Similarity 77.3%; Pred. No. 0.16;
Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAUGCUGAAGCCGACUUCG 23
   ||:|||||:|||||:|
DB 22 CATGCTGAAGCCTCGACTTCG 1

RESULT 2
AAQ73436
ID AAQ73436 standard; DNA; 22 BP.
XX
AC AAQ73436;
XX
DT 18-MAY-1995 (first entry)
XX
DE Histoplasma capsulatum specific DNA probe, complementary sequence.
XX
KW Probe; detection; Histoplasma capsulatum; 18S; rRNA; rDNA; hybridisation;
KW Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;
KW water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.
XX
OS Synthetic.
XX
PN US5352579-A.
XX
PD 04-OCT-1994.
XX
PF 28-JUN-1991; 91US-0720587.
XX
PR 28-JUN-1991; 91US-0720587.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Millman CL;
XX
DR WPI; 1994-316178/39.
XX
PT Hybridisation probe specific for Histoplasma capsulatum -
PT allowing differentiation from all other fungi for detection or
PT quantitation in body fluids, etc.
XX
PS Claim 9; Column 12; 8pp; English.
XX
CC A probe (AAQ73433) or its complement (AAQ73436) and corresponding RNA
CC sequences (AAQ73437 and AAQ86436) used for the specific detection of all
CC strains of Histoplasma capsulatum (H.c.). The probes are manufactured
CC complementary to the H.c. 18S rRNA or rDNA gene. This region also
CC corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.
CC The probe is specific for H.c. and can be used to distinguish the fungus
CC from all others, even its nearest phylogenetic neighbour Blastomyces
CC dermatitidis. Nucleic acid hybridisation of the specific probe is
CC enhanced by the use of helper probes (AAQ73434-5). This method allows
CC the detection and/or the quantitation of H.c. from samples e.g. body
CC fluids, tissue samples, soil and water.
XX
SQ Sequence 22 BP; 5 A; 5 C; 7 G; 5 T; 0 other;

Query Match 95.7%; Score 22; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAUGCUGAAGCCGACUUCG 23
   |||||||:|||||:|
DB 1 CAUGCUGAAGCCGACUUCG 22

RESULT 4

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PT quantitation in body fluids, etc.
XX
PS Claim 4; Column 11; 8pp; English.
XX
CC A probe (AAQ73433) or its complement (AAQ73436) and corresponding RNA
CC sequences (AAQ73437 and AAQ86436) used for the specific detection of all
CC strains of Histoplasma capsulatum (H.c.). The probes are manufactured
CC complementary to the H.c. 18S rRNA or rDNA gene. This region also
CC corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.
CC The probe is specific for H.c. and can be used to distinguish the fungus
CC from all others, even its nearest phylogenetic neighbour Blastomyces
CC dermatitidis. Nucleic acid hybridisation of the specific probe is
CC enhanced by the use of helper probes (AAQ73434-5). This method allows
CC the detection and/or the quantitation of H.c. from samples e.g. body
CC fluids, tissue samples, soil and water.
XX
SQ Sequence 22 BP; 5 A; 5 C; 7 G; 5 T; 0 other;

Query Match 95.7%; Score 22; DB 15; Length 22;
Best Local Similarity 77.3%; Pred. No. 0.16;
Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAUGCUGAAGCCGACUUCG 23
   ||:|||||:|||||:|
DB 22 CATGCTGAAGCCTCGACTTCG 1

RESULT 2
AAQ73436
ID AAQ73436 standard; DNA; 22 BP.
XX
AC AAQ73436;
XX
DT 18-MAY-1995 (first entry)
XX
DE Histoplasma capsulatum specific DNA probe, complementary sequence.
XX
KW Probe; detection; Histoplasma capsulatum; 18S; rRNA; rDNA; hybridisation;
KW Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;
KW water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.
XX
OS Synthetic.
XX
PN US5352579-A.
XX
PD 04-OCT-1994.
XX
PF 28-JUN-1991; 91US-0720587.
XX
PR 28-JUN-1991; 91US-0720587.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Millman CL;
XX
DR WPI; 1994-316178/39.
XX
PT Hybridisation probe specific for Histoplasma capsulatum -
PT allowing differentiation from all other fungi for detection or
PT quantitation in body fluids, etc.
XX
PS Claim 9; Column 12; 8pp; English.
XX
CC A probe (AAQ73433) or its complement (AAQ73436) and corresponding RNA
CC sequences (AAQ73437 and AAQ86436) used for the specific detection of all
CC strains of Histoplasma capsulatum (H.c.). The probes are manufactured
CC complementary to the H.c. 18S rRNA or rDNA gene. This region also
CC corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.
CC The probe is specific for H.c. and can be used to distinguish the fungus
CC from all others, even its nearest phylogenetic neighbour Blastomyces
CC dermatitidis. Nucleic acid hybridisation of the specific probe is
CC enhanced by the use of helper probes (AAQ73434-5). This method allows
CC the detection and/or the quantitation of H.c. from samples e.g. body
CC fluids, tissue samples, soil and water.
XX
SQ Sequence 22 BP; 5 A; 5 C; 7 G; 5 T; 0 other;

Query Match 95.7%; Score 22; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAUGCUGAAGCCGACUUCG 23
   |||||||:|||||:|
DB 1 CAUGCUGAAGCCGACUUCG 22

RESULT 4

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AAQ86436/c  
 ID AAQ86436 standard; RNA; 22 BP.  
 XX  
 AC AAQ86436;  
 XX  
 DT 18-MAY-1995 (first entry)  
 XX  
 DE Histoplasma capsulatum-specific complementary RNA hybridisation probe.  
 XX  
 KW Probe; detection; Histoplasma capsulatum; 18S; rRNA; rDNA; hybridisation;  
 KW Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;  
 KW water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX USS352579-A.  
 PN  
 PD 04-OCT-1994.  
 XX  
 PF 28-JUN-1991; 91US-0720587.  
 XX  
 PR 28-JUN-1991; 91US-0720587.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Milliman CL;  
 XX  
 DR WPI; 1994-316178/39.  
 XX  
 PT Hybridisation probe specific for Histoplasma capsulatum -  
 PT allowing differentiation from all other fungi for detection or  
 PT quantitation in body fluids, etc.  
 XX  
 PS Claim 9; Column 13; 8pp; English.  
 XX  
 CC A probe (AAQ73433) or its complement (AAQ73436) and corresponding RNA  
 CC sequences (AAQ73437 and AAQ86436) used for the specific detection of all  
 CC strains of Histoplasma capsulatum (H.c.). The probes are manufactured  
 CC complementary to the H.c. 18S rRNA or rDNA gene. This region also  
 CC corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.  
 CC The probe is specific for H.c. and can be used to distinguish the fungus  
 CC from all others, even its nearest phylogenetic neighbour Blastomyces  
 CC dermatitidis. Nucleic acid hybridisation of the specific probe is  
 CC enhanced by the use of helper probes (AAQ73434-5). This method allows  
 CC the detection and/or the quantitation of H.c. from samples e.g. body  
 CC fluids, tissue samples, soil and water.  
 XX  
 SQ Sequence 22 BP; 5 A; 5 C; 7 G; 5 U; 0 other;  
 Query Match 95.7%; Score 22; DB 15; Length 22;  
 Best Local Similarity 77.3%; Pred. No. 0.16; Mismatches 0; Indels 0; Gaps 0;  
 Matches 17; Conservative 5;  
 QY 2 CAUGCUGAAGCCUCCGACUUCG 23  
 DB 22 CARGCTGAAGCCCTCGACTTCG 1  
 RESULT 5  
 AAF11545  
 ID AAF11545 standard; cDNA; 568 BP.  
 XX  
 AC AAF11545;  
 XX  
 DT 13-MAR-2001 (first entry)  
 XX  
 DE Aspergillus niger EST SEQ ID NO:4068.  
 XX  
 KW Multiple gene expression; filamentous fungal cell; EST;  
 KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;  
 KW Aspergillus oryzae; Trichoderma reesei; identification; recombination;  
 KW culture condition; environmental stress; spore morphogenesis;  
 KW metabolic pathway engineering; catabolic pathway engineering; ss.

XX Aspergillus niger.  
 OS  
 XX WO2000056762-A2.  
 PN  
 XX  
 PD 28-SEP-2000.  
 XX  
 PF 22-MAR-2000; 2000WO-US07781.  
 XX  
 PR 22-MAR-1999; 99US-0273623.  
 XX  
 PA (NOVO ) NOVO NORDISK BIOTECH INC.  
 PA (NOVO ) NOVO NORDISK AS.  
 XX  
 PI Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;  
 XX WPI; 2000-594572/56.  
 DR  
 XX  
 PT Monitoring differential expression of genes in filamentous fungal cells  
 PT uses fluorescence-labeled nucleic acids isolated from the cells and a  
 PT substrate of expressed sequence tags -  
 XX  
 PS Claim 87; Page 1791-1792; 3161pp; English.  
 CC  
 CC The present invention describes a method for monitoring differential  
 CC expression of genes in a first filamentous fungal (FF) cell relative to  
 CC expression of the same genes in one or more second filamentous fungal  
 CC cells. The method uses fluorescence-labeled nucleic acids isolated from  
 CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs  
 CC are used in the methods for monitoring differential expression of genes  
 CC in a first filamentous fungal (FF) cell relative to expression of the  
 CC same genes in one or more second filamentous fungal cells. Monitoring  
 CC the global expression of genes from FF cells allows the production  
 CC potential of the microorganisms to be improved. New genes may be  
 CC discovered, possible functions of unknown open reading frames can be  
 CC identified and gene copy number variation and stability can be  
 CC monitored. The expression of genes can be used to study how FF cells  
 CC adapt to changes in culture conditions, environmental stress, spore  
 CC morphogenesis, recombination, metabolic or catabolic pathway  
 CC engineering. Using ESTs provides several advantages over genomic or  
 CC random cDNA clones including elimination of redundancy as one spot on an  
 CC array equals one gene or open reading frame, and organisation of the  
 CC microarrays based on function of the gene products to facilitate  
 CC analysis of the results. AAF07478 to AAF11247 represents ESTs from  
 CC Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from  
 CC Aspergillus niger; AAF11854 to AAF14878 represents ESTs from Aspergillus  
 CC niger; AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are  
 CC all specifically claimed in the present invention.  
 XX  
 SQ Sequence 568 BP; 155 A; 116 C; 141 G; 150 T; 6 other;  
 Query Match 91.3%; Score 21; DB 21; Length 568;  
 Best Local Similarity 69.6%; Pred. No. 0.75; Mismatches 1; Indels 0; Gaps 0;  
 Matches 16; Conservative 6;  
 QY 1 RCAUGCUGAAGCCUCCGACUUCG 23  
 DB 156 ACATGCTGAAGCCCTCGACTTCG 178  
 RESULT 6  
 AAZ00859  
 ID AAZ00859 standard; DNA; 1733 BP.  
 XX  
 AC AAZ00859;  
 XX  
 DT 11-OCT-1999 (first entry)  
 XX  
 DE A. fumigatus 18S rRNA DNA.  
 XX  
 KW Detection; diagnosis; 18S rRNA; aspergillosis; oncology;  
 KW invasive infection; haematology; immune system suppression; ss.  
 XX

OS Aspergillus fumigatus.  
 XX DE19806274-A1.  
 XX 19-AUG-1999.  
 XX 16-FEB-1998; 98DE-1006274.  
 XX 16-FEB-1998; 98DE-1006274.  
 XX (BUCH/) BUCHHEIDT D.  
 XX (HEHL/) HEHLMANN R.  
 XX (SKLA/) SKLADNY H.  
 XX Buchheidt D, Hehlmann R, Skladny H;  
 XX WPI; 1999-470047/40.  
 XX Detecting Aspergillus nucleic acid in body samples by two-step  
 PT polymerase chain reaction, for diagnosing aspergillosis  
 XX Claim 2; Fig 1; 16pp; German.  
 XX This invention describes a novel method for detecting Aspergillus nucleic  
 CC acid (I) in a body sample which comprises the isolation of (I) followed  
 CC by a two-step polymerase chain reaction (PCR) amplification of any  
 CC nucleic acid having a sequence essentially homologous to part of the  
 CC 3'-end of the Aspergillus 18S rRNA gene using primers used in the first  
 CC step that do not overlap with those in the second step. The method is  
 CC used for early diagnosis, and monitoring, of aspergillosis, particularly  
 CC invasive infections in hematological-oncological patients with long-term  
 CC overlapping primers, this process provides efficient and reliable  
 CC detection of Aspergillus in clinical situations. It is specific for  
 CC Aspergillus (it detects the species terreus, niger, versicolor, clavatus,  
 CC flavus, and fumigatus, but not oryzae, nor bacteria or fungi from any  
 CC other genera). This sequence represents the DNA sequence of Aspergillus  
 CC fumigatus 18S rRNA.  
 XX Sequence 1733 BP; 446 A; 374 C; 475 G; 438 T; 0 other;  
 SQ  
 Query Match 84.3%; Score 19.4; DB 20; Length 1733;  
 Best Local Similarity 65.2%; Pred. No. 5.5;  
 Matches 15; Conservative 6; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 RCAUGCUGAAAGCCUGACUUCG 23  
 DB 131 ACATGCTAAACCTCGACTTCG 153  
 RESULT 7  
 ID ABA01152  
 XX ABA01152 standard; DNA; 1745 BP.  
 XX ABA01152;  
 XX 24-JAN-2002 (first entry)  
 XX Deuteromycetes polynucleotide SEQ ID 1.  
 XX Aldonic acid; ds.  
 XX Deuteromycetes sp.  
 XX JP2001245657-A.  
 XX 11-SEP-2001.  
 XX 26-DEC-2000; 2000JP-0394766.  
 XX 27-DEC-1999; 99JP-0369714.  
 XX (TAKE-) TAKEHARA KAGAKU KOGYO KK.

PA (OSAKA ) OSAKA CITY.  
 XX WPI; 2002-002933/01.  
 XX A new microbe for producing aldonic acid, comprises a new strain of  
 PT Acinetobacter or Burkholderis -  
 XX Disclosure; Page 17; 22pp; Japanese.  
 XX The present invention relates to a new microbe of Acinetobacter or  
 CC Burkholderis genus producing aldonic acid and oxidizing specifically the  
 CC hemiacetal hydroxy group of a saccharide having said hydroxy group.  
 CC Aldonic acid is used as a mineral reinforcing agent. The present sequence  
 CC was used to illustrate the present invention.  
 XX Sequence 1745 BP; 448 A; 382 C; 465 G; 450 T; 0 other;  
 SQ  
 Query Match 77.4%; Score 17.8; DB 24; Length 1745;  
 Best Local Similarity 65.2%; Pred. No. 36;  
 Matches 15; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 RCAUGCUGAAAGCCUGACUUCG 23  
 DB 145 ACATGCTAAACCCGACTTCG 167  
 RESULT 8  
 ID AAS65314  
 XX AAS65314 standard; cDNA; 492 BP.  
 XX AAS65314;  
 XX 13-FEB-2002 (first entry)  
 XX DNA encoding novel human diagnostic protein #1118.  
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
 XX Homo sapiens.  
 XX WO200175067-A2.  
 PD 11-OCT-2001.  
 XX 30-MAR-2001; 2001WO-US08631.  
 XX 31-MAR-2000; 2000US-0540217.  
 XX 23-AUG-2000; 2000US-0649167.  
 XX (HYSE-) HYSEQ INC.  
 XX Drmanac RT, Liu C, Tang YT;  
 XX WPI; 2001-639362/73.  
 XX P-PSDB; ABG01127.  
 XX New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity -  
 XX Claim 1; SEQ ID No 1118; 103pp; English.  
 XX The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as

CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. AAS64197-AAS94564 represent novel human  
 CC diagnostic coding sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 492 BP; 134 A; 115 C; 142 G; 101 T; 0 other;

Query Match 75.7%; Score 17.4; DB 23; Length 492;  
 Best Local Similarity 61.9%; Pred. No. 49;  
 Matches 13; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 RCAUGCUGAAGCCUGACUU 21  
 Db 378 ACATGCTGAAGCCTAGAGTT 398  
 :||:|||||||:|:|:

## RESULT 9

AAI99683/c  
 ID AAI99683 standard; DNA; 4403765 BP.

XX AC AAI99683;

DT 15-JAN-2002 (first entry)

DE Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 2.

XX Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome;  
 KW variation; epidemiology; patient treatment; epidemic monitoring; ds.  
 XX OS Mycobacterium tuberculosis.

XX PN US6294328-B1.  
 XX PD 25-SEP-2001.

XX PF 24-JUN-1998; 98US-0103840.

XX PR 24-JUN-1998; 98US-0103840.

XX PA (GENO-) INST GENOMIC RES.

XX PI Fleischmann RD, White OR, Fraser CM, Venter JC;

XX DR WPI; 2001-647261/74.

XX Evaluating strain variation of Mycobacterium tuberculosis, comprises  
 PT determining the nucleotide sequence of the strain at positions in the  
 PT genome corresponding to positions where M. tuberculosis strains CDC  
 PT 1551 and H37Rv differ -

PS Claim 4; SEQ ID NO 2; 3pp + Sequence Listing; English.

XX The invention relates to evaluating strain variation within and between  
 CC different populations of the tuberculosis bacterial pathogen,  
 CC Mycobacterium tuberculosis or related Mycobacterium by determining the  
 CC nucleotide sequence of the first strain at positions in the complete  
 CC sequence of the genome that correspond to positions that differ in the  
 CC nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and  
 CC H37Rv (AAI99682). The method is useful for evaluating strain variation of  
 CC M. tuberculosis and has valuable application in the fields of  
 CC tuberculosis genetics, epidemiology, patient treatment and epidemic  
 CC monitoring.

CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from USPTO  
 CC at seqdata.uspto.gov/sequence.html?DocID=6294328B1.

XX SQ Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189 other;  
 Query Match 74.8%; Score 17.2; DB 22; Length 4403765;  
 Best Local Similarity 72.7%; Pred. No. 1.5e+02;  
 Matches 16; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 CAUGCUGAAGCCUGACUUCG 23  
 Db 172071 CATGCTGAAGCCTCGACGCG 172050  
 ||:|:|||||||:|:

## RESULT 10

AAI99682/c  
 ID AAI99682 standard; DNA; 4411529 BP.

XX AC AAI99682;

DT 15-JAN-2002 (first entry)

DE Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 1.

XX Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome;  
 KW variation; epidemiology; patient treatment; epidemic monitoring; ds.  
 XX OS Mycobacterium tuberculosis.

XX PN US6294328-B1.

XX PD 25-SEP-2001.

XX PF 24-JUN-1998; 98US-0103840.

XX PR 24-JUN-1998; 98US-0103840.

XX PA (GENO-) INST GENOMIC RES.

XX PI Fleischmann RD, White OR, Fraser CM, Venter JC;

XX DR WPI; 2001-647261/74.

XX Evaluating strain variation of Mycobacterium tuberculosis, comprises  
 PT determining the nucleotide sequence of the strain at positions in the  
 PT genome corresponding to positions where M. tuberculosis strains CDC  
 PT 1551 and H37Rv differ -

PS Claim 3; SEQ ID NO 1; 3pp + Sequence Listing; English.

XX The invention relates to evaluating strain variation within and between  
 CC different populations of the tuberculosis bacterial pathogen,  
 CC Mycobacterium tuberculosis or related Mycobacterium by determining the  
 CC nucleotide sequence of the first strain at positions in the complete  
 CC sequence of the genome that correspond to positions that differ in the  
 CC nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and  
 CC H37Rv (AAI99682). The method is useful for evaluating strain variation of  
 CC M. tuberculosis and has valuable application in the fields of  
 CC tuberculosis genetics, epidemiology, patient treatment and epidemic  
 CC monitoring.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from USPTO  
 CC at seqdata.uspto.gov/sequence.html?DocID=6294328B1.

XX SQ Sequence 4411529 BP; 758565 A; 1449983 C; 1444602 G; 758379 T; 0 other;  
 Query Match 74.8%; Score 17.2; DB 22; Length 4411529;  
 Best Local Similarity 72.7%; Pred. No. 1.5e+02;  
 Matches 16; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 CAUGCUGAAGCCUGACUUCG 23  
 Db 171902 CATGCTGAAGCCTCGACGCG 171881  
 ||:|:|||||||:|:

```

RESULT 11
ID ABA44550
XX AC ABA44550 standard; DNA; 454 BP.
XX AC ABA44550;
XX DT 01-FEB-2002 (first entry)
XX AC ABA44550;
XX DE Human breast cell single exon nucleic acid probe #3245.
XX DE Human; microarray; single exon probe; gene expression; breast;
XX KW disease; cancer; ss.
XX KW Homo sapiens.
XX OS Homo sapiens.
XX PN WO200157271-A2.
XX PN 09-AUG-2001.
XX PD 30-JAN-2001; 2001WO-US00662.
XX PF 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PI WPI; 2001-496933/54.
XX DR WPI; 2001-496933/54.
XX PT New spatially-addressable set of single exon nucleic acid probes,
XX PT useful for measuring gene expression in sample derived from human
XX PT breast, comprises number of single exon nucleic acid probes -
XX PS Claim 1; SEQ ID NO 3245; 327pp + sequence listing; English.
XX CC The invention relates to a spatially-addressable set of single exon
XX CC nucleic acid probes for measuring gene expression in a sample derived
XX CC from human breast and BT 474 cells. The method involves contacting
XX CC the probes with a collection of detectably labelled nucleic acids
XX CC derived from mRNA of human breast, and then measuring the label
XX CC bound to each probe of the microarray. The probes are useful for
XX CC verifying the expression of regions of genomic DNA predicted to
XX CC encode proteins. They are useful for gene discovery, and for
XX CC determining predisposition and/or prognosing breast disease. Gene
XX CC expression analysis is useful for assessing the toxicity of chemical
XX CC agents on cells. The microarray of this invention presents a far greater
XX CC diversity of probes for measuring gene expression, with far less bias
XX CC than expressed sequence tag microarrays. The method is suitable for
XX CC rapid production of functional information from genomic sequence. The
XX CC present sequence is a single exon nucleic acid probe of the invention.
XX CC Note: The sequence data for this patent did not form part of the
XX CC printed specification, but was obtained in electronic format directly
XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;

Query Match 73.0%; Score 16.8; DB 22; Length 454;
Best Local Similarity 70.0%; Pred. No. 98;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAUGCUGAAGCCCGACUU 21
DB 182 CATGCAGAAAGCCTTACTT 201

RESULT 12
ID ABA44550
XX AC ABA44550 standard; DNA; 454 BP.
XX AC ABA44550;
XX DT 01-FEB-2002 (first entry)
XX AC ABA44550;
XX DE Human foetal liver single exon nucleic acid probe #3302.
XX DE Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX KW Homo sapiens.
XX OS Homo sapiens.
XX PN WO200157277-A2.
XX PN 09-AUG-2001.
XX PD 30-JAN-2001; 2001WO-US00669.
XX PF 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PI WPI; 2001-483447/52.
XX DR WPI; 2001-483447/52.
XX PT Human genome-derived single exon nucleic acid probes useful for
XX PT analyzing gene expression in human fetal liver -
XX PS Claim 1; SEQ ID NO 3302; 639pp + sequence listing; English.
XX CC The invention relates to a single exon nucleic acid probe for
XX CC measuring human gene expression in a sample derived from human foetal
XX CC liver. The single exon nucleic acid probes may be used for predicting,
XX CC measuring and displaying gene expression in samples derived from human
XX CC foetal liver. The present sequence is a single exon nucleic acid
XX CC probe of the invention.
XX CC Note: The sequence data for this patent did not form part of the
XX CC printed specification, but was obtained in electronic format directly
XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;

Query Match 73.0%; Score 16.8; DB 22; Length 454;
Best Local Similarity 70.0%; Pred. No. 98;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAUGCUGAAGCCCGACUU 21
DB 182 CATGCAGAAAGCCTTACTT 201

RESULT 13
ID ABA24760
XX AC ABA24760 standard; DNA; 454 BP.
XX AC ABA24760;
XX DT 23-JAN-2002 (first entry)
XX AC ABA24760;
XX DE Probe #3226 for gene expression analysis in human heart cell sample.
XX KW Human; gene expression; heart; microarray; vascular system; probe;
XX KW cardiovascular disease; hypertension; cardiac arrhythmia;
XX KW congenital heart disease; ss.
XX OS Homo sapiens.

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XX PN WO200157274-A2.
XX PR 09-AUG-2001; 2001WO-US00666.
XX PD
XX PF
XX PP
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488899/53.
XX PT Single exon nucleic acid probes for analyzing gene expression in human
XX PT hearts.
XX PS Claim 1; SEQ ID NO 3226; 530pp; English.
XX CC The present invention relates to single exon nucleic acid probes for
XX CC measuring human gene expression in a sample derived from human heart. The
XX CC present sequence is one such probe. The probes may be used for
XX CC predicting, measuring and displaying gene expression in samples derived
XX CC from the human heart via microarrays. By measuring gene expression, the
XX CC probes are useful for predicting, diagnosing, grading, staging,
XX CC monitoring and prognosing diseases of the human heart and vascular system
XX CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX CC congenital heart disease.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;
XX
XX Query Match 73.0%; Score 16.8; DB 22; Length 454;
XX Best Local Similarity 70.0%; Pred. No. 98;
XX Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 2 CAUGCUGAAGCCUGACUU 21
XX Db ||:|| |||||:||:
XX 182 CATGCAGAAAGCCTCTACTT 201
XX
XX RESULT 14
XX AAK03266
XX ID AAK03266 standard; DNA; 454 BP.
XX AC AAK03266;
XX XX
XX DT 05-NOV-2001 (first entry)
XX PF Human brain expressed single exon probe SEQ ID NO: 3257.
XX DE Human brain expressed exon; gene expression analysis; probe;
XX KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
XX KW epilepsy; cancer; ss.
XX OS Homo sapiens.
XX OS
XX PN WO200157275-A2.
XX PR 09-AUG-2001.
XX PD
XX PF 30-JAN-2001; 2001WO-US00667.
XX PR 04-FEB-2000; 2000US-0180312.
XX PT Human genome-derived single exon nucleic acid probes useful for
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PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX PT Single exon nucleic acid probes for analyzing gene expression in human
XX PT brains.
XX PS Example 4; SEQ ID NO: 3257; 650pp + Sequence Listing; English.
XX CC The present invention provides a number of single exon nucleic acid
XX CC probes which are derived from genomic sequences expressed in the human
XX CC brain. They can be used to measure gene expression in brain cell samples,
XX CC which may enable the diagnosis and improved treatment of nervous system
XX CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX CC epilepsy and cancers. The present sequence is one of the probes of the
XX CC invention.
XX SQ Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;
XX
XX Query Match 73.0%; Score 16.8; DB 22; Length 454;
XX Best Local Similarity 70.0%; Pred. No. 98;
XX Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 2 CAUGCUGAAGCCUGACUU 21
XX Db ||:|| |||||:||:
XX 182 CATGCAGAAAGCCTCTACTT 201
XX
XX RESULT 15
XX AAK28719
XX ID AAK28719 standard; DNA; 454 BP.
XX AC AAK28719;
XX XX
XX DT 06-NOV-2001 (first entry)
XX PF Human bone marrow expressed single exon probe SEQ ID NO: 3276.
XX DE Human; bone marrow expressed exon; gene expression analysis; probe;
XX KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX OS Homo sapiens.
XX OS
XX PN WO200157276-A2.
XX PR 09-AUG-2001.
XX PD
XX PF 30-JAN-2001; 2001WO-US00668.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488900/53.
XX PT Human genome-derived single exon nucleic acid probes useful for
```

PT analyzing gene expression in human bone marrow -  
 XX  
 PS Example 4; SEQ ID NO: 3276; 658pp + Sequence Listing; English.  
 XX  
 CC The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC bone marrow. They can be used to measure gene expression in bone marrow  
 CC samples, which may enable the improved diagnosis and treatment of cancers  
 CC such as lymphoma, leukaemia and myeloma. The present sequence is one of  
 CC the probes of the invention.  
 XX  
 SQ Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;  
 Query Match 73.0%; Score 16.8; DB 22; Length 454;  
 Best Local Similarity 70.0%; Pred. No. 98;  
 Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
 Oy 2 CAUGCUGAAGCCUCGACUU 21  
 |||||  
 Db 182 CATGCAGAAAGCCTCTACTT 201

Search completed: June 12, 2003, 01:44:59  
 Job time : 134.802 secs

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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 01:18:34 ; Search time 22.066 Seconds  
(without alignments)  
319.658 Million cell updates/sec

Title: US-09-674-195C-19

Perfect score: 23

Sequence: 1 rcaugcugaagccugacucg 23

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_NA:\*

1: /cgn2.6/ptodata/1/ina/5A\_COMB.seq:\*

2: /cgn2.6/ptodata/1/ina/5B\_COMB.seq:\*

3: /cgn2.6/ptodata/1/ina/6A\_COMB.seq:\*

4: /cgn2.6/ptodata/1/ina/6B\_COMB.seq:\*

5: /cgn2.6/ptodata/1/ina/PCTUS\_COMB.seq:\*

6: /cgn2.6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	22	95.7	22	1	US-07-720-587A-1
C 2	17.2	74.8	4403765	4	US-09-103-840A-2
C 3	17.2	74.8	4411529	4	US-09-103-840A-1
C 4	16.2	70.4	2033	1	US-08-148-910-14
C 5	16.2	70.4	2033	1	US-08-448-937A-14
C 6	16.2	70.4	2293	4	US-09-645-073-1
C 7	15.8	68.7	522	4	US-09-221-017B-1065
C 8	15.8	68.7	709	4	US-08-998-416-281
C 9	15.8	68.7	738	2	US-08-224-591-13
C 10	15.8	68.7	738	2	US-08-392-338A-22
C 11	15.8	68.7	738	2	US-08-926-789-13
C 12	15.8	68.7	738	3	US-09-166-750-22
C 13	15.8	68.7	738	3	US-09-166-093-22
C 14	15.8	68.7	738	3	US-09-172-019-22
C 15	15.8	68.7	738	3	US-09-166-094-22
C 16	15.8	68.7	738	5	PCT-US93-11138-13
C 17	15.8	68.7	744	2	US-08-392-338A-12
C 18	15.8	68.7	744	3	US-09-166-750-12
C 19	15.8	68.7	744	3	US-09-166-093-12
C 20	15.8	68.7	744	3	US-09-172-019-12
C 21	15.8	68.7	744	3	US-09-166-094-12
C 22	15.8	68.7	758	4	US-09-069-821-1
C 23	15.8	68.7	782	4	US-09-420-592A-1
C 24	15.8	68.7	797	1	US-08-323-445A-3
C 25	15.8	68.7	797	1	US-08-515-903A-3
C 26	15.8	68.7	797	5	PCT-US95-12840-3
C 27	15.8	68.7	803	1	US-08-323-445A-7

28	15.8	68.7	803	1	US-08-515-903A-7	Sequence 7, Appli
29	15.8	68.7	803	5	PCT-US95-12840-7	Sequence 7, Appli
30	15.8	68.7	818	4	US-09-420-592A-3	Sequence 3, Appli
31	15.8	68.7	1460	2	US-08-392-338A-18	Sequence 18, Appl
32	15.8	68.7	1460	3	US-09-166-750-18	Sequence 18, Appl
33	15.8	68.7	1460	3	US-09-166-093-18	Sequence 18, Appl
34	15.8	68.7	1460	3	US-09-172-019-18	Sequence 18, Appl
35	15.8	68.7	1460	3	US-09-166-094-18	Sequence 18, Appl
36	15.6	67.8	1722	1	US-08-055-945-1	Sequence 1, Appli
37	15.4	67.0	9515	1	US-08-920-812-13	Sequence 13, Appl
38	15.4	67.0	9515	1	US-08-920-827-13	Sequence 13, Appl
39	15.4	67.0	9515	1	US-08-921-177-13	Sequence 13, Appl
40	15.4	67.0	9515	1	US-08-362-577C-13	Sequence 13, Appl
41	15.4	67.0	9515	2	US-08-920-828-13	Sequence 13, Appl
42	15.2	66.1	444	1	US-08-093-144-5	Sequence 5, Appli
43	15.2	66.1	444	1	US-08-093-144-6	Sequence 6, Appli
44	15.2	66.1	446	1	US-08-093-144-4	Sequence 4, Appli
45	15.2	66.1	870	1	US-08-411-706-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-07-720-587A-1/c

; Sequence 1, Application US/07720587A

; Patent No. 5352579

; GENERAL INFORMATION:

; APPLICANT: Curt L. Millman

; TITLE OF INVENTION: NUCLEIC ACIDS PROBES

; TITLE OF INVENTION: TO HISTOPLASMA CAPSULATUM

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 611 West Sixth Street

; CITY: Los Angeles

; STATE: California

; COUNTRY: USA

; ZIP: 90017

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

; COMPUTER: IBM PS/2 Model 50Z or 55SX

; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)

; SOFTWARE: WordPerfect (Version 5.0)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/720,587A

; FILING DATE: 19910628

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; PRIOR APPLICATION DATA: including application

; APPLICATION NUMBER: described below:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 193/121

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELE: 67-3510

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 22

; TYPE: NUCLEIC ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

US-07-720-587A-1

Query Match

Best Local Similarity 95.7%; Score 22; DB 1; Length 22;

Matches 17; Conservative 5; Mismatches 0; Indels 0;

Gaps 0;

Qy 2 CAUGCUGAAAGCCUCGACUUCG 23  
||:|||||:|||||:  
Db 22 CATGCTGAAAGCCTCGACTTCG 1

## RESULT 2

US-09-103-840A-2/c  
; Sequence 2, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; FILE REFERENCE: 24366-20007.00  
; CURRENT APPLICATION NUMBER: US/09/103.840A  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 4403765  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; FEATURE:  
; OTHER INFORMATION: CDC 1551  
; OTHER INFORMATION: "n" bases at various positions throughout the sequence  
; OTHER INFORMATION: represent a, t, c or g  
US-09-103-840A-2

Query Match 74.8%; Score 17.2; DB 4; Length 4403765;  
Best Local Similarity 72.7%; Pred. No. 28;  
Matches 16; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CAUGCUGAAAGCCUCGACUUCG 23  
||:|||||:|||||:  
Db 172071 CATGTGAAAGCCTCGACAGG 172050

## RESULT 3

US-09-103-840A-1/c  
; Sequence 1, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; FILE REFERENCE: 24366-20007.00  
; CURRENT APPLICATION NUMBER: US/09/103.840A  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 4411529  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; OTHER INFORMATION: H37RV  
US-09-103-840A-1

Query Match 74.8%; Score 17.2; DB 4; Length 4411529;  
Best Local Similarity 72.7%; Pred. No. 28;  
Matches 16; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CAUGCUGAAAGCCUCGACUUCG 23  
||:|||||:|||||:  
Db 171902 CATGTGAAAGCCTCGACAGG 171881

## RESULT 4

US-08-148-910-14  
; Sequence 14, Application US/08148910  
; Patent No. 5466593  
; GENERAL INFORMATION:  
; APPLICANT: Takeshi SHIMOMURA et al.  
; TITLE OF INVENTION: No. 5466593el Protein and Gene Encoding Said Protein  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch,  
; MEDIUM TYPE: 500 Kb Storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/148,910  
; FILING DATE: No. 5466593ember 5, 1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX: 202-371-8856  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2033 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:  
; ORGANISM: human  
; IMMEDIATE SOURCE:  
; LIBRARY: Pre-made Lambda phage Library,  
; LIBRARY: human liver(49, male) cDNA Library (Stratagene)  
US-08-148-910-14

Query Match 70.4%; Score 16.2; DB 1; Length 2033;  
Best Local Similarity 56.5%; Pred. No. 37;  
Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RCAUGCUGAAGCCUCGACUUCG 23  
||:|||||:|||||:  
Db 350 GCATGCTGCATGCTGCCTTCG 372

## RESULT 5

US-08-448-937A-14  
; Sequence 14, Application US/08448937A  
; Patent No. 5677164  
; GENERAL INFORMATION:  
; APPLICANT: Takeshi SHIMOMURA et al.  
; TITLE OF INVENTION: No. 5677164el Protein and Gene Encoding Said Protein  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch,  
MEDIUM TYPE: 500 Kb Storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/448,937A  
FILING DATE: May 24, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/148,910  
FILING DATE: No. 5677164ember 5, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2033 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
ORIGINAL SOURCE:  
ORGANISM: human  
IMMEDIATE SOURCE:  
LIBRARY: Pre-made Lambda phage Library,  
LIBRARY: human liver(49, male) cdna Library (Stratagene)  
US-08-448-937A-14

Query Match 70.4%; Score 16.2; DB 1; Length 2033;  
Best Local Similarity 56.9%; Pred. No. 37;  
Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 RGAUCGUGAAGCCGACUUCG 23  
DB 350 GCATGCTGCATGCTGCATTCG 372

RESULT 6  
US-09-645-073-1  
Sequence 1, Application US/09645073  
Patent No. 6287800  
GENERAL INFORMATION:  
APPLICANT: Lee, May  
TITLE OF INVENTION: Production of High Titers of Gibberellins GA4 and GA7  
FILE REFERENCE: L02-01NP  
CURRENT APPLICATION NUMBER: US/09/645,073  
CURRENT FILING DATE: 2000-08-25  
PRIOR APPLICATION NUMBER: US 60/151,770  
PRIOR FILING DATE: 1999-08-31  
NUMBER OF SEQ ID NOS: 1  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1  
LENGTH: 2293  
TYPE: DNA  
ORGANISM: Gibberella fujikuroi  
US-09-645-073-1

Query Match 70.4%; Score 16.2; DB 4; Length 2293;  
Best Local Similarity 60.9%; Pred. No. 38;  
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 RGAUCGUGAAGCCGACUUCG 23  
DB 145 ACATGCTAAATCCGACTTCG 167

RESULT 7  
US-09-221-017B-1065  
Sequence 1065, Application US/09221017B  
Patent No. 6444799  
GENERAL INFORMATION:  
APPLICANT: Ross, Bruce C.  
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF  
NUMBER OF SEQUENCES: 1120  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/221,017B  
FILING DATE: 23-DEC-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PP1182  
FILING DATE: 31-DEC-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PP1546  
FILING DATE: 30-JAN-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PP2911  
FILING DATE: 09-APR-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/AU98/01023  
FILING DATE: 10-DEC-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Monroy, Gladys H  
REGISTRATION NUMBER: 32,430  
REFERENCE/DOCKET NUMBER: 27340-20021.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-813-5600  
TELEFAX: 650-494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 1065:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 522 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: UNKNOWN  
ORIGINAL SOURCE:  
ORGANISM: PORPHYROMONAS GINGIVALIS  
FEATURE:  
NAME/KEY: misc-feature  
LOCATION: 1...522  
US-09-221-017B-1065

Query Match 68.7%; Score 15.8; DB 4; Length 522;  
Best Local Similarity 61.9%; Pred. No. 48;  
Matches 13; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 RGAUCGUGAAGCCGACUUCG 21  
DB 337 ACATGCTGGAAGCCTCGGCT 357

RESULT 8  
US-08-998-416-281/c  
Sequence 281, Application US/08998416



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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,936
; FILING DATE: 25-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.0030007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..726
US-08-392-338A-22

Query Match      68.7%  Score 15.8;  DB 2;  Length 738;
Best Local Similarity 63.2%;  Pred. No. 51;
Matches 12;  Conservative 5;  Mismatches 2;  Indels 0;  Gaps 0;

QY      4 UGUGAAAGCCGCGACUUC 22
Db      332 TGCTGAAGGCTCTACTTC 350
      :||:||||| 1:| ||:|

RESULT 11
US-08-926-789-13
; Sequence 13, Application US/08926789
; Patent No. 5990275
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Filipula, David
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,789
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/224,591
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..726
US-08-392-338A-22

Query Match      68.7%  Score 15.8;  DB 2;  Length 738;
Best Local Similarity 63.2%;  Pred. No. 51;
Matches 12;  Conservative 5;  Mismatches 2;  Indels 0;  Gaps 0;

QY      4 UGUGAAAGCCGCGACUUC 22
Db      332 TGCTGAAGGCTCTACTTC 350
      :||:||||| 1:| ||:|

RESULT 12
US-09-166-750-22
; Sequence 22, Application US/09166750
; Patent No. 6025165
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Wood, James F.
; APPLICANT: Hardman, Karl
; APPLICANT: Bird, Robert
; APPLICANT: Filipula, David
; APPLICANT: Rollence, Michelle
; TITLE OF INVENTION: Methods for Producing Multivalent Antigen-Binding
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/166,750
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/392,338
; FILING DATE: 22-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/989,846
; FILING DATE: 20-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,936
; FILING DATE: 25-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.003000C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..726
US-09-166-750-22
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Query Match 68.7%; Score 15.8; DB 3; Length 738;  
Best Local Similarity 63.2%; Pred. No. 51;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 4 UGUGAAGGCCUGGACUUC 22  
Db 332 TGCTGAAGGCTCTACTTC 350  
:|||||:|:|:|

## RESULT 13

US-09-166-093-22  
; Sequence 22, Application US/09166093  
; Patent No. 6027725

## GENERAL INFORMATION:

APPLICANT: Whitlow, Marc  
APPLICANT: Wood, James F.  
APPLICANT: Hardman, Karl  
APPLICANT: Bird, Robert  
APPLICANT: Filpula, David  
APPLICANT: Rollence, Michelle  
TITLE OF INVENTION: Multivalent Antigen-Binding Proteins  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, NW  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/166,093  
FILING DATE: Herewith

## CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/392,338  
FILING DATE: 22-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/989,846  
FILING DATE: 20-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/796,936  
FILING DATE: 25-NOV-1991

ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.003000B  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 22:

## SEQUENCE CHARACTERISTICS:

LENGTH: 738 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both

## FEATURE:

NAME/KEY: CDS  
LOCATION: 1..726

US-09-166-093-22

Query Match 68.7%; Score 15.8; DB 3; Length 738;  
Best Local Similarity 63.2%; Pred. No. 51;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 4 UGUGAAGGCCUGGACUUC 22  
Db 332 TGCTGAAGGCTCTACTTC 350  
:|||||:|:|:|

## RESULT 14

US-09-172-019-22  
; Sequence 22, Application US/09172019  
; Patent No. 6103889

## GENERAL INFORMATION:

APPLICANT: Whitlow, Marc  
APPLICANT: Hardman, Karl  
APPLICANT: Bird, Robert  
APPLICANT: Filpula, David  
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Single-Chain  
Antigen-Binding Proteins (As Amended)  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, NW  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/172,019  
FILING DATE: Herewith

## CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/392,338  
FILING DATE: 22-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/989,846  
FILING DATE: 20-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/796,936  
FILING DATE: 25-NOV-1991

ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.003000D  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 22:

## SEQUENCE CHARACTERISTICS:

LENGTH: 738 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both

## FEATURE:

NAME/KEY: CDS  
LOCATION: 1..726

US-09-172-019-22

Query Match 68.7%; Score 15.8; DB 3; Length 738;  
Best Local Similarity 63.2%; Pred. No. 51;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 4 UGUGAAGGCCUGGACUUC 22  
Db 332 TGCTGAAGGCTCTACTTC 350  
:|||||:|:|:|

## RESULT 15

US-09-166-094-22  
; Sequence 22, Application US/09166094  
; Patent No. 6121424

## GENERAL INFORMATION:

APPLICANT: Whitlow, Marc  
APPLICANT: Wood, James F.

;; APPLICANT: Hardman, Karl  
;; APPLICANT: Bird, Robert  
;; APPLICANT: Filpula, David  
;; APPLICANT: Rollence, Michelle  
;; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins  
;; NUMBER OF SEQUENCES: 23  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
;; STREET: 1100 New York Avenue, NW  
;; CITY: Washington  
;; STATE: D.C.  
;; COUNTRY: U.S.A.  
;; ZIP: 20005  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/166,094  
;; FILING DATE: Herewith  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/392,338  
;; FILING DATE: 22-FEB-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/989,846  
;; FILING DATE: 20-NOV-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/796,936  
;; FILING DATE: 25-NOV-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Goldstein, Jorge A.  
;; REGISTRATION NUMBER: 29,021  
;; REFERENCE/DOCKET NUMBER: 0977.003000A  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 371-2600  
;; TELEFAX: (202) 371-2540  
;; INFORMATION FOR SEQ ID NO: 22:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 738 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: both  
;; TOPOLOGY: both  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: 1..726  
US-09-166-094-22

Query Match 68.7%; Score 15.8; DB 3; Length 738;  
Best Local Similarity 63.2%; Pred. No. 51;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
QY 4 UGCGAAGCCUCGACUUC 22  
Db 332 TGCTGAAGGCTCTACTTC 350

Search completed: June 12, 2003, 04:40:20  
Job time : 42.066 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 01:27:04 ; Search time 134.381 Seconds  
(without alignments)  
239.539 Million cell updates/sec

Title: US-09-674-195C-19  
Perfect score: 23  
Sequence: 1 rcaucgugaagccugacucg 23

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 870385 seqs, 599768693 residues

Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_NA.\*

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- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
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- 11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	16.8	73.0	454	10	US-09-864-761-3226
C 3	16.2	70.4	891	9	US-09-989-643-155
C 4	16.2	70.4	1097	10	US-09-974-300-179
C 5	16.2	70.4	2036	10	US-09-954-456-552
C 6	16.2	70.4	2036	10	US-09-880-107-1612
C 7	16.2	70.4	20556	10	US-09-880-107-3945
C 8	16.2	70.4	177556	9	US-09-952-2130-6
C 9	15.8	68.7	355	10	US-09-783-590-10265
C 10	15.8	68.7	550	9	US-09-991-936-838
C 11	15.8	68.7	723	10	US-09-791-578-5
C 12	15.8	68.7	723	10	US-09-791-540-5
C 13	15.8	68.7	758	9	US-09-956-086-1
C 14	15.8	68.7	758	9	US-09-956-087-1
C 15	15.8	68.7	782	10	US-09-985-442-1
C 16	15.8	68.7	782	10	US-09-791-578-3
C 17	15.8	68.7	782	10	US-09-791-540-3
C 18	15.8	68.7	782	10	US-09-983-580-1
C 19	15.8	68.7	818	9	US-09-985-442-3

20	15.8	68.7	818	10	US-09-983-580-3
21	15.8	68.7	981	10	US-09-770-445-271
C 22	15.8	68.7	1279	9	US-10-165-603-19
C 23	15.6	67.8	310	10	US-09-878-574-665
C 24	15.6	67.8	375	10	US-09-878-574-3603
C 25	15.6	67.8	397	10	US-09-867-701-8410
C 26	15.6	67.8	933	9	US-09-938-842A-536
C 27	15.4	67.0	185548	9	US-10-175-523-62
C 28	15.2	66.1	104	10	US-09-864-761-29160
C 29	15.2	66.1	239	9	US-09-764-891-7021
C 30	15.2	66.1	239	10	US-09-764-864-1677
C 31	15.2	66.1	368	9	US-09-918-995-30049
C 32	15.2	66.1	372	9	US-09-918-995-30320
C 33	15.2	66.1	448	10	US-09-864-761-15514
C 34	15.2	66.1	479	9	US-09-918-995-23618
C 35	15.2	66.1	575	10	US-09-864-761-12559
C 36	15.2	66.1	588	10	US-09-919-580-463
C 37	15.2	66.1	600	10	US-09-864-761-8360
C 38	15.2	66.1	712	9	US-09-774-639-16
C 39	15.2	66.1	712	9	US-09-969-730-68
C 40	15.2	66.1	768	10	US-09-910-943-408
C 41	15.2	66.1	843	9	US-10-164-433-1
C 42	15.2	66.1	861	9	US-10-278-173-83
C 43	15.2	66.1	1186	9	US-09-925-299-98
C 44	15.2	66.1	1186	10	US-09-925-299-98
C 45	15.2	66.1	1413	9	US-09-894-844-25

ALIGNMENTS

RESULT 1  
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; Sequence 1, Application US/10067514  
; Publication No. US20030054531A1  
; GENERAL INFORMATION:  
; APPLICANT: Gretaarsdottir, Solveig  
; APPLICANT: Jonsdottir, Sif  
; APPLICANT: Reynisdottir, Sigridur Th.  
; TITLE OF INVENTION: HUMAN STROKE GENE  
; FILE REFERENCE: 2345.2010-003  
; CURRENT APPLICATION NUMBER: US/10/067,514  
; PRIOR FILING DATE: 2002-02-04  
; PRIOR APPLICATION NUMBER: US 09/811/352  
; PRIOR FILING DATE: 2001-03-19  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1691139  
; TYPE: DNA  
; ORGANISM: Human  
US-10-067-514-1

Query Match 74.8%; Score 17.2; DB 9; Length 1691139;  
Best Local Similarity 63.6%; Pred. No. 45;  
Matches 14; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 CAUCGUGAAGCCUGACUCG 23

Db 758804 CATGCTGAAGCATACACTTCG 758783

RESULT 2  
US-09-864-761-3226  
; Sequence 3226, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; GENE EXPRESSION ANALYSIS BY MICROARRAY

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; FILE REFERENCE: Aecomica-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
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; PRIOR FILING DATE: 2001-01-30
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine
; SEQ ID NO 3226
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL050331.11
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER
; OTHER INFORMATION: EXPRESSED IN BRAIN, SPINAL CORD
; OTHER INFORMATION: EXPRESSED IN PLACENTA
; OTHER INFORMATION: EXPRESSED IN HEART, SKIN
; OTHER INFORMATION: EXPRESSED IN HEART, SKIN
; OTHER INFORMATION: EXPRESSED IN LUNG, SKIN
; OTHER INFORMATION: EXPRESSED IN HBL100, SKIN
; OTHER INFORMATION: EXPRESSED IN BONE MARROW
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER
; US-09-864-761-3226

Query Match 73.0%; Score 16.8
Best Local Similarity 70.0%; Pred. No. 4; Mismatch
Matches 14; Conservative

QY 2 CATGCGAAGACCGCCGACGU 21
||||| ||||| |||
DB 182 CATGCGAAGACCGCTACTT 201

RESULT 3
US-09-989-643-155
; Sequence 155, Application US/09989643
; Publication No. US20030049636A1
; GENERAL INFORMATION:

```

```
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Picard, Francois J.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Species-Specific, Genus-Specific and Universal DNA
; TITLE OF INVENTION: Probes and Amplification Primers to Rapidly Detect and
; TITLE OF INVENTION: Identify Common Bacterial and Fungal Pathogens and
; TITLE OF INVENTION: Associated Antibiotic Resistance Genes from
; FILE REFERENCE: 13287.29
; CURRENT APPLICATION NUMBER: US/09/989,643
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/297,539
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/743,637
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-11-04
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 155
; LENGTH: 891
; TYPE: DNA
; ORGANISM: Fibrobacter succinogenes
US-09-989-643-155

Query Match      70.4%; Score 16.2; DB 9; Length 891;
Best Local Similarity 66.7%; Pred. No. 87;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0

QY    3 AUGCUGAAAGCCUCGACUUC 23
     |:|:|:|:|:|:|:|:|:|:|
DB    158 ATGCTGAATTCGCACCTCG 178

RESULT 4
US-09-974-300-179/c
; Sequence 179, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berkra, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 179
; LENGTH: 1097
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-179

Query Match      70.4%; Score 16.2; DB 10; Length 1097;
Best Local Similarity 71.4%; Pred. No. 89;
Matches 15; Conservative 3; Mismatches 3; Indels 0; Gaps 0

QY    3 AUGCUGAAAGCCUCGACUUC 23
     |:|:|:|:|:|:|:|:|:|:|
DB    335 ATGCTGAAGCGCGACTCCG 315

RESULT 5
US-09-954-456-552
; Sequence 552, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents
; TITLE OF INVENTION: Sets
```

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? FILE REFERENCE: 689230-76
? CURRENT APPLICATION NUMBER: US/09/954,456
? CURRENT FILING DATE: 2001-09-18
? PRIOR APPLICATION NUMBER: US/60/233,617
? PRIOR FILING DATE: 2000-09-18
? PRIOR APPLICATION NUMBER: US/60/234,052
? PRIOR FILING DATE: 2000-09-20
? PRIOR APPLICATION NUMBER: US/60/234,923
? PRIOR FILING DATE: 2000-09-25
? PRIOR APPLICATION NUMBER: US/60/235,134
? PRIOR FILING DATE: 2000-09-25
? PRIOR APPLICATION NUMBER: US/60/235,637
? PRIOR FILING DATE: 2000-09-26
? PRIOR APPLICATION NUMBER: US/60/235,638
? PRIOR FILING DATE: 2000-09-26
? PRIOR APPLICATION NUMBER: US/60/235,711
? PRIOR FILING DATE: 2000-09-27
? PRIOR APPLICATION NUMBER: US/60/235,720
? PRIOR FILING DATE: 2000-09-27
? PRIOR APPLICATION NUMBER: US/60/235,840
? PRIOR FILING DATE: 2000-09-27
? PRIOR APPLICATION NUMBER: US/60/235,863
? PRIOR FILING DATE: 2000-09-27
? NUMBER OF SEQ ID NOS: 2276
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 552
? LENGTH: 2036
? TYPE: DNA
? ORGANISM: Homo sapiens
US-09-954-456-552

```

	Query Match	70.4%	Score 16.2	DB 10	Length 2036
	Best Local Similarity	56.5%	Pred. 10.93		
	Matches 13	Conservative 6	Mismatches 4	Indels 0	Gaps 0
Q7	1	RCAGUCGAAAGCCUCGACUUCG	23		
		::: ::: ::: ::: ::: :::			
Db	353	GCATGCTGCAATGCCGCACTTGC	375		

```

RESULT 6
US-09-880-107-1612
: Sequence 1612, Application US//09880107
: Patent No. US20020142981A1
:
: GENERAL INFORMATION:
:
: APPLICANT: Horne, Darci T.
: APPLICANT: Vockley, Joseph G.
: APPLICANT: Scherf, Uwe
: APPLICANT: Gene Logic, Inc.
:
: TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
:
: FILE REFERENCE: 44921-5028-WO
: CURRENT APPLICATION NUMBER: US/09/880,107
: CURRENT FILING DATE: 2001-06-14
: PRIOR APPLICATION NUMBER: US 60/211,379
: PRIOR FILING DATE: 2000-06-14
: PRIOR APPLICATION NUMBER: US 60/237,054
: PRIOR FILING DATE: 2000-10-02
: NUMBER OF SEQ ID NOS: 3950
: SOFTWARE: PatentIn Ver. 2.1
:
: SEQ ID NO 1612
:
: LENGTH: 2036
:
: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
: FEATURE:
:
: OTHER INFORMATION: Genbank Accession No. US20020142981A1 D14012
:
: US-09-880-107-1612

```

Query Match	70.4%	Score 16.2	DB 10	Length 2036
Best Local Similarity	56.5%	Pred. No. 93		
Matches 13	Conservative	6	Mismatches 4	Indels 0
Gaps				0
1 RCAGUCUGAAACCCUGCAGCAGUCG 23				
:::           :   ::				

```

Db          353  GCATGCTGCATGCTGCATCTTCG 375

RESULT 7
US-09-880-107-3945
: Sequence 3945, Application US/09880107
: Patent No. US20020142981A1
: GENERAL INFORMATION:
:   APPLICANT: Horne, Darci T.
:   APPLICANT: Vockley, Joseph G.
:   APPLICANT: Scherf, Uwe
:   APPLICANT: Gene Logic, Inc.
:   TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
:   FILE REFERENCE: 44921-5028-NO
:   CURRENT APPLICATION NUMBER: US/09/880,107
:   CURRENT FILING DATE: 2001-06-14
:   PRIOR APPLICATION NUMBER: US 60/211,379
:   PRIOR FILING DATE: 2000-06-14
:   PRIOR APPLICATION NUMBER: US 60/237,054
:   PRIOR FILING DATE: 2000-10-02
:   NUMBER OF SEQ ID NOS: 3950
:   SOFTWARE: PatentIn Ver. 2.1
:   SEQ ID NO 3945
:   LENGTH: 20556
:   TYPE: DNA
:   ORGANISM: Homo sapiens
:   FEATURE:
:   OTHER INFORMATION: Genbank Accession No. US20020142981A1 Z69923
US-09-880-107-3945

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Query Match	70.4%	Score 16.2	DB 10	Length 20556
Best Local Similarity	56.5%	Pred. No.1.1e+02		
Matches 13	Conservative	6	Mismatches 4	Indels 0
			Gaps 0	
Oy	1	RCAGGCGAAGCCGCGACGCGG	23	
Db	478	GCAATGCTGATGCCGCGACATTCG	500	

```

: RESULT 8
: US-09-952-213D-6/C
: Sequence 6, Application US/09952213D
: Publication No. US20030096240A1
: GENERAL INFORMATION:
: APPLICANT: MURAD, FERID
: APPLICANT: SHARINA, IRAIDA G.
: APPLICANT: KROMENACKER, J. S.
: APPLICANT: MARTIN, E.
: TITLE OF INVENTION: GENOMIC ORGANIZATION OF MOUSE AND HUMAN SGC
: FILE REFERENCE: UTSH:252US
: CURRENT APPLICATION NUMBER: US/09/952,213D
: CURRENT FILING DATE: 2002-08-16
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 6
: LENGTH: 177556
: TYPE: DNA
: ORGANISM: Mus musculus
: FEATURE:
: NAME/KEY: modified base
: LOCATION: (2293..144567)
: OTHER INFORMATION: N = A, C, T/U OR G
: US-09-952-213D-6

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		70.4%;	Score 16.2;	DB 9;	Length 177556;
Query Match					
Best Local Similarity		56.5%;	Pred. No. 1.3e+02;		
Matches	13;	Conservative	6;	Mismatches	4;
				Indels	0;
				Gaps	0;
QY	1	RCAUCGCGAAGCCUGACUUCG	23		
		:  : :    :	:		
Dd	45084	ACATGATAGTGCCTGGACTTTG	45062		

```
RESULT 9
US-09-783-590-10265/c
; Sequence 10265, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: DILLON, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16.2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12465
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10265
; LENGTH: 365
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (150)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (321)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (329)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (331)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (342)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (349)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (355)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (364)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-10265

Query Match      68.7% Score 15.8; DB 10; Length 365;
Best Local Similarity 57.1% Pred. No. 1.3e+02;
Matches 12; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY      1 RCANGCUGAAGCCUGCAGCU 21
Db      275 ACATGCTGAACCTCACTT 255

RESULT 10
US-09-991-936-838/c
; Sequence 838, Application US/09991936
; Publication No. US20030073827A1
; GENERAL INFORMATION:
; APPLICANT: Brandt, Kevin S.
; APPLICANT: Gaines, Patrick J.
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: FLEA HEAD, NERVE CORD, HINDGUT AND MALPIGHIAN TUBULE
; FILE REFERENCE: FC-6-C1
; CURRENT APPLICATION NUMBER: US/09/991,936
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; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US/09/543,668
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/128,704
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1959
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 838
; LENGTH: 550
; TYPE: DNA
; ORGANISM: Ctenocephalides felis
US-09-991-936-838

Query Match      68.7% Score 15.8; DB 9; Length 550;
Best Local Similarity 63.2% Pred. No. 1.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      4 UGUGAAGCCUGCAGCUC 22
Db      174 TGTGAAGACCTCACTTC 156

RESULT 11
US-09-791-578-5
; Sequence 5, Application US/09791578
; Patent No. US20020061307A1
; GENERAL INFORMATION:
; APPLICANT: WHITLOW, MARC
; SHORR, ROBERT G.L.
; FILIPULA, DAVID R.
; LEE, LINSYNG S.
; TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN
; CORRESPONDENCE ADDRESSES:
; ADDRESSSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/791,578
; FILING DATE: 26-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/069,842
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/050,472
; FILING DATE: 23-JUN-1997
; APPLICATION NUMBER: US 60/063,074
; FILING DATE: 27-OCT-1997
; APPLICATION NUMBER: US 60/067,341
; FILING DATE: 02-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: JORGE A. GOLDSTEIN
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977,1840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 723 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
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NAME/KEY: CDS  
LOCATION: 1..723  
SEQUENCE DESCRIPTION: SEQ ID NO: 5  
US-09-791-578-5

Query Match 68.7%; Score 15.8; DB 10; Length 723;  
Best Local Similarity 63.2%; Pred. No. 1.4e+02;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

DB 332 TGCTGAAGGCTCTACTTC 350

US-09-791-540-5  
Sequence 5, Application US/09791540  
Patent No. US20020098192A1  
GENERAL INFORMATION:  
APPLICANT: WHITLOW, MARC  
SHORR, ROBERT G.L.  
FILPUILA, DAVID R.  
LEE, LIHSYNG S.  
TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN  
POLYPEPTIDES  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVENUE, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/791,540  
FILING DATE: 26-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/069,842  
FILING DATE: 1998-04-30  
APPLICATION NUMBER: US 60/050,472  
FILING DATE: 23-JUN-1997  
APPLICATION NUMBER: US 60/063,074  
FILING DATE: 27-OCT-1997  
APPLICATION NUMBER: US 60/067,341  
FILING DATE: 02-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: JORGE A. GOLDSTEIN  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.1840002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2540  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 723 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..723  
SEQUENCE DESCRIPTION: SEQ ID NO: 5  
US-09-791-540-5

Query Match 68.7%; Score 15.8; DB 10; Length 723;  
Best Local Similarity 63.2%; Pred. No. 1.4e+02;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

DB 332 TGCTGAAGGCTCTACTTC 350

US-09-956-086-1  
Sequence 1, Application US/09956086  
Patent No. US20020155498A1  
GENERAL INFORMATION:  
APPLICANT: FILPUILA, DAVID  
WANG, MAOLIANG  
SHORR, ROBERT  
WHITLOW, MARC  
LEE, LIHSYNG S.  
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS  
CAPABLE OF GLYCOSTYLATION, PRODUCTION AND USES THEREOF  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVE., NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/956,086  
FILING DATE: 20-Sep-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/069,821  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 60/063,074  
FILING DATE: 27-OCT-1997  
APPLICATION NUMBER: US 60/050,472  
FILING DATE: 23-JUN-1997  
APPLICATION NUMBER: US 60/044,449  
FILING DATE: 30-APR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: KIM, JUDITH U.  
REGISTRATION NUMBER: 40,679  
REFERENCE/DOCKET NUMBER: 0977.2280003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)371-2600  
TELEFAX: (202)371-2540  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 758 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cdna  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..747  
SEQUENCE DESCRIPTION: SEQ ID NO: 1  
US-09-956-086-1

Query Match 68.7%; Score 15.8; DB 9; Length 758;  
Best Local Similarity 63.2%; Pred. No. 1.4e+02;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

DB 332 TGCTGAAGGCTCTACTTC 350

RESULT 14  
US-09-956-087-1  
Sequence 1, Application US/099556087  
Patent No. US20020161201A1  
GENERAL INFORMATION:  
APPLICANT: FILIPULA, DAVID  
MANG, MAOLIANG  
SHORR, ROBERT  
WHITLOW, MARC  
LEE, LIHSYNG S.  
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS  
CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVE., NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/956,087  
FILING DATE: 20-SEP-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/069,821  
FILING DATE: 1998-04-30  
APPLICATION NUMBER: US 60/063,074  
FILING DATE: 27-OCT-1997  
APPLICATION NUMBER: US 60/050,472  
FILING DATE: 23-JUN-1997  
APPLICATION NUMBER: US 60/044,449  
FILING DATE: 30-APR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: KIM, JUDITH U.  
REGISTRATION NUMBER: 40,679  
REFERENCE/DOCKET NUMBER: 0977.2280003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)371-2600  
TELEFAX: (202)371-2540  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 758 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..747  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-956-087-1  
Query Match 68.7%; Score 15.8; DB 9; Length 758;  
Best Local Similarity 63.2%; Pred. No. 1.4e+02;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
QY 4 UGUGAAGCCUGACUUC 22  
DB 332 TGCTGAAGGCTCTACTTC 350  
RESULT 15  
US-09-985-442-1  
Sequence 1, Application US/09985442  
Patent No. US20020156248A1  
GENERAL INFORMATION:  
APPLICANT: FILIPULA, DAVID R.

APPLICANT: Mang, Maoliang  
APPLICANT: Whitlow, Marc D.  
TITLE OF INVENTION: NO. US20020156248A1 Method for Targeted Delivery of Nucleic  
FILE REFERENCE: 0977.2300003  
CURRENT APPLICATION NUMBER: US/09/985,442  
CURRENT FILING DATE: 2001-11-02  
PRIOR APPLICATION NUMBER: 09/420,592  
PRIOR FILING DATE: 1998-10-19  
PRIOR APPLICATION NUMBER: 60/104,949  
PRIOR FILING DATE: 1998-10-20  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 1  
LENGTH: 782  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: CC49/218 sfv  
NAME/KEY: CDS  
LOCATION: (1)..(771)  
US-09-985-442-1  
Query Match 68.7%; Score 15.8; DB 9; Length 782;  
Best Local Similarity 63.2%; Pred. No. 1.4e+02;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
QY 4 UGUGAAGCCUGACUUC 22  
DB 332 TGCTGAAGGCTCTACTTC 350

Search completed: June 12, 2003, 04:58:53  
Job time : 140.666 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 00:35:54 ; Search time 844.228 Seconds  
(without alignments)  
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Title: US-09-674-195c-19

Perfect score: 23

Sequence: 1 rcaugcugaagccucgacucg 23

Scoring table: IDENTITY\_NUC  
Gap 10.0 , Gape 1.0

Searched: 16154066 segs, 8097743376 residues 32308132

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estln:\*  
4: em\_estlu:\*  
5: em\_estlov:\*  
6: em\_estlpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estlum:\*  
16: em\_estlom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19.4	84.3	123	12	BF251708 EST418892
2	19.4	84.3	351	12	BF251693 EST418877
3	19.4	84.3	362	12	BF251811 EST419073
4	19.4	84.3	377	12	BF251964 EST419226
5	19.4	84.3	378	12	BF251967 EST419229
6	19.4	84.3	391	12	BF251561 EST418910

7	19.4	84.3	486	10	AW792005	AW792005 D00948-R
8	19.4	84.3	488	12	BF251704	BF251704 EST418888
9	19.4	84.3	502	12	BF252581	BF252581 EST419843
10	19.4	84.3	515	10	AW792430	AW792430 D01189-R
11	19.4	84.3	518	10	BF251715	BF251715 EST418899
12	19.4	84.3	541	12	BF252371	BF252371 EST419633
13	19.4	84.3	546	12	BF253171	BF253171 EST445666
14	19.4	84.3	567	12	BF252094	BF252094 EST419356
15	19.4	84.3	568	12	BF252878	BF252878 EST420141
16	19.4	84.3	572	12	BF252095	BF252095 EST419357
17	19.4	84.3	605	12	BF252135	BF252135 EST419397
18	19.4	84.3	679	12	BF251385	BF251385 EST418646
19	19.4	84.3	687	12	BF251001	BF251001 EST418258
20	19.4	84.3	701	12	BF251666	BF251666 EST418850
21	19.4	84.3	836	12	BF250962	BF250962 EST418219
22	18.4	80.0	222	10	AW791051	AW791051 D00369-R
23	18.4	80.0	905	17	CNS077PT	AL432999 T3 end of
24	18.4	80.0	914	17	CNS079TL	AL435727 T7 end of
25	18.4	80.0	944	17	CNS0787	AL434633 T3 end of
26	18.4	80.0	957	17	CNS0797C	AL434926 T3 end of
27	18.4	80.0	992	17	CNS0784M	AL435352 T3 end of
28	18.4	80.0	997	17	CNS07A19	AL436003 T7 end of
29	18.4	80.0	1008	17	CNS076RE	AL431761 T3 end of
30	18.4	80.0	1012	17	CNS079X1	AL435851 T7 end of
31	18.4	80.0	1020	17	CNS077XC	AL433270 T7 end of
32	18.4	80.0	1031	17	CNS076VJ	AL431909 T7 end of
33	18.4	80.0	1060	17	CNS078BU	AL433900 T3 end of
34	17.8	77.4	176	9	AQ025794	AQ025794 1(2)K0640
35	17.8	77.4	176	9	AI213893	AI213893 2760281.r
36	17.8	77.4	244	9	AI212196	AI212196 9690781.r
37	17.8	77.4	250	9	AA784878	AA784878 9380481.f
38	17.8	77.4	252	9	AI211979	AI211979 v7h0581.f
39	17.8	77.4	260	9	AI329914	AI329914 c1e02ne.r
40	17.8	77.4	269	9	AA966666	AA966666 w7f12a1.r
41	17.8	77.4	273	9	AA966294	AA966294 v7h0581.r
42	17.8	77.4	280	9	AA965352	AA965352 e9d08a1.r
43	17.8	77.4	293	9	AA783904	AA783904 c8b0481.f
44	17.8	77.4	295	9	AA788074	AA788074 r4f0481.f
45	17.8	77.4	295	9	AI327731	AI327731 10c01a1.f

## ALIGNMENTS

RESULT 1  
BF251708 123 bp mRNA linear EST 15-NOV-2001  
EST418892 Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone CIAK37 5' sequence, mRNA sequence.

ACCESSION  
BF251708  
VERSION  
BF251708.1 GI:16931774  
KEYWORDS  
SOURCE  
ORGANISM

Coccidioides immitis.  
Coccidioides immitis  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; mitosporic Onygenales; Coccidioides.  
REFERENCE  
1 (bases 1 to 123)  
AUTHORS  
Gardner, M.J. and Kirkland, T.  
TITLE  
Generation of ESTs from Coccidioides immitis spherule cDNA library  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org

FEATURES  
source  
location/Qualifiers

1..123  
/organism="Coccidioides immitis"  
/db\_xref="taxon:5501"  
/clone="CIAK37"  
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/lab_host="SOLR"
/Note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT      37 a      23 c      27 g      36 t
ORIGIN
Query Match      84.3%; Score 19.4; DB 12; Length 123;
Best Local Similarity 65.2%; Pred. No. 30;
Matches 15; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY      1 RCAGUCGGAAGCCGACGACUUCG 23
Db      58 ACATGCTAATAAACCCTGACTTCG 80

RESULT 2
LOCUS      BF251693      351 bp      mRNA      linear      EST 15-NOV-2001
DEFINITION      EST118877 Coccidioides immitis spherule cDNA library Coccidioides
ACCESSION      BF251693
VERSION      BF251693.1 GI:16931759
KEYWORDS      EST.
SOURCE      Coccidioides immitis.
ORGANISM      Coccidioides immitis
REFERENCE      Gardner,M.J. and Kirkland,T.
AUTHORS      Gardner,M.J. and Kirkland,T.
TITLE      Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL      Unpublished (2000)
COMMENT      Contact: Malcolm J. Gardner
              Department of Eukaryotic Genomics
              The Institute for Genomic Research
              9712 Medical Center Drive, Rockville, MD 20850, USA
              Tel: 301 838 3519
              Fax: 301 838 0208
              Email: gardner@tigr.org.
              Location/Qualifiers
                1..351
                /organism="Coccidioides immitis"
                /db_xref="taxon:5501"
                /clone="CIAAK21"
                /clone_1lb="Coccidioides immitis spherule cDNA library"
                /dev_stage="spherule"
                /lab_host="SOLR"
                /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                XhoI"
BASE COUNT      97 a      69 c      81 g      104 t
ORIGIN
Query Match      84.3%; Score 19.4; DB 12; Length 351;
Best Local Similarity 65.2%; Pred. No. 56;
Matches 15; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY      1 RCAGUCGGAAGCCGACGACUUCG 23
Db      154 ACATGCTAATAAACCCTGACTTCG 176

RESULT 3
LOCUS      BF251811      362 bp      mRNA      linear      EST 15-NOV-2001
DEFINITION      EST419073 Coccidioides immitis spherule cDNA library Coccidioides
ACCESSION      BF251811
VERSION      BF251811.1 GI:16931954
KEYWORDS      EST.
SOURCE      Coccidioides immitis.
ORGANISM      Coccidioides immitis
REFERENCE      Gardner,M.J. and Kirkland,T.
AUTHORS      Gardner,M.J. and Kirkland,T.
TITLE      Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL      Unpublished (2000)
COMMENT      Contact: Malcolm J. Gardner
              Department of Eukaryotic Genomics
              The Institute for Genomic Research
              9712 Medical Center Drive, Rockville, MD 20850, USA
              Tel: 301 838 3519
              Fax: 301 838 0208
              Email: gardner@tigr.org.
              Location/Qualifiers
                1..377
                /organism="Coccidioides immitis"
                /db_xref="taxon:5501"
                /clone="CIAAP15"
                /clone_1lb="Coccidioides immitis spherule cDNA library"
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                /lab_host="SOLR"
                /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                XhoI"
BASE COUNT      103 a      85 c      94 g      95 t
ORIGIN
Query Match      84.3%; Score 19.4; DB 12; Length 377;
Best Local Similarity 65.2%; Pred. No. 58;
Matches 15; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

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REFERENCE      1 (bases 1 to 362)
AUTHORS      Gardner,M.J. and Kirkland,T.
TITLE      Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL      Unpublished (2000)
COMMENT      Contact: Malcolm J. Gardner
              Department of Eukaryotic Genomics
              The Institute for Genomic Research
              9712 Medical Center Drive, Rockville, MD 20850, USA
              Tel: 301 838 3519
              Fax: 301 838 0208
              Email: gardner@tigr.org.
              Location/Qualifiers
                1..362
                /organism="Coccidioides immitis"
                /db_xref="taxon:5501"
                /clone="CIAAM73"
                /clone_1lb="Coccidioides immitis spherule cDNA library"
                /dev_stage="spherule"
                /lab_host="SOLR"
                /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                XhoI"
BASE COUNT      98 a      69 c      84 g      111 t
ORIGIN
Query Match      84.3%; Score 19.4; DB 12; Length 362;
Best Local Similarity 65.2%; Pred. No. 57;
Matches 15; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY      1 RCAGUCGGAAGCCGACGACUUCG 23
Db      149 ACATGCTAATAAACCCTGACTTCG 171

RESULT 4
LOCUS      BF251964      377 bp      mRNA      linear      EST 15-NOV-2001
DEFINITION      EST419226 Coccidioides immitis spherule cDNA library Coccidioides
ACCESSION      BF251964
VERSION      BF251964.1 GI:16932107
KEYWORDS      EST.
SOURCE      Coccidioides immitis.
ORGANISM      Coccidioides immitis
REFERENCE      Gardner,M.J. and Kirkland,T.
AUTHORS      Gardner,M.J. and Kirkland,T.
TITLE      Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL      Unpublished (2000)
COMMENT      Contact: Malcolm J. Gardner
              Department of Eukaryotic Genomics
              The Institute for Genomic Research
              9712 Medical Center Drive, Rockville, MD 20850, USA
              Tel: 301 838 3519
              Fax: 301 838 0208
              Email: gardner@tigr.org.
              Location/Qualifiers
                1..377
                /organism="Coccidioides immitis"
                /db_xref="taxon:5501"
                /clone="CIAAP15"
                /clone_1lb="Coccidioides immitis spherule cDNA library"
                /dev_stage="spherule"
                /lab_host="SOLR"
                /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                XhoI"
BASE COUNT      103 a      85 c      94 g      95 t
ORIGIN
Query Match      84.3%; Score 19.4; DB 12; Length 377;
Best Local Similarity 65.2%; Pred. No. 58;
Matches 15; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

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QY 1 RCAUGCUGAAGCCUGACUUCG 23  
DB 53 ACATGCTAAACCTCGACTTCG 75

RESULT 5  
BF251967  
LOCUS EST419229 Coccidioides immitis spherule cDNA library Coccidioides  
DEFINITION immitis cDNA clone CIAAP18 5' sequence, mRNA sequence.  
ACCESSION BF251967  
VERSION BF251967.1 GI:16932110  
KEYWORDS EST.  
SOURCE Coccidioides immitis.  
ORGANISM Coccidioides immitis  
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
AUTHORS Orygenales; mitosporic Orygenales; Coccidioides.  
TITLE 1 (bases 1 to 378)  
JOURNAL Gardner, M.J. and Kirkland, T.  
COMMENT Generation of ESTs from Coccidioides immitis spherule cDNA library  
Unpublished (2000)  
Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org.

FEATURES  
source  
1..378  
/organism="Coccidioides immitis"  
/db\_xref="taxon:5501"  
/clone\_1ib="Coccidioides immitis spherule cDNA library"  
/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI"

BASE COUNT 104 a 75 c 94 g 105 t

ORIGIN

Query Match 84.3%; Score 19.4; DB 12; Length 378;  
Best Local Similarity 65.2%; Pred. No. 58;  
Matches 15; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 RCAUGCUGAAGCCUGACUUCG 23  
DB 147 ACATGCTAAACCTCGACTTCG 169

RESULT 6  
BF251561  
LOCUS 391 bp mRNA linear EST 15-NOV-2001  
DEFINITION EST418910 Coccidioides immitis spherule cDNA library Coccidioides  
ACCESSION BF251561  
VERSION BF251561.1 GI:16931792  
KEYWORDS EST.  
SOURCE Coccidioides immitis.  
ORGANISM Coccidioides immitis  
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
AUTHORS Orygenales; mitosporic Orygenales; Coccidioides.  
TITLE 1 (bases 1 to 391)  
JOURNAL Gardner, M.J. and Kirkland, T.  
COMMENT Generation of ESTs from Coccidioides immitis spherule cDNA library  
Unpublished (2000)  
Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org.

FEATURES  
source  
Location/Qualifiers  
1..391  
/organism="Coccidioides immitis"  
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/clone\_1ib="CIAAK57"  
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/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI"

BASE COUNT 107 a 76 c 96 g 112 t

ORIGIN

Query Match 84.3%; Score 19.4; DB 12; Length 391;  
Best Local Similarity 65.2%; Pred. No. 59;  
Matches 15; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 RCAUGCUGAAGCCUGACUUCG 23  
DB 154 ACATGCTAAACCTCGACTTCG 176

RESULT 7  
AW792005  
LOCUS 486 bp mRNA linear EST 01-MAY-2001  
DEFINITION D00948-R lambda Zap, Stragene Blumeria graminis f. sp. hordei  
ACCESSION AW792005  
VERSION AW792005.1 GI:13903602  
KEYWORDS EST.  
SOURCE Blumeria graminis f. sp. hordei.  
ORGANISM Blumeria graminis f. sp. hordei  
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;  
AUTHORS Erysiphales; Erysiphaceae; Blumeria.  
TITLE 1 (bases 1 to 486)  
JOURNAL Thomas, S.W., Rasmussen, S.W., Glaring, M.A., Roustner, J.A. and Oliver  
R.P.  
COMMENT Gene identification in the fungal pathogen Blumeria graminis by  
expressed sequence tag analysis  
Unpublished (2000)  
Contact: Rasmussen, S.W.  
Department of Yeast Genetics  
Carlsberg Laboratory  
10 Gl. Carlsbergvej, DK-2500, Copenhagen, Denmark  
Tel: 45 3327 5230  
Fax: 45 3327 4766  
Email: sw@erc.dk  
High quality sequence stop: 486  
POLYA-No.

FEATURES  
source  
Location/Qualifiers  
1..486  
/organism="Blumeria graminis f. sp. hordei"  
/db\_xref="taxon:62688"  
/clone\_1ib="D00948"  
/clone\_1ib="lambda Zap, Stragene"  
/cell\_type="conidia"  
/lab\_host="Hordeum vulgare"

BASE COUNT 138 a 101 c 115 g 132 t

ORIGIN

Query Match 84.3%; Score 19.4; DB 10; Length 486;  
Best Local Similarity 69.6%; Pred. No. 68;  
Matches 16; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 RCAUGCUGAAGCCUGACUUCG 23  
DB 154 ACATGCTAAACCTCGACTTCG 176

RESULT 8  
BF251704  
LOCUS 488 bp mRNA linear EST 15-NOV-2001

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DEFINITION      EST418888 Coccidioides immitis spherule cDNA library Coccidioides
ACCESSION       BF251704
VERSION         BF251704.1
KEYWORDS        GI:16931770
SOURCE          EST.
ORGANISM        Coccidioides immitis.
                Coccidioides immitis
                Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
                Onygenales; mitosporic Onygenales; Coccidioides.
REFERENCE       Gardner,M.J. and Kirkland,T.
AUTHORS         Generation of ESTs from Coccidioides immitis spherule cDNA library
TITLE           Unpublished (2000)
JOURNAL         Contact: Malcolm J. Gardner
                Department of Eukaryotic Genomics
                The Institute for Genomic Research
                9712 Medical Center Drive, Rockville, MD 20850, USA
                Tel: 301 838 3519
                Fax: 301 838 0208
                Email: gardner@tigr.org
FEATURES        Location/Qualifiers
SOURCE          1..488
                /organism="Coccidioides immitis"
                /db_xref="taxon:5501"
                /clone="CIAK33"
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                /dev_stage="spherule"
                /lab_host="SOLR"
                /note="Vector: pBluescript SK(-); Site_1: EcoRI, Site_2:
                xhoI"
BASE COUNT      129 a      97 c      126 g      136 t
ORIGIN
Query Match      84.3%; Score 19.4; DB 12; Length 488;
Beast Local Similarity 65.2%; Pred. NO. 68;
Matches 15; Conservative 6; Mismatches 2; Indels 0; Gaps 0.

QY      1 RCAGCUGAAGGCCGCGACUUCG 23
        |||||: ||| |||: |||||: ||
Db      154 ACATCTAATAAACCTCGACCTTCG 176

RESULT 9
BF252581
LOCUS          BF252581 502 bp mRNA linear EST 15-NOV-2001
DEFINITION    ESF419843 Coccidioides immitis spherule cDNA library Coccidioides
                immitis cDNA clone CIAK33 5' sequence, mRNA sequence.
ACCESSION     BF252581
VERSION       BF252581.1
KEYWORDS      GI:16932724
SOURCE        EST.
ORGANISM      Coccidioides immitis.
                Coccidioides immitis
                Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
                Onygenales; mitosporic Onygenales; Coccidioides.
REFERENCE     Gardner,M.J. and Kirkland,T.
AUTHORS       Generation of ESTs from Coccidioides immitis spherule cDNA library
TITLE         Unpublished (2000)
JOURNAL       Contact: Malcolm J. Gardner
                Department of Eukaryotic Genomics
                The Institute for Genomic Research
                9712 Medical Center Drive, Rockville, MD 20850, USA
                Tel: 301 838 3519
                Fax: 301 838 0208
                Email: gardner@tigr.org
FEATURES      Location/Qualifiers
SOURCE        1..502
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                /clone="CIAK33"
                /clone_1lb="Coccidioides immitis spherule cDNA library"
                /dev_stage="spherule"
                /lab_host="SOLR"

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XhoI"
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Best Local Similarity 65.2%; Pred. No. 69;
Matches 15; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
QY      1 RCAGUCUGAAGCCUCGACUUCG 23
      :|:|:|:| | | | | | | | | | | |
Db      157 ACATGCTAATAAGCCCGACCTTCG 179
RESULT 10
LOCUS      AW792430      515 bp      mRNA      linear      EST 01-MAY-2001
DEFINITION D01189-r Lambda Zap, StrataGene Blumeria graminis f. sp. hordei
            cDNA clone D01189 similar to non-functional folate binding protein,
            mRNA sequence.
ACCESSION   AW792430
VERSION     AW792430.1 GI:13904027
KEYWORDS    EST.
SOURCE      Blumeria graminis f. sp. hordei.
ORGANISM    Blumeria graminis f. sp. hordei
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
            Erysiphales; Erysiphaceae; Blumeria.
REFERENCE   1 (bases 1 to 515)
AUTHORS     Thomas,S.W., Rasmussen,S.W., Glarling,M.A., Roster,J.A. and Oliver
            ,R.P.
TITLE       Gene identification in the fungal pathogen Blumeria graminis by
            expressed sequence tag analysis
JOURNAL     unpublished (2000)
COMMENT     Contact: Rasmussen,S.W.
            Department of Yeast Genetics
            Carlsberg Laboratory
            10 GL. Carlsbergvej, DK-2500, Copenhagen, Denmark
            Tel: 45 3327 5230
            Fax: 45 3327 4766
            Email: sw@erc.dk
            High quality sequence stop: 515
            POLYA-No.
FEATURES
            source          location/Qualifiers
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                        /organism="Blumeria graminis f. sp. hordei"
                        /db_xref="taxon:62688"
                        /clone="D01189"
                        /clone_11b="Lambda Zap, StrataGene"
                        /cell_type="conidia"
                        /lab_host="Hordeum vulgare"
BASE COUNT      150 a      104 c      119 g      142 t
ORIGIN
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Best Local Similarity 69.6%; Pred. No. 70;
Matches 16; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY      1 RCAGUCUGAAGCCUCGACUUCG 23
      :|:|:|:| | | | | | | | | | | |
Db      147 ACATGCTAATAAGCCCGACCTTCG 169
RESULT 11
LOCUS      BF251715      518 bp      mRNA      linear      EST 15-NOV-2001
DEFINITION ESF418899 Coccidioides immitis spherule cDNA library Coccidioides
            immitis cDNA clone CIAK45 5' sequence, mRNA sequence.
ACCESSION   BF251715
VERSION     BF251715.1 GI:16931781
KEYWORDS    EST.
SOURCE      Coccidioides immitis.
ORGANISM    Coccidioides immitis.
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

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REFERENCE  
1 (bases 1 to 518)  
Orygenales; mitosporic Orygenales; Coccidioides.  
AUTHORS  
Gardner, M.J. and Kirkland, T.  
TITLE  
Generation of ESTs from Coccidioides immitis spherule cDNA library  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org

FEATURES  
source  
1. 518  
/organism="Coccidioides immitis"  
/db\_xref="taxon:5501"  
/clone="C1A4K45"  
/clone\_1lb="Coccidioides immitis spherule cDNA library"  
/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT  
141 a 104 c 133 g 140 t

ORIGIN

Query Match  
Best Local Similarity 84.3%; Score 19.4; DB 12; Length 518;  
Matches 15; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY  
1 RCAGUCGAAAGCCUCGACUUCG 23  
:||||: ||| ||:||||: |||  
154 ACATGCTAAACCTGACTTCG 176

DB

RESULT 12  
BF252371 541 bp mRNA linear EST 15-NOV-2001  
LOCUS  
EST419633 Coccidioides immitis spherule cDNA library Coccidioides  
DEFINITION  
Immitis cDNA clone C1A4V41 5' sequence, mRNA sequence.  
ACCESSION  
BF252371  
VERSION  
BF252371.1 GI:16932514  
KEYWORDS  
EST.  
SOURCE  
Coccidioides immitis.  
ORGANISM  
Coccidioides immitis.  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Orygenales; mitosporic Orygenales; Coccidioides.  
1 (bases 1 to 541)  
Gardner, M.J. and Kirkland, T.  
Generation of ESTs from Coccidioides immitis spherule cDNA library  
Unpublished (2000)  
Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org

FEATURES  
source  
1. 541  
/organism="Coccidioides immitis"  
/db\_xref="taxon:5501"  
/clone="C1A4V41"  
/clone\_1lb="Coccidioides immitis spherule cDNA library"  
/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT  
157 a 109 c 133 g 142 t

ORIGIN

Query Match  
Best Local Similarity 84.3%; Score 19.4; DB 12; Length 541;  
Matches 15; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY  
1 RCAGUCGAAAGCCUCGACUUCG 23  
:||||: ||| ||:||||: |||  
153 ACATGCTAAACCTGACTTCG 175

DB

RESULT 13  
BF253171 546 bp mRNA linear EST 15-NOV-2001  
LOCUS  
EST445666 Coccidioides immitis spherule cDNA library Coccidioides  
DEFINITION  
Immitis cDNA clone C1GAB68 5' sequence, mRNA sequence.  
ACCESSION  
BF253171  
VERSION  
BF253171.1 GI:16933314  
KEYWORDS  
EST.  
SOURCE  
Coccidioides immitis.  
ORGANISM  
Coccidioides immitis.  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Orygenales; mitosporic Orygenales; Coccidioides.  
1 (bases 1 to 546)  
Gardner, M.J. and Kirkland, T.  
Generation of ESTs from Coccidioides immitis spherule cDNA library  
Unpublished (2000)  
Other\_ESTs: EST445665  
Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org

FEATURES  
source  
1. 546  
/organism="Coccidioides immitis"  
/db\_xref="taxon:5501"  
/clone="C1GAB68"  
/clone\_1lb="Coccidioides immitis spherule cDNA library"  
/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT  
157 a 109 c 135 g 145 t

ORIGIN

Query Match  
Best Local Similarity 84.3%; Score 19.4; DB 12; Length 546;  
Matches 15; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY  
1 RCAGUCGAAAGCCUCGACUUCG 23  
:||||: ||| ||:||||: |||  
157 ACATGCTAAACCTGACTTCG 179

DB

RESULT 14  
BF252094 567 bp mRNA linear EST 15-NOV-2001  
LOCUS  
EST419356 Coccidioides immitis spherule cDNA library Coccidioides  
DEFINITION  
Immitis cDNA clone C1A4G80 5' sequence, mRNA sequence.  
ACCESSION  
BF252094  
VERSION  
BF252094.1 GI:16932237  
KEYWORDS  
EST.  
SOURCE  
Coccidioides immitis.  
ORGANISM  
Coccidioides immitis.  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Orygenales; mitosporic Orygenales; Coccidioides.  
1 (bases 1 to 567)  
Gardner, M.J. and Kirkland, T.  
Generation of ESTs from Coccidioides immitis spherule cDNA library  
Unpublished (2000)  
Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519



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## OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 22:21:06 ; Search time 348.269 Seconds

(without alignments)  
1921.975 Million cell updates/sec

Title: US-09-674-195c-20

Perfect score: 23  
Sequence: 1 rcgaagucgagcguucagcaug 23Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

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1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rnd:*
36: em_htg_mam:*
37: em_htg_vtl:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	95.7	1704	8 HCC18SRN	275306 H.capsulatu
2	22	95.7	1704	8 HCC18SRN	275307 H.capsulatu
3	22	95.7	1713	8 HCC18SR	X58572 H.capsulatu
4	22	95.7	1726	8 AF320009	AF320009 A.jellomyces
5	20.4	88.7	494	8 AB030916	AB030916 Aspergill
6	20.4	88.7	786	8 AF088252	AF088252 Teloschis
7	20.4	88.7	969	8 AF113712	AF113712 Dibaeis b
8	20.4	88.7	990	8 AF107345	AF107345 Dibaeis b
9	20.4	88.7	1031	8 AF203458	AF203458 Cycloaneus
10	20.4	88.7	1054	8 AB030917	AB030917 Aspergill
11	20.4	88.7	1479	8 AEU05438	U04338 Amylocarpus
12	20.4	88.7	1648	8 SC072712	U72712 Siphula cer
13	20.4	88.7	1673	8 AN18SR	X78538 A.niger (ls
14	20.4	88.7	1678	8 PVT13996	Y13996 Paecilomyces
15	20.4	88.7	1686	8 AF113713	AF113713 Dibaeis b
16	20.4	88.7	1687	8 AF184749	AF184749 Bunodopis
17	20.4	88.7	1692	8 AF113710	AF113710 Siphula p
18	20.4	88.7	1696	8 AF113711	AF113711 Siphula p
19	20.4	88.7	1701	8 AF085473	AF085473 Dibaeis b
20	20.4	88.7	1721	8 AF242259	AF242259 Acrosporm
21	20.4	88.7	1732	8 AB008408	AB008408 Aspergill
22	20.4	88.7	1733	8 AB008397	AB008397 Aspergill
23	20.4	88.7	1733	8 AB008413	AB008413 Aspergill
24	20.4	88.7	1733	8 D63695	D63695 Aspergillus
25	20.4	88.7	1733	8 D63697	D63697 Aspergillus
26	20.4	88.7	1734	8 AB006716	AB006716 Talaromyces
27	20.4	88.7	1737	8 AF053479	AF053479 Leveillul
28	20.4	88.7	1746	8 AF053726	AF053726 Kirschsche
29	20.4	88.7	1770	8 AB002079	AB002079 Aspergill
30	20.4	88.7	1771	8 AB002066	AB002066 Aspergill
31	20.4	88.7	1772	8 AF053729	AF053729 Helicascu
32	20.4	88.7	1774	8 AB003947	AB003947 Talaromyces
33	20.4	88.7	1776	8 AB003946	AB003946 Penicilliu
34	20.4	88.7	1777	8 AB003808	AB003808 Aspergill
35	20.4	88.7	1989	8 CSP301706	ALJ301706 Capnobotr
36	20.4	88.7	2150	8 AB003945	AB003945 Penicilliu
37	20.4	88.7	2734	8 AR0421692	ALJ421692 Anaplychl
38	20.4	88.7	2737	8 PPR421689	ALJ421689 Physconia
39	19.4	84.3	1759	8 AB005561	AB005561 Kockovaesi
40	18.8	81.7	144	8 AB046947	AB046947 Endophyte
41	18.8	81.7	144	8 AB046948	AB046948 Endophyte
42	18.8	81.7	144	8 AB046949	AB046949 Endophyte
43	18.8	81.7	192	8 AF062662	AF062662 Endophyte
44	18.8	81.7	192	8 AF062664	AF062664 Endophyte
45	18.8	81.7	192	8 AF062675	AF062675 Endophyte

## ALIGNMENTS

RESULT 1  
HCC18SRN/c  
LOCUS HCC18SRN 1704 bp DNA linear PLN 10-DEC-1999  
DEFINITION H.capsulatum ssp. duboisii 18S rRNA gene.  
ACCESSION Z75306.1  
VERSION Z75306.1 GI:1419549  
KEYWORDS 18S ribosomal RNA; 18S rRNA gene; small subunit ribosomal RNA.  
SOURCE  
ORGANISM Ajellomyces capsulatus  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; Onygenaceae; Ajellomyces.  
REFERENCE  
AUTHORS Okeke,C.N., Kappe,R., Zakikhani,S., Nolte,O. and Sonntag,H.G.  
TITLE Ribosomal genes of Histoplasma capsulatum var. duboisii and var. farciniosum

JOURNAL Mycoses 41 (9-10), 355-362 (1998)  
 MEDLINE 99114487  
 PUBMED 9916456  
 REFERENCE 2 (bases 1 to 1704)  
 AUTHORS Kappe, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-JUL-1996) Reinhard Kappe, Hygiene & Med.  
 Microbiology, University of Heidelberg, Hygiene Institute, Im  
 Neuenheimer Feld 324, Heidelberg, D-69120, Germany

FEATURES  
 source Location/Qualifiers  
 1. 1704

organism="Ajellomyces capsulatus"  
 strain="CBS175.57"  
 sub\_species="duboisii"  
 db\_xref="taxon:5037"  
 1. 1704  
 gene /gene="18S rRNA"  
 1. 1704  
 rRNA /gene="18S rRNA"  
 /product="18S ribosomal RNA"

BASE COUNT 432 a 365 c 470 g 437 t  
 ORIGIN

Query Match 95.7%; Score 22; DB 8; Length 1704;  
 Best Local Similarity 77.3%; Pred. No. 1.8;  
 Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGAAGUCGAGCCUUCAGCAUG 23  
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 DB 133 CGAAGTCGAGCGCTTCAGCATG 112

RESULT 2  
 HCF18SR/c 1704 bp DNA linear PLN 10-DEC-1999  
 LOCUS HCF18SRRN  
 DEFINITION H.capsulatum ssp. farciminosum 18S rRNA gene.  
 ACCESSION Z75307  
 VERSION 275307.1 GI:1419550  
 KEYWORDS 18S ribosomal RNA; 18S rRNA gene; small subunit ribosomal RNA.  
 SOURCE Ajellomyces capsulatus.  
 ORGANISM Ajellomyces capsulatus.  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 Onygenales; Onygenaceae; Ajellomyces.  
 1 (bases 1 to 1704)  
 Okeke, C.N., Kappe, R., Zakikhani, S., Nolte, O. and Sonntag, H. G.  
 Ribosomal genes of Histoplasma capsulatum var. duboisii and var.  
 farciminosum  
 Mycoses 41 (9-10), 355-362 (1998)

JOURNAL Mycoses 41 (9-10), 355-362 (1998)  
 MEDLINE 99114487  
 PUBMED 9916456  
 REFERENCE 2 (bases 1 to 1704)  
 AUTHORS Kappe, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-JUL-1996) Reinhard Kappe, Hygiene & Med.  
 Microbiology, University of Heidelberg, Hygiene Institute, Im  
 Neuenheimer Feld 324, Heidelberg, D-69120, Germany

FEATURES  
 source Location/Qualifiers  
 1. 1704

organism="Ajellomyces capsulatus"  
 strain="CBS205.35, CBS478.64"  
 sub\_species="farciminosum"  
 db\_xref="taxon:5037"  
 1. 1704  
 gene /gene="18S rRNA"  
 1. 1704  
 rRNA /gene="18S rRNA"  
 /product="18S ribosomal RNA"

BASE COUNT 432 a 364 c 471 g 437 t  
 ORIGIN

Query Match 95.7%; Score 22; DB 8; Length 1704;  
 Best Local Similarity 77.3%; Pred. No. 1.8;  
 Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGAAGUCGAGCCUUCAGCAUG 23  
 |||||:|||||:|||||:|||||:|  
 DB 133 CGAAGTCGAGCGCTTCAGCATG 112

RESULT 3  
 HCF18SR/c 1713 bp DNA linear PLN 30-JUN-1993  
 LOCUS HCF18SR  
 DEFINITION H.capsulatum DNA for 18S ribosomal RNA, partial.  
 ACCESSION X58572 S45469  
 VERSION X58572.1 GI:2759  
 KEYWORDS 18S ribosomal RNA  
 SOURCE Ajellomyces capsulatus.  
 ORGANISM Ajellomyces capsulatus.  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 Onygenales; Onygenaceae; Ajellomyces.  
 1 (bases 1 to 1713)  
 Bowman, B.H.  
 Direct Submission  
 Submitted (19-MAR-1991) B.H. Bowman, Roche Molecular Systems, 1145  
 Atlantic Avenue, Alameda CA 94501, USA  
 2 (bases 1 to 1713)  
 Bowman, B.H., Taylor, J.W. and White, T.J.  
 Molecular evolution of the fungi: human pathogens  
 Mol. Biol. Evol. 9 (5), 893-904 (1992)  
 92408455  
 MEDLINE 1528111  
 PUBMED 1528111

REFERENCE  
 AUTHORS Bowman, B.H., Taylor, J.W. and White, T.J.  
 TITLE Molecular evolution of the fungi: human pathogens  
 JOURNAL Mol. Biol. Evol. 9 (5), 893-904 (1992)  
 92408455  
 MEDLINE 1528111  
 PUBMED 1528111  
 REFERENCE  
 AUTHORS Barbee, M.L. and Taylor, J.W.  
 TITLE Convergence in ascospore discharge mechanism among pyrenomyce  
 fungi based on 18S ribosomal RNA gene sequence  
 Mol. Phylogenet. Evol. 1 (1), 59-71 (1992)  
 94115689  
 MEDLINE 1342925  
 PUBMED 1342925

JOURNAL  
 MEDLINE 94115689  
 PUBMED 1342925  
 REMARK Annotation  
 FEATURES  
 source Location/Qualifiers  
 1. 1713

organism="Ajellomyces capsulatus"  
 strain="ATCC 11408"  
 db\_xref="taxon:5037"  
 <1..>1713  
 /product="18S ribosomal RNA"  
 /note="missing approx. 38 bases from 5' and 49 from 3'  
 end of coding region"

BASE COUNT 434 a 368 c 473 g 438 t  
 ORIGIN

Query Match 95.7%; Score 22; DB 8; Length 1713;  
 Best Local Similarity 77.3%; Pred. No. 1.8;  
 Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGAAGUCGAGCCUUCAGCAUG 23  
 |||||:|||||:|||||:|||||:|  
 DB 153 CGAAGTCGAGCGCTTCAGCATG 132

RESULT 4  
 AF320009/c 1726 bp DNA linear PLN 13-FEB-2001  
 LOCUS AF320009  
 DEFINITION Ajellomyces capsulatus ATCC26032 18S ribosomal RNA gene, partial  
 sequence.  
 ACCESSION AF320009  
 VERSION AF320009.1 GI:12751371  
 KEYWORDS

SOURCE Ajellomyces capsulatus.  
 ORGANISM Ajellomyces capsulatus.  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 Onygenales; Onygenaceae; Ajellomyces.  
 1 (bases 1 to 1726)  
 Kasuga, T., White, T.J. and Taylor, J.W.  
 The Molecular Clock in Fungi in the Class Plectomycetes  
 unpublished

REFERENCE  
 AUTHORS Kasuga, T., White, T.J. and Taylor, J.W.  
 TITLE The Molecular Clock in Fungi in the Class Plectomycetes  
 JOURNAL unpublished

REFERENCE 2 (bases 1 to 1726)  
 AUTHORS Kasuga,T., White,T.J. and Taylor,J.W.  
 JOURNAL Direct Submission  
 Submitted (07-NOV-2000) Roche Molecular Systems, 1145 Atlantic Ave., Alameda, CA 94501, USA  
 FEATURES  
 source  
 1. 1726  
 /organism="Afjelovices capsulatus"  
 /strain="ATCC26032: G217B"  
 /db\_xref="ATCC:26032"  
 /db\_xref="taxon:5037"  
 /note="class 2 North American population"  
 <1. >1726  
 /product="18S ribosomal RNA"  
 BASE COUNT 440 a 371 c 475 g 440 t  
 ORIGIN

Query Match 95.7%; Score 22; DB 8; Length 1726;  
 Best Local Similarity 77.3%; Pred. No. 1.8;  
 Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGAAGUCGAGCCTTCAGCATG 23  
 |||||:|||||:|||||:|  
 Db 153 CGAAGTCGAGCCTTCAGCATG 132

RESULT 5  
 AB030916/c 494 bp DNA linear PLN 19-AUG-1999  
 LOCUS Aspergillus niger gene for 18S rRNA, partial sequence.  
 ACCESSION AB030916  
 VERSION AB030916.1 GI:5738920  
 KEYWORDS 18S rRNA; 18S ribosomal RNA.  
 SOURCE Aspergillus niger (strain:IEF1) DNA.  
 ORGANISM Aspergillus niger  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

REFERENCE 1 (bases 1 to 494)  
 AUTHORS Shintani,T. and Matsumoto,Y.  
 JOURNAL Aspergillus niger gene for 18S rRNA, partial sequence  
 REFERENCE 2 (bases 1 to 494)  
 Shintani,T. and Matsumoto,Y.  
 Direct Submission  
 Submitted (10-AUG-1999) Tomoyoshi Shintani, Industrial Research Center of Ehime Prefecture, Laboratory of Food Process, 487-2 Kumeboba, Matsuyama, Ehime 791-1101, Japan  
 (E-mail:shintani@iri.pref.ehime.jp, URL:www.iri.pref.ehime.jp, Tel:81-89-976-7612, Fax:81-89-976-7313)  
 FEATURES  
 source  
 1. 494  
 /organism="Aspergillus niger"  
 /strain="IEF1"  
 /db\_xref="taxon:5061"  
 <1. >494  
 /product="18S ribosomal RNA"  
 BASE COUNT 141 a 100 c 121 g 131 t 1 others  
 ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 494;  
 Best Local Similarity 72.7%; Pred. No. 11;  
 Matches 16; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 2 CGAAGUCGAGCCTTCAGCATG 23  
 |||||:|||||:|||||:|  
 Db 171 CGAAGTCGAGCCTTCAGCATG 150

RESULT 6  
 AF088252/c 786 bp DNA linear PLN 17-JUN-1999  
 LOCUS Teloschistes cf. chrysophthalmus Feige and Mies ESS-6640 18S  
 DEFINITION ribosomal RNA, partial sequence.

ACCESSION AF088252  
 VERSION AF088252.1 GI:4731142  
 KEYWORDS Teloschistes cf. chrysophthalmus Feige and Mies ESS-6640.  
 SOURCE Teloschistes cf. chrysophthalmus Feige and Mies ESS-6640  
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes; Lecanorales; Teloschistiales; Teloschistaceae; Teloschistes.

REFERENCE 1 (bases 1 to 786)  
 AUTHORS Stenroos,S.K. and Depriest,P.T.  
 JOURNAL SSU rDNA phylogeny of cladoniiform lichens  
 REFERENCE 2 (bases 1 to 786)  
 AUTHORS Am. J. Bot. 85, 1548-1559 (1998)  
 TITLE Depriest,P.T., Ivanova,N. and Gargas,A.  
 JOURNAL Direct Submission  
 Submitted (31-AUG-1998) Department of Botany, NHB-166, Smithsonian Institution, National Museum of Natural History, 10th & Constitution Avenue NW, Washington, DC 20560-0166, USA  
 FEATURES  
 source  
 1. 786  
 /organism="Teloschistes cf. chrysophthalmus Feige and Mies ESS-6640"  
 /specimen\_voucher="Feige & Mies ESS-6640 (US)"  
 /db\_xref="taxon:88650"  
 /country="Cape Verde:Sanro Antao, 1988"  
 <1. >786  
 /product="18S ribosomal RNA"  
 /note="small subunit ribosomal RNA"  
 BASE COUNT 208 a 161 c 198 g 219 t  
 ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 786;  
 Best Local Similarity 72.7%; Pred. No. 12;  
 Matches 16; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 2 CGAAGUCGAGCCTTCAGCATG 23  
 |||||:|||||:|||||:|  
 Db 134 CGAAGTCGAGCCTTCAGCATG 113

RESULT 7  
 AF113712/c 969 bp DNA linear PLN 06-DEC-1999  
 LOCUS Dibaetis baecomyces small subunit ribosomal RNA gene, partial sequence.  
 ACCESSION AF113712  
 VERSION AF113712.1 GI:6502558  
 KEYWORDS Dibaetis baecomyces.  
 SOURCE Dibaetis baecomyces.  
 ORGANISM Dibaetis baecomyces  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes; Lecanoromycetes incertae sedis; Icmadophiliaceae; Dibaetis.

REFERENCE 1 (bases 1 to 969)  
 AUTHORS Platt,J.L. and Spatafora,J.W.  
 JOURNAL Evolutionary relationships of nonsexual lichenized fungi: molecular SSU and LSU rDNA analyses  
 REFERENCE 2 (bases 1 to 969)  
 AUTHORS Platt,J.L. and Spatafora,J.W.  
 JOURNAL Direct Submission  
 Submitted (16-DEC-1998) Department of Botany & Plant Pathology, Oregon State University, 2082 Cordley Hall, Corvallis, OR 97331-2902, USA  
 FEATURES  
 source  
 1. 969  
 /organism="Dibaetis baecomyces"  
 /db\_xref="taxon:83478"  
 <1. >969  
 /product="small subunit ribosomal RNA"  
 BASE COUNT 268 a 189 c 243 g 268 t 1 others  
 ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 969;

Best Local Similarity 72.7%; Pred. No. 12;  
Matches 16; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGAAGUCGAGGCUUUCAGCAG 23  
DB 128 CGAAGTCGAGGTTTTCAGCATG 107

RESULT 8  
AF107345/c  
LOCUS Dibaels baecomyces small subunit ribosomal RNA gene, partial  
DEFINITION  
ACCESSION AF107345  
VERSION AF107345.1 GI:6318520  
KEYWORDS  
SOURCE Dibaels baecomyces.  
ORGANISM Dibaels baecomyces.  
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;  
AUTHORS Platt,J.L., Camacho,F.J. and Spatafora,J.W.  
TITLE 1 (bases 1 to 90)  
JOURNAL Evolution of the lichen symbiosis within the Lecaniales; molecular  
AUTHORS phylogenetic hypotheses for Dibaels and Baecomyces  
TITLE Unpublished  
JOURNAL 2 (bases 1 to 90)  
AUTHORS Platt,J.L. and Spatafora,J.W.  
TITLE Direct Submission  
JOURNAL Submitted (18-NOV-1998) Botany & Plant Pathology, Oregon State  
FEATURES University, 2082 Cordley Hall, Corvallis, OR 97331, USA  
SOURCE Location/Qualifiers  
1..90  
/organism="Dibaels baecomyces"  
/isolate="OSC56400"  
/db\_xref="taxon:83478"  
rRNA <1..>90  
/product="small subunit ribosomal RNA"  
BASE COUNT 269 a 189 c 248 g 284 t  
ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 90;  
Best Local Similarity 72.7%; Pred. No. 12;  
Matches 16; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGAAGUCGAGGCUUUCAGCAG 23  
DB 117 CGAAGTCGAGGTTTTCAGCATG 96

RESULT 9  
AF203458/c  
LOCUS Cycloaneuema minus small subunit ribosomal RNA gene, partial  
DEFINITION  
ACCESSION AF203458  
VERSION AF203458.1 GI:9622908  
KEYWORDS  
SOURCE Cycloaneuema minus.  
ORGANISM Cycloaneuema minus.  
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;  
AUTHORS Rhytismatales; Rhytismatales; Cycloaneuema.  
TITLE 1 (bases 1 to 1031)  
JOURNAL Gerandt,D.S., Platt,J.L., Stone,J.K., Spatafora,J.W.,  
AUTHORS Holst-Jensen,A., Hamelin,R.C. and Kohn,L.M.  
TITLE Phylogenetics of Helotiales and Rhytismatales based on partial  
JOURNAL small subunit nuclear ribosomal DNA sequences  
AUTHORS Mycologia 93 (5), 915-933 (2001)  
TITLE 2 (bases 1 to 1031)  
JOURNAL Gerandt,D.S., Platt,J.L., Stone,J.K., Spatafora,J.W.,  
AUTHORS Holst-Jensen,A., Hamelin,R.C. and Kohn,L.M.  
TITLE Direct Submission  
JOURNAL Submitted (12-NOV-1999) Department of Botany and Plant Pathology,  
ORIGIN Oregon State University, 2082 Cordley Hall, Corvallis, OR

97331-2902, USA  
FEATURES Location/Qualifiers  
SOURCE 1..1031  
/organism="Cycloaneuema minus"  
/strain="93197"  
/specific\_host="Pinus sylvestris"  
/db\_xref="taxon:64355"  
rRNA <1..>1031  
/product="small subunit ribosomal RNA"  
BASE COUNT 275 a 203 c 264 g 289 t  
ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 1031;  
Best Local Similarity 72.7%; Pred. No. 12;  
Matches 16; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGAAGUCGAGGCUUUCAGCAG 23  
DB 117 CGAAGTCGAGGCTTTTCAGCATG 96

RESULT 10  
AB030917/c  
LOCUS Aspergillus niger var. awamori gene for 18S rRNA, partial sequence.  
DEFINITION  
ACCESSION AB030917  
VERSION AB030917.1 GI:5738921  
KEYWORDS 18S rRNA; 18S ribosomal RNA.  
SOURCE Aspergillus niger var. awamori (strain: IEF2) DNA.  
ORGANISM Aspergillus awamori  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
REFERENCE 1 (bases 1 to 1054)  
AUTHORS Shintani,T. and Matsumoto,Y.  
TITLE Aspergillus awamori gene for 18S rRNA, partial sequence  
JOURNAL Published Only in Database (1999)  
REFERENCE 2 (bases 1 to 1054)  
AUTHORS Shintani,T. and Matsumoto,Y.  
TITLE Direct Submission  
JOURNAL Submitted (10-AUG-1999) Tomoyoshi Shintani, Industrial Research  
Center of Ehime Prefecture, Laboratory of Food Process; 487-2  
Kumekubota, Matsuyama, Ehime 791-1101, Japan  
E-mail:shintani@iri.pref.ehime.jp, URL:www.iri.pref.ehime.jp,  
Tel:81-89-976-7612, Fax:81-89-976-7313  
FEATURES Location/Qualifiers  
SOURCE 1..1054  
/organism="Aspergillus awamori"  
/strain="IEF2"  
/db\_xref="taxon:105351"  
/note="synonym:Aspergillus awamori"  
rRNA <1..>1054  
/product="18S ribosomal RNA"  
BASE COUNT 288 a 215 c 274 g 277 t  
ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 1054;  
Best Local Similarity 72.7%; Pred. No. 12;  
Matches 16; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGAAGUCGAGGCUUUCAGCAG 23  
DB 155 CGAAGTCGAGGTTTTCAGCATG 134

RESULT 11  
AE045438/c  
LOCUS Amylocarpus encephaloides small subunit rRNA gene.  
DEFINITION  
ACCESSION AE045438  
VERSION AE045438.1 GI:1736923  
KEYWORDS  
SOURCE Amylocarpus encephaloides.  
ORGANISM Amylocarpus encephaloides

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanomyces;  
Helotiales; Helotiales incertae sedis; Amylocarpus.  
REFERENCE  
1 (bases 1 to 1479)  
AUTHORS  
Landvik,S., Shaller,N.F.J. and Eriksson,O.E.  
TITLE  
SSU rDNA sequences support for a close relationship between the  
Elaphomyces and the Eurotiales and Orygenales  
JOURNAL  
Mycoscience 37, 237-241 (1996)  
REFERENCE  
2 (bases 1 to 1479)  
AUTHORS  
Landvik,S., Shaller,N.F.J. and Eriksson,O.E.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (11-JAN-1996) Sara Landvik, Ecological Botany, Umea,  
S-90187, Sweden  
FEATURES  
Source  
1.1479  
/organism="Amylocarpus encephaloides"  
/strain="UME 29765"  
/db\_xref="taxon:45428"  
rRNA  
1.1479  
/product="small subunit ribosomal RNA"  
BASE COUNT  
382 a 300 c 399 g 398 t  
ORIGIN  
Query Match 88.7%; Score 20.4; DB 8; Length 1479;  
Best Local Similarity 72.7%; Pred. No.12;  
Matches 16; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
QY 2 CGAAGCGAGCGCCUUCAGCAUG 23  
Db 108 CGAAGTCGAGCGTTTTCAGCATG 87  
RESULT 12  
SCU072712/c 1648 bp DNA linear PLN 30-JUL-1997  
LOCUS  
Siphula ceratites 18S small subunit ribosomal RNA gene, complete  
DEFINITION  
sequence.  
ACCESSION  
U72712.1 GI:2286071  
VERSION  
U72712.1 GI:2286071  
KEYWORDS  
Siphula ceratites.  
SOURCE  
Siphula ceratites  
ORGANISM  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanomyces;  
Lecanoromycetes incertae sedis; Icmadophyllaceae; Siphula.  
REFERENCE  
1 (bases 1 to 1648)  
AUTHORS  
Stenroos,S., Lontander,K. and Tehler,A.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (27-SEP-1996) Botany, National Museum of Natural History,  
Smithsonian Institution, NHB-166, 10th St. & Constitution Ave.,  
Washington, DC 20560, USA  
FEATURES  
Source  
1.1648  
Location/Qualifiers  
/organism="Siphula ceratites"  
/db\_xref="taxon:53373"  
rRNA  
1.1648  
/product="18S small subunit ribosomal RNA"  
BASE COUNT  
424 a 343 c 442 g 439 t  
ORIGIN  
Query Match 88.7%; Score 20.4; DB 8; Length 1648;  
Best Local Similarity 72.7%; Pred. No.12;  
Matches 16; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
QY 2 CGAAGCGAGCGCCUUCAGCAUG 23  
Db 110 CGAAGTCGAGCGTTTTCAGCATG 89  
RESULT 13  
AN18SRR 1673 bp DNA linear PLN 13-MAR-1995  
LOCUS  
A.niger (isolate CBS102.12) 18S rRNA gene.  
DEFINITION  
X78538  
ACCESSION  
X78538.1 GI:469079  
VERSION

KEYWORDS  
18S ribosomal RNA.  
SOURCE  
Aspergillus niger.  
ORGANISM  
Aspergillus niger  
REFERENCE  
1 (bases 1 to 1673)  
AUTHORS  
Melchers,W.J., Verweij,P.E., van den Hurk,P., van Belkum,A., De  
Pauw,B.E., Hoogkamp-Korstanje,J.A. and Mels,J.F.  
TITLE  
General primer-mediated PCR for detection of Aspergillus species  
JOURNAL  
J. Clin. Microbiol. 32 (7), 1710-1717 (1994)  
MEDLINE  
95014936  
PUBMED  
7929762  
REFERENCE  
2 (bases 1 to 1673)  
AUTHORS  
Melchers,W.J.G.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (25-MAR-1994) W.J.G. Melchers, Department of Medical  
Microbiology, University of Nijmegen, P O Box 9101, 6500 HB  
Nijmegen, NETHERLANDS  
FEATURES  
Source  
1.1673  
Location/Qualifiers  
/organism="Aspergillus niger"  
/isolate="CBS102.12"  
/db\_xref="taxon:5061"  
rRNA  
<1.1673  
/product="18S ribosomal RNA"  
/evidence="experimental"  
BASE COUNT  
423 a 365 c 458 g 426 t 1 others  
ORIGIN  
Query Match 88.7%; Score 20.4; DB 8; Length 1673;  
Best Local Similarity 72.7%; Pred. No.12;  
Matches 16; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
QY 2 CGAAGCGAGCGCCUUCAGCAUG 23  
Db 131 CGAAGTCGAGCGTTTTCAGCATG 110  
RESULT 14  
PVY13996 1678 bp DNA linear PLN 23-JUL-1997  
LOCUS  
Paecilomyces variotii 18S rRNA gene.  
DEFINITION  
Y13996  
ACCESSION  
Y13996.1 GI:2224834  
VERSION  
18S ribosomal RNA; 18S rRNA gene.  
KEYWORDS  
Paecilomyces variotii.  
SOURCE  
Paecilomyces variotii  
ORGANISM  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae;  
Paecilomyces.  
REFERENCE  
1 (bases 1 to 1678)  
AUTHORS  
Zakikhani,S., Okeke,C.N. and Kappe,R.  
TITLE  
18S rDNA sequence of Paecilomyces variotii CBS339.51  
JOURNAL  
Unpublished  
REFERENCE  
2 (bases 1 to 1678)  
AUTHORS  
Kappe,R.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (24-JUN-1997) Kappe R., Hygiene Institute, University of  
Heidelberg, Im Neuenheimer Feld 324 D-69120 GERMANY  
FEATURES  
Source  
1.1678  
Location/Qualifiers  
/organism="Paecilomyces variotii"  
/strain="CBS339.51"  
/isolate="Man, sputum"  
/db\_xref="taxon:45996"  
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rRNA  
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/product="18S ribosomal RNA"  
/evidence="experimental"  
BASE COUNT  
422 a 363 c 467 g 426 t  
ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 1678;  
 Best Local Similarity 72.7%; Pred. No. 12;  
 Matches 16; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 2 CGAAGUCGAGCCUUCACGCAUG 23  
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 DB 105 CGAAGTCGAGGTTTCACGATG 84

## RESULT 15

AF113713/C

LOCUS AF113713 1686 bp DNA linear PLN 06-DEC-1999  
 DEFINITION Dibaels baemyces isolate OSC53939 small subunit ribosomal RNA  
 gene, partial sequence.

ACCESSION AF113713  
 VERSION AF113713.1 GI:6502559

KEYWORDS  
 SOURCE

ORGANISM  
 Dibaels baemyces.

REFERENCE  
 AUTHORS Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;  
 Lecanoromycetes incertae sedis; Lecanophylaceae; Dibaels.  
 1 (bases 1 to 1686)

TITLE Platt,J.L. and Spatafora,J.W.  
 Evolutionary relationships of nonsexual lichenized fungi: molecular  
 phylogenetic hypotheses for the genera Siphula and Thamolia from  
 SSU and LSU rDNA analyses

JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1686).  
 AUTHORS Platt,J.L. and Spatafora,J.W.  
 TITLE Direct Submission

JOURNAL Submitted (16-DEC-1998) Department of Botany & Plant Pathology,  
 Oregon State University, 2082 Cordley Hall, Corvallis, OR  
 97331-2902, USA

FEATURES  
 source Location/Qualifiers

1..1686  
 /organism="Dibaels baemyces"  
 /isolate="OSC53939"  
 /db\_xref="taxon:83478"  
 <1..>1686

BASE COUNT 441 a 346 c 438 g 460 t 1 others  
 ORIGIN

Query Match 88.7%; Score 20.4; DB 8; Length 1686;  
 Best Local Similarity 72.7%; Pred. No. 12;  
 Matches 16; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 2 CGAAGUCGAGCCUUCACGCAUG 23  
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 DB 128 CGAAGTCGAGGTTTCACGATG 107

Search completed: June 12, 2003, 02:33:54  
 Job time : 348.269 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 11, 2003, 22:17:41 ; Search time 117.802 Seconds

(Without alignments)  
439.686 Million cell updates/sec

Title: US-09-674-195c-20

Perfect score: 23

Sequence: 1 tcgaagucgagcgccuucagcgcaug 23

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	22	95.7	22	15	AAO73433	Histoplasma capsul
2	22	95.7	22	15	AAO73436	Histoplasma capsul
3	22	95.7	22	15	AAO73437	Histoplasma capsul
4	22	95.7	22	15	AAO86436	Histoplasma capsul
5	20.4	88.7	22	21	AAE11545	Histoplasma capsul
6	18.8	81.7	1733	20	AAZ00859	Aspergillus niger
7	17.2	74.8	1745	24	ABA01152	A. fumigatus 16S r
8	17.2	74.8	4403765	22	AAI99683	Deuteromyces pol
9	17.2	74.8	4411529	22	AAI99682	Mycobacterium tube

C 10	16.8	73.0	454	22	ABA44550	Human breast cell
C 11	16.8	73.0	454	22	ABA54997	Human foetal liver
C 12	16.8	73.0	454	22	ABA24760	Probe #3226 for ge
C 13	16.8	73.0	454	22	AAK03266	Human brain expres
C 14	16.8	73.0	454	22	AAK28719	Human bone marrow
C 15	16.8	73.0	454	22	AAI13296	Probe #3229 for ge
C 16	16.8	73.0	454	22	AAI134650	Probe #3336 used t
C 17	16.8	73.0	454	22	AAI03197	Probe #3188 used t
C 18	16.8	73.0	454	22	ABSO3233	Human genome deriv
C 19	16.8	73.0	492	24	AA565314	DNA sequencing novel
C 20	16.8	73.0	891	19	AAV37154	DNA sequence used
C 21	16.8	73.0	891	19	AAH01747	Fibroblast succin
C 22	16.4	71.3	7584	22	AAH01747	Rhodococcus corall
C 23	16.4	71.3	7600	21	AAH01747	Rhodococcus sp. OH
C 24	16.2	70.4	351	21	AA51878	Human secreted pro
C 25	16.2	70.4	654	21	AA53824	Neisseria gonorrhoe
C 26	16.2	70.4	846	23	AA590625	DNA encoding novel
C 27	16.2	70.4	1097	23	ABK72888	Bacillus lichenifo
C 28	16.2	70.4	1922	12	AAQ14716	Nitrosomonas SPN 3
C 29	16.2	70.4	1922	12	AAQ14716	DNA encoding novel
C 30	16.2	70.4	3002	23	ABK72888	Drosophila melanog
C 31	16.2	70.4	4448	20	AAZ20564	Polynucleotide seq
C 32	16.2	70.4	7264	23	ABL29848	Drosophila melanog
C 33	16.2	70.4	9228	23	ABL11660	N. meningitidis pa
C 34	16.2	70.4	17381	21	AAH1493	Neisseria meningit
C 35	16.2	70.4	349980	21	AAH21607	N. meningitidis B
C 36	16.2	70.4	143768	21	AAH81490	Cat flea head and
C 37	15.8	68.7	550	21	AAH94343	Human cDNA 5'-end
C 38	15.8	68.7	695	22	AAK91828	Human cDNA clone r
C 39	15.8	68.7	695	22	AAK93228	Sequence encoding
C 40	15.8	68.7	738	14	AAQ43293	CC49 VL / 217 / 4-
C 41	15.8	68.7	738	15	AAQ66841	DNA encoding a pro
C 42	15.8	68.7	738	20	AAK04747	Fusion polypeptide
C 43	15.8	68.7	738	21	AAV99764	DNA encoding bival
C 44	15.8	68.7	738	20	AAH95090	DNA encoding bival
C 45	15.8	68.7	738	21	AAH95622	DNA encoding a sin

## ALIGNMENTS

RESULT 1  
AAO73433 standard; DNA; 22 BP.  
XX  
XX AAO73433;  
AC  
XX 18-MAY-1995 (first entry)  
DT  
XX  
XX  
DE Histoplasma capsulatum-specific DNA hybridisation probe.  
KW Probe: detection; Histoplasma capsulatum; 18S; rRNA; rDNA; hybridisation;  
KW Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;  
KW water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.  
XX  
XX Synthetic.  
OS  
XX  
XX US5352579-A.  
PN  
XX  
XX 04-OCT-1994.  
PD  
XX  
XX 28-JUN-1991; 91US-0720587.  
PR  
XX  
XX 28-JUN-1991; 91US-0720587.  
PA  
XX  
XX (GENP-) GEN-PROBE INC.  
PI  
XX  
XX Millman CL;  
XX  
XX WPI; 1994-316178/39.  
DR  
XX  
XX Hybridisation probe specific for Histoplasma capsulatum -  
PT allowing differentiation from all other fungi for detection or

PT quantitation in body fluids, etc.  
 XX  
 PS Claim 4; Column 11; 8bp; English.  
 XX  
 CC A probe (AAO73433) or its complement (AAO73436) and corresponding RNA  
 CC sequences (AAO73437 and AAO86436) used for the specific detection of all  
 CC strains of Histoplasma capsulatum (H.c.). The probes are manufactured  
 CC complementary to the H.c. 18S rRNA or rDNA gene. This region also  
 CC corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.  
 CC The probe is specific for H.c. and can be used to distinguish the fungus  
 CC from all others, even its nearest phylogenetic neighbour Blastomyces  
 CC dermatitidis. Nucleic acid hybridisation of the specific probe is  
 CC enhanced by the use of helper probes (AAO73434-5). This method allows  
 CC the detection and/or the quantitation of H.c. from samples e.g. body  
 CC fluids, tissue samples, soil and water.  
 XX  
 SO Sequence 22 BP; 5 A; 5 C; 7 G; 5 T; 0 other;  
 Query Match 95.7%; Score 22; DB 15; Length 22;  
 Best Local Similarity 77.3%; Pred. No. 0.16;  
 Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
 OY 2 CGAAGTCGAGCGCTTCACGATG 23  
 DB 1 CGAAGTCGAGCGCTTCACGATG 22  
 RESULT 2  
 AAO73436/C  
 ID AAO73436 standard; DNA; 22 BP.  
 XX  
 AC AAO73436;  
 XX  
 DT 18-MAY-1995 (first entry)  
 XX  
 DE Histoplasma capsulatum specific DNA probe, complementary sequence.  
 XX  
 KW Probe: detection; Histoplasma capsulatum; 18S; rRNA; rDNA; hybridisation;  
 KW Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;  
 KW water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.  
 OS Synthetic.  
 XX  
 PN US5352579-A.  
 XX  
 PD 04-OCT-1994.  
 XX  
 PF 28-JUN-1991; 91US-0720587.  
 XX  
 PR 28-JUN-1991; 91US-0720587.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 PI Millman CL;  
 XX  
 DR WPI; 1994-316178/39.  
 XX  
 PT Hybridisation probe specific for Histoplasma capsulatum -  
 PT allowing differentiation from all other fungi for detection or  
 PT quantitation in body fluids, etc.  
 PS Claim 9; Column 12; 8bp; English.  
 XX  
 CC A probe (AAO73433) or its complement (AAO73436) and corresponding RNA  
 CC sequences (AAO73437 and AAO86436) used for the specific detection of all  
 CC strains of Histoplasma capsulatum (H.c.). The probes are manufactured  
 CC complementary to the H.c. 18S rRNA or rDNA gene. This region also  
 CC corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.  
 CC The probe is specific for H.c. and can be used to distinguish the fungus  
 CC from all others, even its nearest phylogenetic neighbour Blastomyces  
 CC dermatitidis. Nucleic acid hybridisation of the specific probe is  
 CC enhanced by the use of helper probes (AAO73434-5). This method allows  
 CC the detection and/or the quantitation of H.c. from samples e.g. body

CC fluids, tissue samples, soil and water.  
 XX  
 SO Sequence 22 BP; 5 A; 7 C; 5 G; 5 T; 0 other;  
 Query Match 95.7%; Score 22; DB 15; Length 22;  
 Best Local Similarity 77.3%; Pred. No. 0.16;  
 Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
 OY 2 CGAAGTCGAGCGCTTCACGATG 23  
 DB 22 CGAAGTCGAGCGCTTCACGATG 1  
 RESULT 3  
 AAO73437/C  
 ID AAO73437 standard; RNA; 22 BP.  
 XX  
 AC AAO73437;  
 XX  
 DT 18-MAY-1995 (first entry)  
 XX  
 DE Histoplasma capsulatum-specific RNA hybridisation probe.  
 XX  
 KW Probe: detection; Histoplasma capsulatum; 18S; rRNA; rDNA; hybridisation;  
 KW Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;  
 KW water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.  
 OS Synthetic.  
 XX  
 PN US5352579-A.  
 XX  
 PD 04-OCT-1994.  
 XX  
 PF 28-JUN-1991; 91US-0720587.  
 XX  
 PR 28-JUN-1991; 91US-0720587.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 PI Millman CL;  
 XX  
 DR WPI; 1994-316178/39.  
 XX  
 PT Hybridisation probe specific for Histoplasma capsulatum -  
 PT allowing differentiation from all other fungi for detection or  
 PT quantitation in body fluids, etc.  
 PS Claim 9; Column 12-13; 8bp; English.  
 XX  
 CC A probe (AAO73433) or its complement (AAO73436) and corresponding RNA  
 CC sequences (AAO73437 and AAO86436) used for the specific detection of all  
 CC strains of Histoplasma capsulatum (H.c.). The probes are manufactured  
 CC complementary to the H.c. 18S rRNA or rDNA gene. This region also  
 CC corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.  
 CC The probe is specific for H.c. and can be used to distinguish the fungus  
 CC from all others, even its nearest phylogenetic neighbour Blastomyces  
 CC dermatitidis. Nucleic acid hybridisation of the specific probe is  
 CC enhanced by the use of helper probes (AAO73434-5). This method allows  
 CC the detection and/or the quantitation of H.c. from samples e.g. body  
 CC fluids, tissue samples, soil and water.  
 XX  
 SO Sequence 22 BP; 5 A; 7 C; 5 G; 5 T; 0 other;  
 Query Match 95.7%; Score 22; DB 15; Length 22;  
 Best Local Similarity 77.3%; Pred. No. 0.16;  
 Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
 OY 2 CGAAGTCGAGCGCTTCACGATG 23  
 DB 22 CGAAGTCGAGCGCTTCACGATG 1  
 RESULT 4

AA086436  
ID AA086436 standard; RNA; 22 BP.  
XX  
AC AA086436;  
XX  
DT 18-MAY-1995 (first entry)  
XX  
DE Histoplasma capsulatum-specific complementary RNA hybridisation probe.  
XX  
KW Probe: detection; Histoplasma capsulatum; 18S; rRNA; rDNA; hybridisation;  
KW Saccharomyces cerevisiae; fungus; phylogenetic; helper probe; soil;  
KW water; Blastomyces dermatitidis; quantitation; sample; body fluid; ss.  
XX  
OS Synthetic.  
XX  
PN US5352579-A.  
XX  
PD 04-OCT-1994.  
XX  
PF 28-JUN-1991; 91US-0720587.  
XX  
PR 28-JUN-1991; 91US-0720587.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Millman CL;  
XX  
DR WPI: 1994-316178/39.  
XX  
PT Hybridisation probe specific for Histoplasma capsulatum -  
PT allowing differentiation from all other fungi for detection or  
PT quantitation in body fluids, etc.  
XX  
PS Claim 9; Column 13; 8pp; English.  
XX  
CC A probe (AA073433) or its complement (AA073436) and corresponding RNA  
CC sequences (AA073437 and AA086436) used for the specific detection of all  
CC strains of Histoplasma capsulatum (H.c.). The probes are manufactured  
CC complementary to the H.c. 18S rRNA or rDNA gene. This region also  
CC corresponds to the bases 172-193 of Saccharomyces cerevisiae 18S rRNA.  
CC The probe is specific for H.c. and can be used to distinguish the fungus  
CC from all others, even its nearest phylogenetic neighbour Blastomyces  
CC dermatitidis. Nucleic acid hybridisation of the specific probe is  
CC enhanced by the use of helper probes (AA073434-5). This method allows  
CC the detection and/or the quantitation of H.c. from samples e.g. body  
CC fluids, tissue samples, soil and water.  
XX  
SQ Sequence 22 BP; 5 A; 5 C; 7 G; 5 U; 0 other;  
Query Match 95.7%; Score 22; DB 15; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGAAGUCGAGGCUUUCAGCAUG 23  
Db 1 CGAAGUCGAGGCUUUCAGCAUG 22

RESULT 5  
AA086436/c  
ID AA086436 standard; cDNA; 568 BP.  
XX  
AC AA086436;  
XX  
DT 13-MAR-2001 (first entry)  
XX  
DE Aspergillus niger EST SEQ ID NO:4068.  
XX  
KW Multiple gene expression; filamentous fungal cell; EST;  
KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;  
KW Aspergillus oryzae; Trichoderma reesei; identification; recombination;  
KW culture condition; environmental stress; spore morphogenesis;  
KW metabolic pathway engineering; catabolic pathway engineering; ss.

XX  
OS Aspergillus niger.  
XX  
PN WO200056762-A2.  
XX  
PD 28-SEP-2000.  
XX  
PF 22-MAR-2000; 2000WO-US07781.  
XX  
PR 22-MAR-1999; 99US-0273623.  
XX  
PA (NOVO ) NOVO NORDISK BIOTECH INC.  
XX  
PA (NOVO ) NOVO NORDISK AS.  
XX  
PI Berka RM, Rey MM, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;  
XX  
DR WPI: 2000-594572/56.  
XX  
PT Monitoring differential expression of genes in filamentous fungal cells  
PT uses fluorescence-labeled nucleic acids isolated from the cells and a  
PT substrate of expressed sequence tags -  
XX  
PS Claim 87; Page 1791-1792; 3161pp; English.  
XX  
CC The present invention describes a method for monitoring differential  
CC expression of genes in a first filamentous fungal (FF) cell relative to  
CC expression of the same genes in one or more second filamentous fungal  
CC cells. The method uses fluorescence-labeled nucleic acids isolated from  
CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs  
CC are used in the methods for monitoring differential expression of genes  
CC in a first filamentous fungal (FF) cell relative to expression of the  
CC same genes in one or more second filamentous fungal cells. Monitoring  
CC the global expression of genes from FF cells allows the production  
CC potential of the microorganisms to be improved. New genes may be  
CC discovered, possible functions of unknown open reading frames can be  
CC identified and gene copy number variation and stability can be  
CC monitored. The expression of genes can be used to study how FF cells  
CC adapt to changes in culture conditions, environmental stress, spore  
CC morphogenesis, recombination, metabolic or catabolic pathway  
CC engineering. Using ESTs provides several advantages over genomic or  
CC random cDNA clones including elimination of redundancy as one spot on an  
CC array equals one gene or open reading frame, and organisation of the  
CC microarrays based on function of the gene products to facilitate  
CC analysis of the results. AA07478 to AA07478 represents ESTs from  
CC Fusarium venenatum; AA07478 to AA07478 represents ESTs from  
CC niger; AA07478 to AA07478 represents ESTs from Aspergillus  
CC niger; AA07478 to AA07478 represents ESTs from Trichoderma reesei; and  
CC all specifically claimed in the present invention.  
XX  
SQ Sequence 568 BP; 155 A; 116 C; 141 G; 150 T; 6 other;  
Query Match 88.7%; Score 20.4; DB 21; Length 568;  
Best Local Similarity 72.7%; Pred. No. 1.5;  
Matches 16; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 2 CGAAGUCGAGGCUUUCAGCAUG 23  
Db 178 CGAAGUCGAGGCUUUCAGCAUG 157

RESULT 6  
AA086436/c  
ID AA086436 standard; DNA; 1733 BP.  
XX  
AC AA086436;  
XX  
DT 11-OCT-1999 (first entry)  
XX  
DE A. fumigatus 18S rRNA DNA.  
XX  
KW Detection; diagnosis; 18S rRNA; aspergillosis; oncology;  
KW invasive infection; haematology; immune system suppression; ss.

OS Aspergillus fumigatus.  
XX DE19806274-A1.  
PN 19-AUG-1999.  
PD 16-FEB-1998; 98DE-1006274.  
XX 16-FEB-1998; 98DE-1006274.  
XX 16-FEB-1998; 98DE-1006274.  
PR (BUCH/) BUCHHEIDT D.  
XX (HEHL/) HEHLMANN R.  
PA (SKLA/) SKLADNY H.  
XX Buchheidt D, Hehlmann R, Skladny H;  
PI WPI, 1999-470047/40.  
DR  
XX Detecting Aspergillus nucleic acid in body samples by two-step  
PT polymerase chain reaction, for diagnosing aspergilliosis  
PS Claim 2; Fig 1; 16pp; German.  
XX  
XX This invention describes a novel method for detecting Aspergillus nucleic  
CC acid (I) in a body sample which comprises the isolation of (I) followed  
CC by a two-step polymerase chain reaction (PCR) amplification of any  
CC nucleic acid having a sequence essentially homologous to part of the  
CC 3'-end of the Aspergillus 18S rRNA gene using primers used in the first  
CC step that do not overlap with those in the second step. The method is  
CC used for early diagnosis, and monitoring, of aspergilliosis, particularly  
CC invasive infections in hematological-oncological patients with long-term  
CC suppression of the immune system. Unlike the known method using  
CC overlapping primers, this process provides efficient and reliable  
CC detection of Aspergillus in clinical situations. It is specific for  
CC Aspergillus (it detects the species terreus, niger, versicolor, clavatus,  
CC flavus, and fumigatus, but not oryzae, nor bacteria or fungi from any  
CC other genera). This sequence represents the DNA sequence of Aspergillus  
CC fumigatus 18S rRNA.  
XX  
SQ Sequence 1733 BP; 446 A; 374 C; 475 G; 438 T; 0 other;  
XX  
Query Match 81.7%; Score 18.8; DB 20; Length 1733;  
Best Local Similarity 68.2%; Pred. No. 11;  
Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
QY 2 CGAAGTCGAGCGGCTTTCAGCATG 23  
DB 153 CGAAGTCGAGCGGCTTTCAGCATG 132  
XX  
RESULT 7  
ID ABA01152 standard; DNA; 1745 BP.  
XX ABA01152;  
AC 24-JAN-2002 (first entry)  
DT 24-JAN-2002 (first entry)  
XX Deuteromycetes polynucleotide SEQ ID 1.  
DE Deuteromycetes polynucleotide SEQ ID 1.  
XX Aldonic acid; ds.  
KM Aldonic acid; ds.  
XX Deuteromycetes sp.  
OS Deuteromycetes sp.  
XX JP2001245657-A.  
PN 11-SEP-2001.  
XX 26-DEC-2000; 2000JP-0394766.  
XX 27-DEC-1999; 99JP-0369714.  
XX (TAKE-) TAKEHARA KAGAKU KOGYO KK.  
PA

PA (OSAKA ) OSAKA CITY.  
XX WPI; 2002-002933/01.  
DR A new microbe for producing aldonic acid, comprises a new strain of  
XX Actinobacter or Burkholderis -  
PT Actinobacter or Burkholderis -  
XX Disclosure; Page 17; 22pp; Japanese.  
PS  
XX The present invention relates to a new microbe of Actinobacter or  
CC Burkholderis genus producing aldonic acid and oxidizing specifically the  
CC hemiacetal hydroxy group of a saccharide having said hydroxy group.  
CC Aldonic acid is used as a mineral reinforcing agent. The present sequence  
CC was used to illustrate the present invention.  
XX  
SQ Sequence 1745 BP; 448 A; 382 C; 465 G; 450 T; 0 other;  
XX  
Query Match 74.8%; Score 17.2; DB 24; Length 1745;  
Best Local Similarity 63.6%; Pred. No. 72;  
Matches 14; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
QY 2 CGAAGTCGAGCGGCTTTCAGCATG 23  
DB 167 CGAAGTCGAGCGGCTTTCAGCATG 146  
XX  
RESULT 8  
ID AA199683 standard; DNA; 4403765 BP.  
XX AA199683;  
AC 15-JAN-2002 (first entry)  
DT Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 2.  
XX Mycobacterium tuberculosis strain H37Rv; strain CDC 1551; genome;  
DE Mycobacterium tuberculosis; patient treatment; epidemic monitoring; ds.  
XX Mycobacterium tuberculosis.  
OS Mycobacterium tuberculosis.  
XX US6294328-B1.  
PN 25-SEP-2001.  
XX 24-JUN-1998; 98US-0103840.  
PF 24-JUN-1998; 98US-0103840.  
XX 24-JUN-1998; 98US-0103840.  
PR (GENO-) INST GENOMIC RES.  
XX (GENO-) INST GENOMIC RES.  
PA Fletschmann RD, White OR, Fraser CM, Venter JC;  
XX Fletschmann RD, White OR, Fraser CM, Venter JC;  
PI WPI; 2001-647261/74.  
DR  
XX Evaluating strain variation of Mycobacterium tuberculosis, comprises  
PT determining the nucleotide sequence of the strain at positions in the  
PT genome corresponding to positions where M. tuberculosis strains CDC  
PT 1551 and H37Rv differ -  
XX  
PS Claim 4; SEQ ID NO 2; 3pp + Sequence Listing; English.  
XX  
The invention relates to evaluating strain variation within and between  
CC different populations of the tuberculosis bacterial pathogen,  
CC Mycobacterium tuberculosis or related Mycobacterium by determining the  
CC nucleotide sequence of the first strain at positions in the complete  
CC sequence of the genome that correspond to positions that differ in the  
CC nucleotide sequences of M. tuberculosis strains CDC 1551 (AA199683) and  
CC H37Rv (AA199682). The method is useful for evaluating strain variation of  
CC M. tuberculosis and has valuable application in the fields of  
CC tuberculosis genetics, epidemiology, patient treatment and epidemic  
CC monitoring.  
CC Note: The sequence data for this patent did not form part of the printed

```

RESULT 10
ID ABA44550/c
XX ABA44550 standard; DNA; 454 BP.
AC ABA44550;
XX
XX
DT 01-FEB-2002 (first entry)
XX
DE Human breast cell single exon nucleic acid probe #3245.
XX
KW Human; microarray; single exon probe; gene expression; breast;
disease; cancer; ss.
OS Homo sapiens.
PN WO200157271-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00662.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0633366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-496933/54.
XX
DR
XX
PT New spatially-addressable set of single exon nucleic acid probes,
PT useful for measuring gene expression in sample derived from human
PR breast, comprises number of single exon nucleic acid probes
XX
PS Claim 1; SEQ ID NO 3245; 327bp + sequence listing; English.
XX
XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and B7 474 cells. The method involves contacting
CC the probes with a collection of detectably labeled nucleic acids
CC derived from mRNA of human breast, and then measuring the label
CC bound to each probe of the microarray. The probes are useful for
CC verifying the expression of regions of genomic DNA predicted to
CC encode proteins. They are useful for gene discovery, and for
CC determining predisposition and/or prognosing breast disease. Gene
CC expression analysis is useful for assessing the toxicity of chemical
CC agents on cells. The microarray of this invention presents a far greater
CC diversity of probes for measuring gene expression, with far less bias
CC than expressed sequence tag microarrays. The method is suitable for
CC rapid production of functional information from genomic sequence. The
CC present sequence is a single exon nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX
SQ Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;
XX
XX
Query Match 73.0%; Score 16.8; DB 22; Length 454;
Best Local Similarity 65.0%; Pred. No. 97;
Matches 13; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
XX
4 AAGTCGAGGCGCTTCGATG 23
|||||:|||||:|||||
201 AAGTAGAGGCTTTCGATG 182

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```

RESULT 11
ABA54997/C
ID ABA54997 standard; DNA: 454 BP.
XX
AC ABA54997;
XX
DT 01-FEB-2002 (first entry)
XX
DE Human foetal liver single exon nucleic acid probe #3302.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00669.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI: 2001-483447/52.
XX
DR Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human fetal liver.
XX
PS Claim 1; SEQ ID NO 3302; 639pp + sequence listing; English.
XX
CC The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal
CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC foetal liver. The present sequence is a single exon nucleic acid
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;

Query Match 73.0%; Score 16.8; DB 22; Length 454;
Best Local Similarity 65.0%; Pred. NO. 97;
Matches 13; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 4 AAGUCGAGCCUUCAGCAUG 23
DB 201 AAGTAGAGCCTTTCGATG 182

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```

XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00666.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI: 2001-488899/53.
XX
DR Single exon nucleic acid probes for analyzing gene expression in human
PT hearts.
XX
PS Claim 1; SEQ ID NO 3226; 530pp; English.
XX
CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived
CC from the human heart via microarrays. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognosing diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;

Query Match 73.0%; Score 16.8; DB 22; Length 454;
Best Local Similarity 65.0%; Pred. NO. 97;
Matches 13; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 4 AAGUCGAGCCUUCAGCAUG 23
DB 201 AAGTAGAGCCTTTCGATG 182

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```

RESULT 12
ABA24760/C
ID ABA24760 standard; DNA: 454 BP.
XX
AC ABA24760;
XX
DT 23-JAN-2002 (first entry)
XX
DE Probe #3226 for gene expression analysis in human heart cell sample.
XX
KW Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.

```

```

RESULT 13
AAK03266/C
ID AAK03266 standard; DNA: 454 BP.
XX
AC AAK03266;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe SEQ ID NO: 3257.
XX
KW Human; brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00667.

```

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XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains -
XX
XX Example 4; SEQ ID NO: 3257; 650pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is one of the probes of the
XX invention.
XX
XX Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;
XX
XX Query Match 73.0%; Score 16.8; DB 22; Length 454;
XX Best Local Similarity 65.0%; Pred. No. 97;
XX Matches 13; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
OY 4 AAGCGAGCGCTTCTGCATG 23
DB 201 AAGTAGAGGCTTCTGCATG 182
XX
XX RESULT 14
XX ID AAK28719 standard; DNA; 454 BP.
XX AC AAK28719;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human bone marrow expressed single exon probe SEQ ID NO: 3276.
XX
XX Human bone marrow expressed exon; gene expression analysis; probe;
XX microarray; cancer; leukemia; lymphoma; myeloma; ss.
XX
XX Homo sapiens.
XX
XX WO200157276-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00668.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488900/53.
XX

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XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human bone marrow -
XX
XX Example 4; SEQ ID NO: 3276; 658pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX bone marrow. They can be used to measure gene expression in bone marrow
XX samples, which may enable the improved diagnosis and treatment of cancers
XX such as lymphoma, leukemia and myeloma. The present sequence is one of
XX the probes of the invention.
XX
XX Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;
XX
XX Query Match 73.0%; Score 16.8; DB 22; Length 454;
XX Best Local Similarity 65.0%; Pred. No. 97;
XX Matches 13; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
OY 4 AAGCGAGCGCTTCTGCATG 23
DB 201 AAGTAGAGGCTTCTGCATG 182
XX
XX RESULT 15
XX ID AAI13296 standard; DNA; 454 BP.
XX AC AAI13296;
XX
XX 12-OCT-2001 (first entry)
XX
XX Probe #3229 for gene expression analysis in human cervical cell sample.
XX
XX Probe; human; microarray; gene expression; cervical epithelial cell;
XX cervical cancer; ss.
XX
XX Homo sapiens.
XX
XX WO200157276-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00670.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488901/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human cervical epithelial cells -
XX
XX Claim 25; SEQ ID NO 3229; 487pp; English.
XX
XX The present invention relates to human single exon nucleic acid probes
XX (SENPs). The present sequence is one such probe. The SENPs are derived
XX from human HeLa cells. The SENPs can be used to produce a single exon
XX microarray, which can be used for measuring human gene expression in a
XX sample derived from human cervical epithelial cells. By measuring gene
XX expression, the probes are therefore useful in grading and/or staging
XX of diseases of the cervix, notably cervical cancer.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX

```

CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 454 BP; 135 A; 84 C; 120 G; 115 T; 0 other;

Query Match 73.0%; Score 16.8; DB 22; Length 454;  
 Best Local Similarity 65.0%; Pred. No. 97;  
 Matches 13; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 4 AAGGCGAGGCTTTCGATG 23  
 DB 201 AAGTACAGGCTTTCGATG 182

Search completed: June 12, 2003, 01:45:17  
 Job time : 135.802 secs

GenCore version 5.1.6  
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OK nucleic - nucleic search, using sw model

Run on: June 12, 2003, 01:18:34 ; Search time 22.066 Seconds

(without alignments)  
319.658 Million cell updates/sec

Title: US-09-674-195C-20

Sequence: 1 rcgaagcagcagcagcagcagcagc 23

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

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2: /cgn2\_6/ptodata/1/lna/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/1/lna/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/1/lna/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/1/lna/PCITUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/1/lna/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	22	95.7	22	1	US-07-720-587A-1
2	17.2	74.8	4403765	4	US-09-103-840A-2
3	17.2	74.8	4411529	4	US-09-103-840A-1
4	16.2	70.4	1722	1	US-08-055-945-1
5	15.8	68.7	738	2	US-08-224-591-13
6	15.8	68.7	738	2	US-08-392-338A-22
7	15.8	68.7	738	2	US-08-926-789-13
8	15.8	68.7	738	3	US-09-166-750-22
9	15.8	68.7	738	3	US-09-166-093-22
10	15.8	68.7	738	3	US-09-172-019-22
11	15.8	68.7	738	5	US-09-166-094-22
12	15.8	68.7	738	5	PCT-US93-11138-13
13	15.8	68.7	744	2	US-08-392-338A-12
14	15.8	68.7	744	3	US-09-166-750-12
15	15.8	68.7	744	3	US-09-166-093-12
16	15.8	68.7	744	3	US-09-172-019-12
17	15.8	68.7	744	3	US-09-166-094-12
18	15.8	68.7	758	4	US-09-069-821-1
19	15.8	68.7	782	4	US-09-420-592A-1
20	15.8	68.7	797	1	US-08-323-445A-3
21	15.8	68.7	797	1	US-08-515-903A-3
22	15.8	68.7	797	5	PCT-US95-12840-3
23	15.8	68.7	803	1	US-08-323-445A-7
24	15.8	68.7	803	1	US-08-515-903A-7
25	15.8	68.7	803	5	PCT-US95-12840-7
26	15.8	68.7	818	4	US-09-420-592A-3
27	15.8	68.7	870	1	US-08-411-706-1

C 28	15.8	68.7	1460	2	US-08-392-338A-18	Sequence 18, App1
C 29	15.8	68.7	1460	3	US-09-166-750-18	Sequence 18, App1
C 30	15.8	68.7	1460	3	US-09-166-093-18	Sequence 18, App1
C 31	15.8	68.7	1460	3	US-09-172-019-18	Sequence 18, App1
C 32	15.8	68.7	1460	3	US-09-166-094-18	Sequence 18, App1
C 33	15.8	68.7	12412	1	US-08-390-878-18	Sequence 18, App1
C 34	15.8	68.7	4403765	4	US-09-103-840A-2	Sequence 2, App1
C 35	15.6	67.8	2033	1	US-08-148-910-14	Sequence 14, App1
C 36	15.6	67.8	2293	1	US-08-448-937A-14	Sequence 14, App1
C 37	15.6	67.8	2293	1	US-09-645-073-1	Sequence 14, App1
C 38	15.4	67.0	9515	1	US-08-920-812-13	Sequence 13, App1
C 39	15.4	67.0	9515	1	US-08-920-827-13	Sequence 13, App1
C 40	15.4	67.0	9515	1	US-08-921-177-13	Sequence 13, App1
C 41	15.4	67.0	9515	1	US-08-362-577C-13	Sequence 13, App1
C 42	15.4	67.0	9515	2	US-08-920-828-13	Sequence 13, App1
C 43	15.2	66.1	5222	4	US-09-221-017B-1065	Sequence 1065, App
C 44	15.2	66.1	705	4	US-08-928-416-281	Sequence 281, App
C 45	15.2	66.1	1029	2	US-08-899-011-1	Sequence 1, App1

#### ALIGNMENTS

RESULT 1  
US-07-720-587A-1  
Sequence 1, Application US/07720587A

Patent No. 5352579

GENERAL INFORMATION:

APPLICANT: Curt L. Millman

TITLE OF INVENTION: NUCLEIC ACIDS PROBES

TITLE OF INVENTION: TO HISTOPLASMA CAPSULATUM

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESS: 611 West Sixth Street

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90017

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)

SOFTWARE: WordPerfect (Version 5.0)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07720,587A

FILING DATE: 19910628

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: including application

PRIOR APPLICATION DATA: described below:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Wardburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 193/121

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 22

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

US-07-720-587A-1

Query Match 95.7% Score 22; DB 1; Length 22;  
Best Local Similarity 77.3% Pred. No. 0.022;  
Matches 17; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGAAGUCGAGCCUUCACGAUG 23  
|||||:|||||:|||||:1  
DB 1 CGAAGTCGAGGCTTCACCATG 22

## RESULT 2

US-09-103-840A-2  
; Sequence 2, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; TITLE OF INVENTION: TUBERCULOSIS  
; FILE REFERENCE: 24366-20007.00  
; CURRENT APPLICATION NUMBER: US/09/103,840A  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 4403765  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; FEATURE:  
; OTHER INFORMATION: CDC 1551  
; OTHER INFORMATION: "n" bases at various positions throughout the sequence  
US-09-103-840A-2

Query Match 74.8%; Score 17.2; DB 4; Length 4403765;  
Best Local Similarity 63.6%; Pred. No. 28;  
Matches 14; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGAAGUCGAGCCUUCACGAUG 23  
|||:|||||:|||||:1  
DB 172050 CGCTGTGAGGCTTCACCATG 172071

## RESULT 3

US-09-103-840A-1  
; Sequence 1, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; TITLE OF INVENTION: TUBERCULOSIS  
; FILE REFERENCE: 24366-20007.00  
; CURRENT APPLICATION NUMBER: US/09/103,840A  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 4411529  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; OTHER INFORMATION: H37Rv  
US-09-103-840A-1

Query Match 74.8%; Score 17.2; DB 4; Length 4411529;  
Best Local Similarity 63.6%; Pred. No. 28;  
Matches 14; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGAAGUCGAGCCUUCACGAUG 23  
|||:|||||:|||||:1  
DB 171881 CGCTGTGAGGCTTCACCATG 171902

## RESULT 4

US-08-055-945-1  
; Sequence 1, Application US/08055945  
; Patent No. 5462855  
; GENERAL INFORMATION:  
; APPLICANT: Springer, Wolfgang; Rast, Hans George;  
; APPLICANT: L boerding, Antonius; and Kanne, Reinhard  
; TITLE OF INVENTION: A METHOD FOR THE DETECTION AND  
; TITLE OF INVENTION: QUANTITATIVE DETERMINATION OF  
; TITLE OF INVENTION: NITROSOMONAS STRAINS IN  
; TITLE OF INVENTION: WASTEWATERS OR SOILS  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SPRUNG HORN KRAMER & WOODS  
; STREET: 1140 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 1.2 MB  
; MEDIUM TYPE: storage  
; COMPUTER: NEC Powermate 1 Plus  
; OPERATING SYSTEM: DOS  
; SOFTWARE: WordPerfect 5.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/055,945  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/692,745  
; FILING DATE: NO. 5462855e  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kuit G. Briscoe  
; REGISTRATION NUMBER: 33,141  
; REFERENCE/DOCKET NUMBER: Bayer 8194-KGB  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 391-0520  
; TELEFAX: (212) 382-0949  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1722 bp  
; TYPE: Nucleotide  
; STRANDEDNESS: Double  
; TOPOLOGY: Linear  
; MOLECULE TYPE: genomic DNA  
US-08-055-945-1

Query Match 70.4%; Score 16.2; DB 1; Length 1722;  
Best Local Similarity 60.9%; Pred. No. 35;  
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 RCGAAGUCGAGCCUUCACGAUG 23  
:||||:|||||:|||||:1  
DB 397 CGGATGTCGAGGCTATCTCCGTG 419

## RESULT 5

US-08-224-591-13/c  
; Sequence 13, Application US/08224591  
; Patent No. 5856456  
; GENERAL INFORMATION:  
; APPLICANT: Whitlow, Marc  
; APPLICANT: Filippula, David  
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/224,591  
FILING DATE: Herewith  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/002,845  
FILING DATE: 15-JAN-1993  
APPLICATION NUMBER: US 07/980,529  
FILING DATE: 20-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.1920002/JAG  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 738 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(1..726)  
US-08-224-591-13

Query Match 68.7%; Score 15.8; DB 2; Length 738;  
Best Local Similarity 68.4%; Pred. No. 49;  
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGUGAGGCUUCAGCA 21  
Db 350 GAAGTAGAGCCTTCAGCA 332

RESULT 6  
US-08-392-338A-22/c  
Sequence 22, Application US/08392338A  
Patent No. 5869620  
GENERAL INFORMATION:  
APPLICANT: Whitlow, Marc  
APPLICANT: Wood, James F.  
APPLICANT: Hardman, Karl  
APPLICANT: Bird, Robert  
APPLICANT: Filpula, David  
TITLE OF INVENTION: Multivalent Antigen-Binding Proteins  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, NW  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/392,338A  
FILING DATE: 22-FEB-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/989,846  
FILING DATE: 20-NOV-1992  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/796,936  
FILING DATE: 23-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.0030007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 738 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..726  
US-08-392-338A-22

Query Match 68.7%; Score 15.8; DB 2; Length 738;  
Best Local Similarity 68.4%; Pred. No. 49;  
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGUGAGGCUUCAGCA 21  
Db 350 GAAGTAGAGCCTTCAGCA 332

RESULT 7  
US-08-926-789-13/c  
Sequence 13, Application US/08926789  
Patent No. 5980275  
GENERAL INFORMATION:  
APPLICANT: Whitlow, Marc  
APPLICANT: Filpula, David  
TITLE OF INVENTION: Linker for Linked Fusion Polypeptides  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/926,789  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/224,591  
FILING DATE:  
APPLICATION NUMBER: US 08/002,845  
FILING DATE: 15-JAN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/980,529  
FILING DATE: 20-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.1920002/JAG  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 738 base pairs  
TYPE: nucleic acid

US-09-166-750-22

DB 350 GAAGTAGAGCCCTTTCACCA 332

```

RESULT 10
US-09-172-019-22/c
: Sequence 22, Application US/09172019
: Patent No. 6103889
: GENERAL INFORMATION:
: APPLICANT: Whittlow, Marc
: APPLICANT: Hardman, Karl
: APPLICANT: Bird, Robert
: APPLICANT: Filpula, David
: TITLE OF INVENTION: Nucleic Acid Molecules Encoding Single-Chain
: TITLE OF INVENTION: Antigen-Binding Proteins (As Amended)
: NUMBER OF SEQUENCES: 23
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
: STREET: 1100 New York Avenue, NW
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentia Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/172,019
: FILING DATE: Herewith
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/392,338
: FILING DATE: 22-FEB-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/989,846
: FILING DATE: 20-NOV-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/796,936
: FILING DATE: 25-NOV-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Goldstein, Jorge A.
: REGISTRATION NUMBER: 29,021
: REFERENCE/DOCKET NUMBER: 0977.003000D
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 371-2600
: TELEFAX: (202) 371-2540
: INFORMATION FOR SEQ ID NO: 22:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 738 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: both
: TOPOLOGY: both
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..726
: US-09-172-019-22

Query Match          68.7%; Score 15.8; DB 3; Length 738;
Best Local Similarity 68.4%; Pred. No. 49;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY      3 GAAGUCGAGCGCUCUOCACGA 21
      |||||:||||:|||||
Db      350 GAAGTAGAGCCTTCACGA 332

RESULT 11
US-09-166-094-22/c
: Sequence 22, Application US/09166094
: Patent No. 6121424
: GENERAL INFORMATION:
: APPLICANT: Whittlow, Marc
: APPLICANT: Wood, James F.
: APPLICANT: Hardman, Karl

```

```

? APPLICANT: Bird, Robert
? APPLICANT: Filpula, David
? APPLICANT: Rolence, Michelle
? TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
? NUMBER OF SEQUENCES: 23
? CORRESPONDENCE ADDRESSES:
? ADDRESSSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
? STREET: 1100 New York Avenue, NW
? CITY: Washington
? STATE: D.C.
? COUNTRY: U.S.A.
? ZIP: 20005
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/166,094
? FILING DATE: Herewith
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/392,338
? FILING DATE: 22-FEB-1995
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/989,846
? FILING DATE: 20-NOV-1992
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/796,936
? FILING DATE: 25-NOV-1991
? ATTORNEY/AGENT INFORMATION:
? NAME: Goldstein, Jorge A.
? REGISTRATION NUMBER: 29,021
? REFERENCE/DOCKET NUMBER: .0977.003000A
? TELECOMMUNICATION INFORMATION:
? TELEFAX: (202) 371-2540
? INFORMATION FOR SEQ ID NO: 22:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 738 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: both
? TOPOLOGY: both
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..726
? US-09-166-094-22
?
? Query Match 68.7% Score 15.8; DB 3; Length 738;
? Best Local Similarity 68.4%; Pred. No. 49;
? Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0.
?
? Oy 3 GAAGUCGAGCGCUUCACGA 21
? Db 350 GAAGTAGAGCCTTCACGA 332
?
? RESULT 12
? PCT-US93-11138-13/c
? Sequence 13, Application PC/TUS9311138
? GENERAL INFORMATION:
? APPLICANT: Enzon, Inc.
? TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
? NUMBER OF SEQUENCES: 14
? CORRESPONDENCE ADDRESSES:
? ADDRESSSEE: Sterne, Kessler, Goldstein & Fox
? STREET: 1100 New York Avenue, N.W.
? CITY: Washington
? STATE: D.C.
? COUNTRY: U.S.A.
? ZIP: 20005-3934
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11138
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/980,529
FILING DATE: 20-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,845
FILING DATE: 15-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.2006604/JAG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 738 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: 1..738
PCT-US93-11138-13

Query Match      68.7% Score 15.8; DB 5; Length 738;
Best Local Similarity 68.4%; Pred. No. 49;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY      3 GAAGUCGAGCCUUCACGA 21
      ||||| ||| |:::|||||
Db      350 GAAGTAGAGCCTTCACGA 332

RESULT 13
US-08-392-338A-12/C
Sequence 12, Application US/08392338A
Patent No. 5869620
GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
APPLICANT: Wood, James F.
APPLICANT: Hardman, Karl
APPLICANT: Bird, Robert
APPLICANT: Filpula, David
TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,338A
FILING DATE: 22-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/989,846
FILING DATE: 20-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,936
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FILING DATE: 25-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.0030007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 744 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: 1..732
US-08-392-338A-12

Query Match      68.7% Score 15.8; DB 2; Length 744;
Best Local Similarity 68.4%; Pred. No. 49;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY      3 GAAGUCGAGCCUUCACGA 21
      ||||| ||| |:::|||||
Db      350 GAAGTAGAGCCTTCACGA 332

RESULT 14
US-09-166-750-12/C
Sequence 12, Application US/09166750
Patent No. 6025165
GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
APPLICANT: Wood, James F.
APPLICANT: Hardman, Karl
APPLICANT: Bird, Robert
APPLICANT: Filpula, David
APPLICANT: Rollence, Michelle
TITLE OF INVENTION: Methods for Producing Multivalent Antigen-Binding
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/166,750
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/392,338
FILING DATE: 22-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/989,846
FILING DATE: 20-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,936
FILING DATE: 25-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.003000C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
```

TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 744 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..732  
US-09-166-750-12

Query Match  
Best Local Similarity 68.7%; Score 15.8; DB 3; length 744;  
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGUCGAGCCUUCAGCA 21  
|||||  
Db 350 GAAGTAGAGCCTTCAGCA 332

RESULT 15  
US-09-166-093-12/c

Sequence 12, Application US/09166093  
Patent No. 6027725

GENERAL INFORMATION:

APPLICANT: Whitlow, Marc  
APPLICANT: Wood, James F.

APPLICANT: Hardman, Karl  
APPLICANT: Bird, Robert

APPLICANT: Filpula, David  
APPLICANT: Rollence, Michelle

TITLE OF INVENTION: Multivalent Antigen-Binding Proteins  
NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Avenue, NW  
CITY: Washington

STATE: D.C.  
COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/166,093  
FILING DATE: Herewith

CLASSIFICATION:  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/392,338  
FILING DATE: 22-FEB-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/989,846

FILING DATE: 20-NOV-1992  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/796,936  
FILING DATE: 25-NOV-1991

ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.

REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.003000B

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:  
LENGTH: 744 base pairs

TYPE: nucleic acid  
STRANDEDNESS: both

TOPOLOGY: both  
FEATURE:

NAME/KEY: CDS  
LOCATION: 1..732  
US-09-166-093-12

Query Match  
Best Local Similarity 68.7%; Score 15.8; DB 3; length 744;  
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGUCGAGCCUUCAGCA 21  
|||||  
Db 350 GAAGTAGAGCCTTCAGCA 332

Search completed: June 12, 2003, 04:40:53  
Job time : 55.066 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 01:27:04 ; Search time 134.361 Seconds  
(without alignments)  
239.539 Million cell updates/sec

Title: US-09-674-195c-20

Perfect score: 23  
Sequence: 1 rcgaagucgagcucnucagcaug 23

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

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12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.2	74.8	1691139	9	US-10-067-514-1
2	16.8	73.0	454	10	US-09-864-761-3226
3	16.8	73.0	891	9	US-09-989-643-155
4	16.2	70.4	1097	10	US-09-974-300-179
5	15.8	68.7	550	9	US-09-991-936-838
6	15.8	68.7	723	10	US-09-791-578-5
7	15.8	68.7	723	9	US-09-791-540-5
8	15.8	68.7	758	9	US-09-956-086-1
9	15.8	68.7	758	9	US-09-956-087-1
10	15.8	68.7	782	9	US-09-985-442-1
11	15.8	68.7	782	10	US-09-791-578-3
12	15.8	68.7	782	10	US-09-791-540-3
13	15.8	68.7	782	10	US-09-983-580-1
14	15.8	68.7	818	9	US-09-985-442-3
15	15.8	68.7	818	10	US-09-983-580-3
16	15.8	68.7	981	10	US-09-770-445-271
17	15.8	68.7	1279	9	US-10-165-603-19
18	15.8	68.7	1413	9	US-09-894-844-25
19	15.8	68.7	1579	10	US-09-822-849A-139

20	15.6	67.8	310	10	US-09-878-574-665	Sequence 665, App
21	15.6	67.8	375	10	US-09-878-574-3603	Sequence 3603, App
22	15.6	67.8	397	10	US-09-867-701-8410	Sequence 8410, App
23	15.6	67.8	933	9	US-09-938-842A-536	Sequence 536, App
24	15.6	67.8	1014	10	US-09-815-242-7828	Sequence 7828, App
25	15.6	67.8	2036	10	US-09-954-456-552	Sequence 552, App
26	15.6	67.8	2036	10	US-09-880-107-1612	Sequence 1612, App
27	15.6	67.8	20556	10	US-09-880-107-3945	Sequence 3945, App
28	15.6	67.8	177556	9	US-09-952-2130-6	Sequence 6, Appl1
29	15.4	67.0	351	10	US-09-770-791-655	Sequence 695, App
30	15.2	66.1	365	10	US-09-783-590-10265	Sequence 10265, A
31	15.2	66.1	427	10	US-09-960-352-3997	Sequence 3997, App
32	15.2	66.1	477	10	US-09-864-761-2467	Sequence 2467, App
33	15.2	66.1	761	10	US-09-770-445-961	Sequence 961, App
34	15.2	66.1	768	10	US-09-910-943-408	Sequence 408, App
35	15.2	66.1	843	9	US-10-164-433-1	Sequence 1, Appl1
36	15.2	66.1	1186	9	US-09-925-299-98	Sequence 98, Appl1
37	15.2	66.1	1186	9	US-09-925-299-98	Sequence 98, Appl1
38	15.2	66.1	1602	9	US-10-198-846-13522	Sequence 13522, A
39	15.2	66.1	1604	9	US-10-114-893-187	Sequence 187, App
40	15.2	66.1	3119	10	US-09-867-701-10873	Sequence 10873, A
41	15.2	66.1	7090	9	US-09-832-292-28	Sequence 28, Appl1
42	15.2	66.1	8268	9	US-10-074-095-868	Sequence 868, App
43	15.2	66.1	8268	10	US-09-764-860-868	Sequence 868, App
44	15.2	66.1	8272	9	US-10-074-095-867	Sequence 867, App
45	15.2	66.1	8272	10	US-09-764-860-867	Sequence 867, App

## ALIGNMENTS

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RESULT 1
US-10-067-514-1
; Sequence 1, Application US/10067514
; Publication No US20030054531A1
; GENERAL INFORMATION:
; APPLICANT: Grelatsdotlir, Solveig
; APPLICANT: Jonasdottir, Sif
; APPLICANT: Reynisdottir, Sigridur Th.
; TITLE OF INVENTION: HUMAN STROKE GENE
; FILE REFERENCE: 2345.2010-003
; CURRENT APPLICATION NUMBER: US/10/067, 514
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: US 09/811/352
; FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1691139
; TYPE: DNA
; ORGANISM: Human
; US-10-067-514-1

Query Match      74.8% Score 17.2; DB 9; Length 1691139;
Best Local Similarity 63.6%; Pred. No. 41;
Matches 14; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      2 CGAAGUCGAGCUCUUCAGCAUG 23
DB      758783 CGAAGCTATGCTTCAGCATG 758804

RESULT 2
US-09-864-761-3226/c
; Sequence 3226, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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FILE REFERENCE: Aesomica-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GR 24263, 6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 3226  
LENGTH: 454  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AL050331.11  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.99  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2  
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.2  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3  
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.3  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4  
US-09-864-761-3226

Query Match 73.0%, Score 16.8; DB 10; Length 454;  
Best Local Similarity 65.0%; Pred. No. 36;  
Matches 13; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 4 AAGUCAGCCUUCAGCAUG 23  
|||:|||||:|||||  
DB 201 AAGTAGAGCTTTCGATG 182

RESULT 3  
US-09-989-643-155/c  
Sequence 155, Application US/09989643  
Publication No. US20030049636a1  
GENERAL INFORMATION:

APPLICANT: Bergeron, Michel G.  
APPLICANT: Picard, Francois J.  
APPLICANT: Ouellette, Marc  
APPLICANT: Roy, Paul H.  
TITLE OF INVENTION: Species-Specific, Genus-Specific and Universal DNA  
TITLE OF INVENTION: Probes and Amplification Primers to Rapidly Detect and  
TITLE OF INVENTION: Identify Common Bacterial and Fungal Pathogens and  
TITLE OF INVENTION: Associated Antibiotic Resistance Genes from  
FILE REFERENCE: 12287/29  
CURRENT APPLICATION NUMBER: US/09/989,643  
CURRENT FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/297,539  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-09  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/743,637  
PRIOR FILING DATE: EARLIER FILING DATE: 1996-11-04  
NUMBER OF SEQ ID NOS: 174  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 155  
LENGTH: 891  
TYPE: DNA  
ORGANISM: Fibrobacter succinogenes  
US-09-989-643-155

Query Match 73.0%, Score 16.8; DB 9; Length 891;  
Best Local Similarity 59.1%; Pred. No. 38;  
Matches 13; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 1 RCGAAGUCAGCCUUCAGCAU 22  
|||:|||||:|||||  
DB 179 ACGAGTCGAGATTTCGAT 158

RESULT 4  
US-09-974-300-179  
Sequence 179, Application US/09974300  
Patent No. US20020146721A1  
GENERAL INFORMATION:  
APPLICANT: Berka, Randy M.  
APPLICANT: Clausen, Ib Groth  
TITLE OF INVENTION: Methods For Monitoring Multiple Gene  
TITLE OF INVENTION: Expression  
FILE REFERENCE: 10085,500-US  
CURRENT APPLICATION NUMBER: US/09/974,300  
CURRENT FILING DATE: 2001-10-05  
PRIOR APPLICATION NUMBER: 09/680,598  
PRIOR FILING DATE: 2000-10-06  
PRIOR APPLICATION NUMBER: 60/279,526  
PRIOR FILING DATE: 2001-03-27  
NUMBER OF SEQ ID NOS: 8481  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 179  
LENGTH: 1097  
TYPE: DNA  
ORGANISM: Bacillus licheniformis  
US-09-974-300-179

Query Match 70.4%, Score 16.2; DB 10; Length 1097;  
Best Local Similarity 61.9%; Pred. No. 79;  
Matches 13; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 CGAAGUCAGCCUUCAGCAU 22  
|||:|||||:|||||  
DB 315 CCGAGTCGCGCCCTTTCAGCAT 335

RESULT 5  
US-09-991-936-838  
Sequence 838, Application US/09991936  
Publication No. US20030073827A1  
GENERAL INFORMATION:  
APPLICANT: Brandt, Kevin S.  
APPLICANT: Gaines, Patrick J.  
APPLICANT: Stinchcomb, Dan T.

APPLICANT: Wisniewski, Nancy  
TITLE OF INVENTION: FLEA HEAD, NERVE CORD, HINDGUT AND MALPIGHIAN TUBULE  
FILE REFERENCE: FC-6-C1  
CURRENT APPLICATION NUMBER: US/09/991,936  
PRIORITY FILING DATE: 2001-11-21  
PRIORITY APPLICATION NUMBER: US/09/543,668  
PRIORITY FILING DATE: 2000-04-07  
PRIORITY APPLICATION NUMBER: 60/128,704  
PRIORITY FILING DATE: 1999-04-09  
NUMBER OF SEQ ID NOS: 1959  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 838  
LENGTH: 550  
TYPE: DNA  
ORGANISM: Ctenocephalides felis  
US-09-991-936-838

Query Match 68.7%; Score 15.8; DB 9; Length 550;  
Best Local Similarity 68.4%; Pred. No. 1.2e+02;  
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGUCGAGCGUUCAGCA 21  
|||||:|||||:|||||  
Db 156 GAAGTGGAGCGTTTCACGA 174

RESULT 6  
US-09-791-578-5/c  
Sequence 5, Application US/09791578  
Patent No. US20020061307A1  
GENERAL INFORMATION:  
APPLICANT: WHITLOW, MARC  
SHORR, ROBERT G.L.  
FILIPULA, DAVID R.  
LEE, LIHSYNG S.  
TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN  
POLYPEPTIDES  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVENUE, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/791,578  
FILING DATE: 26-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 09/069,842  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 60/050,472  
FILING DATE: 23-JUN-1997  
APPLICATION NUMBER: US 60/063,074  
FILING DATE: 27-OCT-1997  
APPLICATION NUMBER: US 60/067,341  
FILING DATE: 02-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: JORGE A. GOLDSTEIN  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.1840002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:

LENGTH: 723 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..723  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-791-578-5

Query Match 68.7%; Score 15.8; DB 10; Length 723;  
Best Local Similarity 68.4%; Pred. No. 1.2e+02;  
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGUCGAGCGUUCAGCA 21  
|||||:|||||:|||||  
Db 350 GAAGTGGAGCGTTTCACGA 332

RESULT 7  
US-09-791-540-5/c  
Sequence 5, Application US/09791540  
Patent No. US20020098192A1  
GENERAL INFORMATION:  
APPLICANT: WHITLOW, MARC  
SHORR, ROBERT G.L.  
FILIPULA, DAVID R.  
LEE, LIHSYNG S.  
TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN  
POLYPEPTIDES  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVENUE, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/791,540  
FILING DATE: 26-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 09/069,842  
FILING DATE: 1998-04-30  
APPLICATION NUMBER: US 60/050,472  
FILING DATE: 23-JUN-1997  
APPLICATION NUMBER: US 60/063,074  
FILING DATE: 27-OCT-1997  
APPLICATION NUMBER: US 60/067,341  
FILING DATE: 02-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: JORGE A. GOLDSTEIN  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.1840002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 723 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..723  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-791-540-5

Query Match 68.7%: Score 15.8; DB 10; Length 723;

Best Local Similarity 68.4%: Pred. No. 1.2e+02;

Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGUCGAGCGUUCACGA 21

Db 350 GAAGTAGAGCCTTCACGA 332

RESULT 8

US-09-956-086-1/c

; Sequence 1, Application US/09956086

; Patent No. US20020155498A1

GENERAL INFORMATION:

APPLICANT: FILIPULA, DAVID

WANG, MAOLING

SHORR, ROBERT

WHITLOW, MARC

LEE, LISHYNG S.

TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS

CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESSES:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN &amp; FOX P.L.L.C.

STREET: 1100 NEW YORK AVE., NW, SUITE 600

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/956.086

FILING DATE: 20-Sep-2001

CLASSIFICATION: &lt;unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/069,821

FILING DATE: &lt;unknown&gt;

APPLICATION NUMBER: US 60/063,074

FILING DATE: 27-OCT-1997

APPLICATION NUMBER: US 60/050,472

FILING DATE: 23-JUN-1997

APPLICATION NUMBER: US 60/044,449

FILING DATE: 30-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: KIM, JUDITH U.

REGISTRATION NUMBER: 40,679

REFERENCE/DOCKET NUMBER: 0977.2280003

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)371-2600

TELEFAX: (202)371-2540

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 758 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..747

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-956-086-1

Query Match 68.7%: Score 15.8; DB 9; Length 758;

Best Local Similarity 68.4%: Pred. No. 1.2e+02;

Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGUCGAGCGUUCACGA 21

Db 350 GAAGTAGAGCCTTCACGA 332

RESULT 9

US-09-956-087-1/c

; Sequence 1, Application US/09956087

; Patent No. US20020161201A1

GENERAL INFORMATION:

APPLICANT: FILIPULA, DAVID

WANG, MAOLING

SHORR, ROBERT

WHITLOW, MARC

LEE, LISHYNG S.

TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS

CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESSES:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN &amp; FOX P.L.L.C.

STREET: 1100 NEW YORK AVE., NW, SUITE 600

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/956.087

FILING DATE: 20-Sep-2001

CLASSIFICATION: &lt;unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/069,821

FILING DATE: 1998-04-30

APPLICATION NUMBER: US 60/063,074

FILING DATE: 27-OCT-1997

APPLICATION NUMBER: US 60/050,472

FILING DATE: 23-JUN-1997

APPLICATION NUMBER: US 60/044,449

FILING DATE: 30-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: KIM, JUDITH U.

REGISTRATION NUMBER: 40,679

REFERENCE/DOCKET NUMBER: 0977.2280003.

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)371-2600

TELEFAX: (202)371-2540

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 758 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..747

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-956-087-1

Query Match 68.7%: Score 15.8; DB 9; Length 758;

Best Local Similarity 68.4%: Pred. No. 1.2e+02;

Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGUCGAGCGUUCACGA 21

Db 350 GAAGTAGAGCCTTCACGA 332

RESULT 10

US-09-985-442-1/C  
Sequence 1, Application US/09985442  
Patent No. US20020156248A1  
GENERAL INFORMATION:  
APPLICANT: FILIPULA, David R.  
APPLICANT: Wang, Maoliang  
APPLICANT: Whitlow, Marc D.  
TITLE OF INVENTION: NO. US20020156248A1 Method for Targeted Delivery of Nucleic Acids  
FILE REFERENCE: 0977.2300003  
CURRENT APPLICATION NUMBER: US/09/985,442  
CURRENT FILING DATE: 2001-11-02  
PRIOR APPLICATION NUMBER: 09/420,592  
PRIOR FILING DATE: 1999-10-19  
PRIOR APPLICATION NUMBER: 60/104,949  
PRIOR FILING DATE: 1998-10-20  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 1  
LENGTH: 782  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: CC49/218 sfv  
NAME/KEY: CDS  
LOCATION: (1)..(771)  
US-09-985-442-1

Query Match 68.7%; Score 15.8; DB 9; Length 782;  
Best Local Similarity 68.4%; Pred. No. 1.2e+02;  
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGUCGAGCCUUCACGA 21  
DB 350 GAAGTAGAGCCTTCACGA 332

RESULT 11  
US-09-791-578-3/C  
Sequence 3, Application US/09791578  
Patent No. US20020061307A1  
GENERAL INFORMATION:  
APPLICANT: WHITLOW, MARC  
SHORR, ROBERT G.L.  
FILIPULA, DAVID R.  
LEE, LHSYNG S.  
TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN  
POLYPEPTIDES  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVENUE, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/791,578  
FILING DATE: 26-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/069,842  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 60/050,472  
FILING DATE: 23-JUN-1997  
APPLICATION NUMBER: US 60/063,074  
FILING DATE: 27-OCT-1997  
APPLICATION NUMBER: US 60/067,341  
FILING DATE: 02-DEC-1997

ATTORNEY/AGENT INFORMATION:  
NAME: JORGE A. GOLDSTEIN  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.1840002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 782 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..771  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-791-578-3

Query Match 68.7%; Score 15.8; DB 10; Length 782;  
Best Local Similarity 68.4%; Pred. No. 1.2e+02;  
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAAGUCGAGCCUUCACGA 21  
DB 350 GAAGTAGAGCCTTCACGA 332

RESULT 12  
US-09-791-540-3/C  
Sequence 3, Application US/09791540  
Patent No. US20020098192A1  
GENERAL INFORMATION:  
APPLICANT: WHITLOW, MARC  
SHORR, ROBERT G.L.  
FILIPULA, DAVID R.  
LEE, LHSYNG S.  
TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN  
POLYPEPTIDES  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVENUE, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/791,540  
FILING DATE: 26-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/069,842  
FILING DATE: 1998-04-30  
APPLICATION NUMBER: US 60/050,472  
FILING DATE: 23-JUN-1997  
APPLICATION NUMBER: US 60/063,074  
FILING DATE: 27-OCT-1997  
APPLICATION NUMBER: US 60/067,341  
FILING DATE: 02-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: JORGE A. GOLDSTEIN  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.1840002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540

```

; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 782 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: both
;   TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 1..771
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-791-540-3

Query Match      68.7%; Score 15.8; DB 10; Length 782;
Best Local Similarity 68.4%; Pred. No. 1.2e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      3 GAAGUCGAGCCUUCACGA 21
      ||||| ||| |:::|||||
DB      350 GAAGTAGAGCCTTCACGA 332

RESULT 13
US-09-983-580-1/c
; Sequence 1, Application US/09983580
; Patent No. US20020151061A1
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: NO. US20020151061A1 Method for Targeted Delivery of Nucleic Acid
; FILE REFERENCE: 0977.2300002
; CURRENT APPLICATION NUMBER: US/09/983,580
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/420,592
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 782
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CC49/218 sfv
; NAME/KEY: CDS
; LOCATION: (1)..(771)
US-09-983-580-1

Query Match      68.7%; Score 15.8; DB 10; Length 782;
Best Local Similarity 68.4%; Pred. No. 1.2e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      3 GAAGUCGAGCCUUCACGA 21
      ||||| ||| |:::|||||
DB      350 GAAGTAGAGCCTTCACGA 332

RESULT 14
US-09-985-442-3/c
; Sequence 3, Application US/09985442
; Patent No. US20020156248A1
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: NO. US20020156248A1 Method for Targeted Delivery of Nucleic Acid
; FILE REFERENCE: 0977.2300003
; CURRENT APPLICATION NUMBER: US/09/985,442
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/420,592
; PRIOR FILING DATE: 1999-10-19
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; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 818
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CC49/218 sfv
; NAME/KEY: CDS
; LOCATION: (1)..(807)
US-09-985-442-3

Query Match      68.7%; Score 15.8; DB 9; Length 818;
Best Local Similarity 68.4%; Pred. No. 1.3e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      3 GAAGUCGAGCCUUCACGA 21
      ||||| ||| |:::|||||
DB      350 GAAGTAGAGCCTTCACGA 332

RESULT 15
US-09-983-580-3/c
; Sequence 3, Application US/09983580
; Patent No. US20020151061A1
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: NO. US20020151061A1 Method for Targeted Delivery of Nucleic Acid
; FILE REFERENCE: 0977.2300002
; CURRENT APPLICATION NUMBER: US/09/983,580
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/420,592
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 818
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CC49/218 sfv
; NAME/KEY: CDS
; LOCATION: (1)..(807)
US-09-983-580-3

Query Match      68.7%; Score 15.8; DB 10; Length 818;
Best Local Similarity 68.4%; Pred. No. 1.3e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      3 GAAGUCGAGCCUUCACGA 21
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DB      350 GAAGTAGAGCCTTCACGA 332

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Title: US-09-674-195C-20

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Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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8: em\_hlc:\*  
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27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	18.8	81.7	362	12	BF251811 EST419073
4	18.8	81.7	377	12	BF251964 EST419226
5	18.8	81.7	378	12	BF251967 EST419229
6	18.8	81.7	391	12	BF251561 EST418910

C 7	18.8	81.7	486	10	AW792005	AW792005 D00948-R
C 8	18.8	81.7	488	12	BF251704	BF251704 EST418888
C 9	18.8	81.7	502	12	BF252581	BF252581 EST419843
C 10	18.8	81.7	515	10	AW792430	AW792430 D01189-R
C 11	18.8	81.7	518	12	BF251715	BF251715 EST418899
C 12	18.8	81.7	541	12	BF252371	BF252371 EST419633
C 13	18.8	81.7	546	12	BF252094	BF252094 EST419356
C 14	18.8	81.7	557	12	BF252094	BF252094 EST419357
C 15	18.8	81.7	568	12	BF252878	BF252878 EST420141
C 16	18.8	81.7	572	12	BF252095	BF252095 EST419357
C 17	18.8	81.7	603	12	BF252135	BF252135 EST419397
C 18	18.8	81.7	679	12	BF251385	BF251385 EST418646
C 19	18.8	81.7	687	12	BF251001	BF251001 EST418258
C 20	18.8	81.7	701	12	BF251666	BF251666 EST418850
C 21	18.8	81.7	836	12	BF250962	BF250962 EST418219
C 22	18.4	80.0	578	14	W36400	W36400 mb/510.r1
C 23	17.8	77.4	222	10	AW791051	AW791051 D00369-R
C 24	17.8	77.4	661	17	BH738995	BH738995 BOHYR88TR
C 25	17.8	77.4	735	17	BH532538	BH532538 BCGM057TR
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C 28	17.8	77.4	914	17	CNS079PT	AL435727 T7 end of
C 29	17.8	77.4	944	17	CNS07827	AL434633 T3 end of
C 30	17.8	77.4	957	17	CNS0797C	AL434926 T3 end of
C 31	17.8	77.4	992	17	CNS0784M	AL433532 T3 end of
C 32	17.8	77.4	997	17	CNS076RE	AL436003 T3 end of
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C 35	17.8	77.4	1020	17	CNS076VC	AL433270 T7 end of
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C 40	17.2	74.8	176	9	A1213893	A1213893 27a0281.f
C 41	17.2	74.8	244	9	A1212196	A1212196 w9f07a1.f
C 42	17.2	74.8	250	9	AA784878	AA784878 g3a04a1.f
C 43	17.2	74.8	252	9	A1211979	A1211979 v7h05a1.f
C 44	17.2	74.8	260	9	A1329914	A1329914 cle02ne.r
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#### ALIGNMENTS

RESULT 1  
LOCUS BF251708 123 bp mRNA linear EST 15-NOV-2001  
DEFINITION BF251708 Coccidioides immitis spherule CDNA library Coccidioides immitis CDNA clone CIAK37 5' sequence, mRNA sequence.

ACCESSION BF251708 GI:169311774  
VERSION BF251708.1  
KEYWORDS EST.  
SOURCE Coccidioides immitis.  
ORGANISM Coccidioides immitis.  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; Mitosporic Onygenales; Coccidioides.

REFERENCE 1 (bases 1 to 123)  
AUTHORS Gardner, M.J. and Kirkland, T.  
TITLE Generation of ESTs from Coccidioides immitis spherule CDNA library  
JOURNAL Unpublished (2000)  
COMMENT Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org.

FEATURES  
source location/Qualifiers

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/organism="Coccidioides immitis"  
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/clone\_lib="Coccidioides immitis spherule CDNA library"

/dev\_stage="spherule"  
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XhoI"

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Best Local Similarity 68.2%; Pred. No. 58;  
Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

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80 CGAAGTCGAGGTTTTCAGCATG 59

RESULT 2  
BF251693/c 351 bp mRNA linear EST 15-NOV-2001  
LOCUS EST18877 Coccidioides immitis spherule cDNA library Coccidioides  
DEFINITION immitis cDNA clone CIAAK21 5' sequence, mRNA sequence.  
ACCESSION BF251693  
VERSION BF251693.1 GI:16931759  
KEYWORDS EST  
SOURCE Coccidioides immitis.  
ORGANISM Coccidioides immitis  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; Mitosporic Onygenales; Coccidioides.  
1 (bases 1 to 351)  
Gardner, M.J. and Kirkland, T.  
Generation of ESTs from Coccidioides immitis spherule cDNA library  
Unpublished (2000)  
Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org.  
Location/Qualifiers  
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/clone="CIAAK21"  
/clone\_1lb="Coccidioides immitis spherule cDNA library"  
/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI"

BASE COUNT 97 a 69 c 81 g 104 t

ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 351;  
Best Local Similarity 68.2%; Pred. No. 1.1e+02;  
Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 2 CGAAGUCGAGCCTTTCAGCATG 23  
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176 CGAAGTCGAGGTTTTCAGCATG 155

RESULT 3  
BF251811/c 362 bp mRNA linear EST 15-NOV-2001  
LOCUS EST19073 Coccidioides immitis spherule cDNA library Coccidioides  
DEFINITION immitis cDNA clone CIAAM73 5' sequence, mRNA sequence.  
ACCESSION BF251811  
VERSION BF251811.1 GI:16931954  
KEYWORDS EST  
SOURCE Coccidioides immitis.  
ORGANISM Coccidioides immitis  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; Mitosporic Onygenales; Coccidioides.

1 (bases 1 to 362)  
Gardner, M.J. and Kirkland, T.  
Generation of ESTs from Coccidioides immitis spherule cDNA library  
Unpublished (2000)  
Contact: Malcolm J. Gardner  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org.  
Location/Qualifiers  
1..362  
/organism="Coccidioides immitis"  
/db\_xref="taxon:5501"  
/clone="CIAAM73"  
/clone\_1lb="Coccidioides immitis spherule cDNA library"  
/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI"

BASE COUNT 98 a 69 c 84 g 111 t

ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 362;  
Best Local Similarity 68.2%; Pred. No. 1.1e+02;  
Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 2 CGAAGUCGAGCCTTTCAGCATG 23  
|||||:|||||:::|||||:  
171 CGAAGTCGAGGTTTTCAGCATG 150

RESULT 4  
BF251964/c 377 bp mRNA linear EST 15-NOV-2001  
LOCUS EST19226 Coccidioides immitis spherule cDNA library Coccidioides  
DEFINITION immitis cDNA clone CIAAP15 5' sequence, mRNA sequence.  
ACCESSION BF251964  
VERSION BF251964.1 GI:16932107  
KEYWORDS EST  
SOURCE Coccidioides immitis.  
ORGANISM Coccidioides immitis  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; Mitosporic Onygenales; Coccidioides.  
1 (bases 1 to 377)  
Gardner, M.J. and Kirkland, T.  
Generation of ESTs from Coccidioides immitis spherule cDNA library  
Unpublished (2000)  
Contact: Malcolm J. Gardner  
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Email: gardner@tigr.org.  
Location/Qualifiers  
1..377  
/organism="Coccidioides immitis"  
/db\_xref="taxon:5501"  
/clone="CIAAP15"  
/clone\_1lb="Coccidioides immitis spherule cDNA library"  
/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI"

BASE COUNT 103 a 85 c 94 g 95 t

ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 377;  
Best Local Similarity 68.2%; Pred. No. 1.1e+02;  
Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAAGCGAGCCUUCAGCAUG 23  
 DB 75 CGAAGTCGAGGTTTTCAGCATG 54

RESULT 5  
 LOCUS BF251967/c 378 bp mRNA linear EST 15-NOV-2001  
 DEFINITION EST419229 Coccidioides immitis spherule cDNA library Coccidioides immitis cDNA clone CIAK57 5' sequence, mRNA sequence.

ACCESSION BF251967  
 VERSION BF251967.1 GI:16932110  
 KEYWORDS EST.  
 SOURCE Coccidioides immitis.  
 ORGANISM Coccidioides immitis  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; mitosporic Onygenales; Coccidioides.

REFERENCE  
 AUTHORS Gardner M.J. and Kirkland T.  
 TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Malcolm J. Gardner  
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 Fax: 301 838 0208  
 Email: gardneretlgr.org.

FEATURES  
 source  
 1..378  
 location/Qualifiers  
 /organism="Coccidioides immitis"  
 /db\_xref="taxon:5501"  
 /clone\_lib="Coccidioides immitis spherule cDNA library"  
 /dev\_stage="spherule"  
 /lab\_host="SOLR"  
 /note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT 104 a 75 c 94 g 105 t  
 ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 378;  
 Best Local Similarity 68.2%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAAGCGAGCCUUCAGCAUG 23  
 DB 169 CGAAGTCGAGGTTTTCAGCATG 148

RESULT 6  
 LOCUS BF251561/c 391 bp mRNA linear EST 15-NOV-2001  
 DEFINITION EST418910 Coccidioides immitis spherule cDNA library Coccidioides immitis cDNA clone CIAK57 5' sequence, mRNA sequence.

ACCESSION BF251561  
 VERSION BF251561.1 GI:16931792  
 KEYWORDS EST.  
 SOURCE Coccidioides immitis.  
 ORGANISM Coccidioides immitis  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; mitosporic Onygenales; Coccidioides.

REFERENCE  
 AUTHORS Gardner M.J. and Kirkland T.  
 TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Malcolm J. Gardner  
 Department of Eukaryotic Genomics  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301 838 3519  
 Fax: 301 838 0208  
 Email: gardneretlgr.org.

FEATURES  
 source  
 location/Qualifiers  
 1..391  
 /organism="Coccidioides immitis"  
 /db\_xref="taxon:5501"  
 /clone\_lib="Coccidioides immitis spherule cDNA library"  
 /dev\_stage="spherule"  
 /lab\_host="SOLR"  
 /note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT 107 a 76 c 96 g 112 t  
 ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 391;  
 Best Local Similarity 68.2%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAAGCGAGCCUUCAGCAUG 23  
 DB 176 CGAAGTCGAGGTTTTCAGCATG 155

RESULT 7  
 LOCUS AW792005/c 486 bp mRNA linear EST 01-MAY-2001  
 DEFINITION D00948-R lambda zap, StrataGene Blumeria graminis f. sp. hordei cDNA clone D00948 similar to non-functional folate binding protein, mRNA sequence.

ACCESSION AW792005  
 VERSION AW792005.1 GI:13903602  
 KEYWORDS EST.  
 SOURCE Blumeria graminis f. sp. hordei.  
 ORGANISM Blumeria graminis f. sp. hordei  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes; Erysiphales; Erysiphaceae; Blumeria.

REFERENCE  
 AUTHORS Thomas S.W., Rasmussen S.W., Glaring M.A., Rousster J.A. and Oliver R.P.  
 TITLE Gene identification in the fungal pathogen Blumeria graminis by expressed sequence tag analysis  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Rasmussen S.W.  
 Department of Yeast Genetics  
 Carlsberg Laboratory  
 10 GI. Carlsbergvej, DK-2500, Copenhagen, Denmark  
 Tel: 45 3327 5230  
 Fax: 45 3327 4766  
 Email: svre@carl.dk  
 High quality sequence stop: 486  
 POLYA-NO.

FEATURES  
 source  
 location/Qualifiers  
 1..486  
 /organism="Blumeria graminis f. sp. hordei"  
 /db\_xref="taxon:6268"  
 /clone\_lib="D00948"  
 /clone\_lib="lambda zap, StrataGene"  
 /cell\_type="conidia"  
 /lab\_host="Hordeum vulgare"

BASE COUNT 138 a 101 c 115 g 132 t  
 ORIGIN

Query Match 81.7%; Score 18.8; DB 10; Length 486;  
 Best Local Similarity 68.2%; Pred. No. 1.3e+02;  
 Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAAGCGAGCCUUCAGCAUG 23  
 DB 176 CGAAGTCGAGGTTTTCAGCATG 155

RESULT 8  
 LOCUS BF251704/c 488 bp mRNA linear EST 15-NOV-2001

DEFINITION EST418888 Coccidioides immitis spherule cDNA library Coccidioides immitis cDNA clone CIAK33 5' sequence, mRNA sequence.

ACCESSION BF251704

VERSION BF251704.1 GI:16931770

KEYWORDS EST.

SOURCE Coccidioides immitis.

ORGANISM Coccidioides immitis

REFERENCE Gardner, M.J. and Kirkland, T. 1 (bases 1 to 488) Orygenales; mitosporic Orygenales; Coccidioides.

AUTHORS Gardner, M.J. and Kirkland, T.

TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library

JOURNAL Unpublished (2000)

COMMENT Contact: Malcolm J. Gardner  
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Location/Qualifiers

1. .488

/organism="Coccidioides immitis"

/db\_xref="taxon:5501"

/clone="CIAK33"

/clone\_lib="Coccidioides immitis spherule cDNA library"

/dev\_stage="spherule"

/lab\_host="SOLR"

/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT 129 a 97 c 126 g 136 t

ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 488;  
Best Local Similarity 68.2%; Pred. No. 1.3e+02;  
Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAAGUCGAGCGUUCAGCAGG 23  
|||||:|||||:|||||:|

Db 176 CGAAGTCGAGGTTTACGATG 155

RESULT 9  
BF252581/c 502 bp mRNA linear EST 15-NOV-2001

LOCUS EST418843 Coccidioides immitis spherule cDNA library Coccidioides immitis cDNA clone CIAK35 5' sequence, mRNA sequence.

ACCESSION BF252581

VERSION BF252581.1 GI:16932724

KEYWORDS EST.

SOURCE Coccidioides immitis.

ORGANISM Coccidioides immitis

REFERENCE Gardner, M.J. and Kirkland, T. 1 (bases 1 to 502) Orygenales; mitosporic Orygenales; Coccidioides.

AUTHORS Gardner, M.J. and Kirkland, T.

TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library

JOURNAL Unpublished (2000)

COMMENT Contact: Malcolm J. Gardner  
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Location/Qualifiers

1. .502

/organism="Coccidioides immitis"

/db\_xref="taxon:5501"

/clone="CIAK35"

/clone\_lib="Coccidioides immitis spherule cDNA library"

/dev\_stage="spherule"

/lab\_host="SOLR"

/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT 142 a 101 c 126 g 133 t

ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 502;  
Best Local Similarity 68.2%; Pred. No. 1.3e+02;  
Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAAGUCGAGCGUUCAGCAGG 23  
|||||:|||||:|||||:|

Db 179 CGAAGTCGAGGTTTACGATG 158

RESULT 10  
AM792430/c 515 bp mRNA linear EST 01-MAY-2001

LOCUS D01189-R Lambda Zap, Stratagene Blumeria graminis f. sp. hordei cDNA clone D01189 similar to non-functional folate binding protein, mRNA sequence.

ACCESSION AM792430

VERSION AM792430.1 GI:13904027

KEYWORDS EST.

SOURCE Blumeria graminis f. sp. hordei.

ORGANISM Blumeria graminis f. sp. hordei

REFERENCE Eukaryotes; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes; Erysiphales; Erysiphaceae; Blumeria. 1 (bases 1 to 515) Thomas, S.W., Rasmussen, S.W., Glaring, M.A., Rousster, J.A. and Oliver, R.P.

AUTHORS Thomas, S.W., Rasmussen, S.W., Glaring, M.A., Rousster, J.A. and Oliver, R.P.

TITLE Gene identification in the fungal pathogen Blumeria graminis by expressed sequence tag analysis

JOURNAL Unpublished (2000)

COMMENT Contact: Rasmussen, S.W.  
Department of Yeast Genetics  
Carlsberg Laboratory  
10 GL. Carlsbergvej, DK-2500, Copenhagen, Denmark  
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Fax: 45 3327 4766  
Email: svr@erc.dk

Location/Qualifiers

1. .515

/organism="Blumeria graminis f. sp. hordei"

/db\_xref="taxon:62688"

/clone="D01189"

/clone\_lib="Lambda Zap, Stratagene"

/cell\_type="conidia"

/lab\_host="Hordeum vulgare"

BASE COUNT 150 a 104 c 119 g 142 t

ORIGIN

Query Match 81.7%; Score 18.8; DB 10; Length 515;  
Best Local Similarity 68.2%; Pred. No. 1.3e+02;  
Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAAGUCGAGCGUUCAGCAGG 23  
|||||:|||||:|||||:|

Db 169 CGAAGTCGAGGCTTTACGATG 148

RESULT 11  
BF251715/c 518 bp mRNA linear EST 15-NOV-2001

LOCUS EST418899 Coccidioides immitis spherule cDNA library Coccidioides immitis cDNA clone CIAK45 5' sequence, mRNA sequence.

ACCESSION BF251715

VERSION BF251715.1 GI:16931781

KEYWORDS EST.

SOURCE Coccidioides immitis.

ORGANISM Coccidioides immitis

REFERENCE Gardner, M.J. and Kirkland, T. 1 (bases 1 to 518) Orygenales; mitosporic Orygenales; Coccidioides.

AUTHORS Gardner, M.J. and Kirkland, T.

TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library

JOURNAL Unpublished (2000)

COMMENT Contact: Malcolm J. Gardner  
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Location/Qualifiers

1. .518

/organism="Coccidioides immitis"

/db\_xref="taxon:5501"

/clone="CIAK45"

/clone\_lib="Coccidioides immitis spherule cDNA library"

/dev\_stage="spherule"

/lab\_host="SOLR"

Onygenales; mitosporic Onygenales; Coccidioides.  
REFERENCE 1 (bases 1 to 518)  
AUTHORS Gardner, M.J. and Kirkland, T.  
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library  
JOURNAL Unpublished (2000)  
COMMENT Contact: Malcolm J. Gardner  
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Email: gardner@tigr.org.

FEATURES  
source  
1. 518  
/organism="Coccidioides immitis"  
/db\_xref="taxon:5501"  
/clone="C1A4V45"  
/clone\_1lb="Coccidioides immitis spherule cDNA library"  
/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT 141 a 104 c 133 g 140 t  
ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 518;  
Best Local Similarity 68.2%; Pred. No. 1.3e+02;  
Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAAGUCGAGCCUUCAGCAUG 23  
|||||:|||||:::|||||:  
Db 176 CGAAGTCGAGGTTTATGCAATG 155

RESULT 12  
BF252371/c 541 bp mRNA linear EST 15-NOV-2001  
LOCUS EST419363 Coccidioides immitis spherule cDNA library Coccidioides  
DEFINITION Immitis cDNA clone C1A4V41 5' sequence, mRNA sequence.  
ACCESSION BF252371  
VERSION BF252371.1 GI:16932514  
KEYWORDS EST.  
SOURCE Coccidioides immitis.  
ORGANISM Coccidioides immitis.  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; mitosporic Onygenales; Coccidioides.  
REFERENCE 1 (bases 1 to 541)  
AUTHORS Gardner, M.J. and Kirkland, T.  
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library  
JOURNAL Unpublished (2000)  
COMMENT Contact: Malcolm J. Gardner  
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Fax: 301 838 0208  
Email: gardner@tigr.org.

FEATURES  
source  
1. 541  
/organism="Coccidioides immitis"  
/db\_xref="taxon:5501"  
/clone="C1A4V41"  
/clone\_1lb="Coccidioides immitis spherule cDNA library"  
/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT 157 a 109 c 133 g 142 t  
ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 541;  
Best Local Similarity 68.2%; Pred. No. 1.4e+02;  
Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAAGUCGAGCCUUCAGCAUG 23  
|||||:|||||:::|||||:  
Db 175 CGAAGTCGAGGTTTATGCAATG 154

RESULT 13  
BF253171/c 546 bp mRNA linear EST 15-NOV-2001  
LOCUS EST445666 Coccidioides immitis spherule cDNA library Coccidioides  
DEFINITION Immitis cDNA clone C1GAB68 5' sequence, mRNA sequence.  
ACCESSION BF253171  
VERSION BF253171.1 GI:16933314  
KEYWORDS EST.  
SOURCE Coccidioides immitis.  
ORGANISM Coccidioides immitis.  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; mitosporic Onygenales; Coccidioides.  
REFERENCE 1 (bases 1 to 546)  
AUTHORS Gardner, M.J. and Kirkland, T.  
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library  
JOURNAL Unpublished (2000)  
COMMENT Other-ESTs: EST445665  
Contact: Malcolm J. Gardner  
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Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org.

FEATURES  
source  
1. 546  
/organism="Coccidioides immitis"  
/db\_xref="taxon:5501"  
/clone="C1GAB68"  
/clone\_1lb="Coccidioides immitis spherule cDNA library"  
/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT 157 a 109 c 135 g 145 t  
ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 546;  
Best Local Similarity 68.2%; Pred. No. 1.4e+02;  
Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAAGUCGAGCCUUCAGCAUG 23  
|||||:|||||:::|||||:  
Db 179 CGAAGTCGAGGTTTATGCAATG 158

RESULT 14  
BF252094/c 567 bp mRNA linear EST 15-NOV-2001  
LOCUS EST419356 Coccidioides immitis spherule cDNA library Coccidioides  
DEFINITION Immitis cDNA clone C1A4Q80 5' sequence, mRNA sequence.  
ACCESSION BF252094  
VERSION BF252094.1 GI:16932237  
KEYWORDS EST.  
SOURCE Coccidioides immitis.  
ORGANISM Coccidioides immitis.  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; mitosporic Onygenales; Coccidioides.  
REFERENCE 1 (bases 1 to 567)  
AUTHORS Gardner, M.J. and Kirkland, T.  
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library  
JOURNAL Unpublished (2000)  
COMMENT Contact: Malcolm J. Gardner  
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The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519

Fax: 301 838 0208  
Email: gardner@tigr.org.  
Location/Qualifiers

FEATURES  
SOURCE  
1. 567  
/organism="Coccidioides immitis"  
/db\_xref="taxon:5501"

/clone="C1A080"  
/clone\_1lb="Coccidioides immitis spherule cDNA library"  
/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI"

BASE COUNT 161 a 118 c 142 g 146 t  
ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 567;  
Best Local Similarity 68.2%; Pred. NO. 1.4e+02;  
Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 2 CGAAGUCGAGCGUUCAGCAG 23  
||||:||||:||||:|  
Db 182 CGAAGTCGAGCTTTTACATG 161

RESULT 15  
BF252878 568 bp mRNA linear EST 15-NOV-2001  
LOCUS BF252878/c  
DEFINITION EST420141 Coccidioides immitis spherule cDNA library Coccidioides  
immitis cDNA clone C1AB92 5' sequence, mRNA sequence.

ACCESSION BF252878  
VERSION BF252878.1 GI:16933021  
KEYWORDS EST.

SOURCE  
ORGANISM Coccidioides immitis.  
Coccidioides immitis.  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Onygenales; Microsporid Onygenales; Coccidioides.

REFERENCE  
AUTHORS Gardner, M.J. and Kirkland, T.  
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library  
JOURNAL Unpublished (2000)  
COMMENT Contact: Malcolm J. Gardner  
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9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301 838 3519  
Fax: 301 838 0208  
Email: gardner@tigr.org

FEATURES  
SOURCE  
Location/Qualifiers  
1. 568  
/organism="Coccidioides immitis"  
/db\_xref="taxon:5501"

/clone="C1AB92"  
/clone\_1lb="Coccidioides immitis spherule cDNA library"  
/dev\_stage="spherule"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI"

BASE COUNT 162 a 117 c 143 g 146 t  
ORIGIN

Query Match 81.7%; Score 18.8; DB 12; Length 568;  
Best Local Similarity 68.2%; Pred. NO. 1.4e+02;  
Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 2 CGAAGUCGAGCGUUCAGCAG 23  
||||:||||:||||:|  
Db 182 CGAAGTCGAGCTTTTACATG 161

Search completed: June 12, 2003, 04:35:08  
Job time : 844.943 secs